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Stealing into the wild: conservation science, plant breeding and the makings of new seed enclosures

Maywa Montenegro de Wit

Faced with pressing climatic changes, scientific and industrial interests are vying to develop crops that can survive drought, floods and shifting pest regimes. Increasingly, they look for solutions in an unlikely place: the gene pools of wild plants. Crop wild relatives (CWR) – species closely related to crops, including their ancestors – offer breeders the allure of retracing the domestication bottleneck, infusing genomes of modern crops with ‘lost’ genetic variety. Yet wild relatives also confront threats from climate change, urbanization and expansion of industrial agri-food. Thus, CWR, seen as both salvational and threatened, have become an international conservation and food-security priority. It is my contention that, in their common project to harness wild-relative potential, conservation and breeding science are co-evolving to extend seed commodity relations into new spheres. I examine enclosures along two fronts: first within ‘systematic CWR conservation’, where ‘in situ’ approaches, typically regarded as empowering and sustainable alternatives to ‘ex situ’, instead may support a complementary system of value extraction; second, in breeding and biotechnology research, which produces new value for CWR while profoundly shaping upstream conservation priorities. An important finding is that although today’s ‘ex situ-centric’ complementarity favors dispossession, an ‘in situ-centric’ approach could foster democratic renewal of biocultural diversity.

Keywords: crop wild relatives; primitive accumulation; climate change; biotechnology; conservation science; ex situ/in situ; intellectual property

Introduction

If you have not yet heard that wild weeds can feed the world, you soon will. With climate change already affecting crop systems worldwide, scientists increasingly say we have no choice but to adapt agriculture to drought, floods and shifting pest regimes. While some research communities focus on agronomic practices – changes to cropping, soil, water and biodiversity strategies – another large subset of research is trained on crops themselves, improving seeds at the core of production. Much of their emphasis is on genetics. To quote an influential Nature article, ‘We will have to give crops a genetic helping hand, infusing them with new genes to allow them to better cope with new climates, and the new pests and diseases they will bring’ (Guarino and Lobell 2011).

Such statements call to mind industry’s invocations for genetically modified seed. Yet it is not the promise of GMOs being spoken of here. Today, another possibility is inciting the attention of governments, companies, scientists and conservation professionals who work in the field of plant genetic resource for food and agriculture, or PGRFA. Crop wild relatives (CWR), defined as ‘species closely related to domesticated crops, including their wild
progenitors’,1 offer the potential to infuse crops with traits necessary to cope with climate change. By dint of being wild, these species have evolved adaptations to extreme conditions – precisely the rugged adaptions agriculture now needs. Many of these hardy traits were winnowed out of the domesticated gene pool when ancestral farmers instigated seed sowing more than 10,000 years ago. Researchers suggest that reintroducing CWR traits offers a chance to retrace this genetic bottleneck, accessing an abundance of genetic variety that was inadvertently ‘lost’. The incentives for retracing and rewilding are clear. The paradox? Like many wild plants, CWR are themselves threatened by climate change, development and other anthropogenic forces, agriculture included.

Because CWRs are increasingly seen as both important and threatened, their conservation has become an international priority, with two apparently rivaling conservation paradigms in play. Ex situ strategies focus on collecting seeds for storage in gene banks, identifying critical sites and species for wild relative collection. They address what is seen as a gene-bank ‘gap’: a deficiency of CWRs in global PGRFA repositories. By contrast, in situ programs stress the ‘dynamic evolution of diversity’ found only in natural settings. Centered on conserving crop relatives in situ – that is, ‘in the ecosystems and native habitats where they have acquired their distinctive characteristics’ (CBD 1992) – they underscore ecology as the essential means of maintaining and renewing diversity in populations of wild relatives. In the past five years, major CWR initiatives have been launched on both ex situ and in situ fronts, in response to a widely perceived failure of CWR conservation efforts to date: a lack of ‘systematic’ planning and implementation (Heywood et al. 2007; Maxted and Kell 2009; Hunter et al. 2012; Vincent et al. 2013; Dempeewolf et al. 2014; Kell et al. 2015). With efforts underway to lay the scientific basis for such a systematic practice, conservation science is producing new knowledge about wild relatives: where they exist, how their diversity is spatially distributed, whether their genotypes have adapted to particularly climate-hardy local ecologies and landscapes. In parallel, breeding science, propelled by advances in molecular breeding and biotechnology, is now bringing previously ‘unwieldy’ wild relatives into reach for crop improvement. In the genes of these ‘exotics’, many breeders believe, lie latent capacities to develop crops with greater yield, greater resistance to drought, pests and disease, even higher quality foods.

It is my contention that, in their common project to harness the potential of wild relatives, conservation science and plant breeding science are now co-evolving to enable a new frontier of primitive accumulation to materialize. The collection and conservation of CWR – in banks and on land – provide the foundation from which valuable traits can be extracted and bred or engineered into new climate-hardy varieties. The scientific strategies are internally related and co-productive. Crop development relies fundamentally on the conservation of wild relatives – in and ex situ – for access to germplasm and related genetic information. There is no breeding or biotechnology without genetic diversity – and hence without sustained conservation. But conservation science – its priorities, its objectives and even its basis of legitimacy – hinges, then, on ‘use’ and its valorization. The marketable form comes to exert a backwards pressure on conservation: delimiting what is important to

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1 Progenitors’ indicates the ‘parents’ of current cultivated crops – that is, the wild species that were domesticated by ancient farmers. The term CWR includes the progenitors as well as other more or less closely related species. An example is domesticated sweet potato (Ipomoea batatas (L.) Lam.) which is thought to have originated from cross-species hybridization involving I. trifida, I. littoralis and/or I. leucantha. These progenitors are among the 14 species scientists count as the close relatives of cultivated sweet potato (Khoury et al. 2015).
salvage and why. As a result, multiple enclosures could develop: around germplasm, around wild landscapes, around agroecosystems and traditional knowledge.

In order to better understand how these interrelated enclosures cohere, it helps to begin upstream, with the production of scientific knowledge itself. How are conservation plans being designed? What values are embedded in the measures and priorities that guide CWR planning? Who is participating in breeding new crops from ancestral DNA?

Looking at the discourses and practices of CWR science, I have found that ex situ and in situ are commonly framed as antagonistic strategies. Ex situ is the colonial paradigm of exploitative collection and off-site storage. In situ is the anti-colonial response: a liberatory strategy of place-based renewal. In CWRs, we find a decidedly different ontology taking shape, in which land-based and bank-based strategies not are only nonrival, but are complementary. The character of complementarity may, however, be highly uneven – or ‘ex situ-centric’ (cf. Graddy-Lovelace 2015). By favoring a flow of material, epistemic and economic value away from local sites and peoples, I will argue, complementarity is helping forge a frontier of primitive accumulation for wild relative social and ecological value. But complementarity need not take this tenor, and the sciences of conservation and breeding could support paradigms for CWR characterized by in situ-centricity: in which the flow of genetic resources and rights gravitates towards the landscapes and agrarian societies with whom wild relative diversity has co-evolved.

This paper begins with a brief review of primitive accumulation, before turning to narratives of climate change, food security and biodiversity preservation – the entwined justifications for saving and using CWR. Systematic conservation is then explored, with a look at the scientific practices of counting, prioritizing and establishing plans for collections and protected areas. Next, I consider advances in breeding science, which are not only producing new value for wild relatives – especially in the form of climate-hardy crops – but are also profoundly shaping conservation priorities. I then examine the potential for primitive accumulation to emerge vis-à-vis these scientific developments, in terms of uneven geographical distribution of CWR, market potential, international genetic governance and data-fication.

**Primitive accumulation: seed enclosures from domesticated to wild**

In his groundbreaking work, *First the seed* (1988), Kloppenburg recounts a history of plant biotechnology through the lens of primitive accumulation. Scientific technology and changing legal standards helped guide germplasm into property form, reshaping long-standing relations between farmers and their seed. But conformity to capital was not easily achieved – or easily kept. It required nothing less than new configurations of nature, state and market, which Kloppenburg considers along three main strands: (1) the privatization and commodification of plant genetic resources; (2) a division of labor between public and private research; and (3) the highly uneven, and unjust, international flow of plant genetic resources between countries.

Like Berlan and Lewontin’s earlier work (1986), Kloppenburg’s interrogation of the seed stems from its dual nature: as a living, reproducing organism, the seed links both ends of the production process. It is at once the means of production and the result of production, a potential exchange-value if sold, or a use-value if replanted. This regenerative capacity of germplasm, at once cultural and biological, has been antagonistic to enclosure for most of human history – exemplifying the variety of natural and social obstacles to the penetration of agriculture by capital (Mann and Dickinson 1978; Friedmann 1980). As a result, until the 1930s, farmers in both the global North and South enjoyed nearly complete...
sovereignty over their seeds (Aoki 2008; Kloppenburg 2010). They decided what to plant, which varieties to crop under what conditions, and whether to eat or replant the fruits of their harvests. Surely such decisions were not altogether egalitarian – patriarchy and other status divisions have long configured uneven access in traditional and indigenous communities. But, as Zimmerer (1996) argues, most agrarian cultures operating on bases of gift and reciprocity worked to facilitate, rather than restrict, wide dissemination of seed.

However, in just the past 85 years, the combined forces of crop biotechnology and intellectual property rights (IPR) have moved swiftly to enclose common genetic heritage as private property, turning public goods into private benefits. Biological and legal strategies have been complementary here. The development of hybrid seeds, beginning in the 1930s, separated farmers from effective biological reproduction of their own germplasm. Since hybridized seeds do not ‘breed true’ from one generation to the next, the incentive to replant seeds was replaced by the requirement to purchase anew. In the same decade, Congress passed the Plant Patent Act, the first legal enclosure in a line of progressively restrictive IPR legislation. The 1961 establishment of the Union for the Protection of New Varieties of Plants (UPOV) in Europe, followed by the 1970 Plant Variety Protection (PVP) Act in the United States, instituted exclusive breeders’ rights but with important exemptions for scientists and farmers. Since the 1980s, the strictest form of IPR – the utility patent – has been applied in both the US and Europe, while revisions to UPOV (1991) have come to mimic patents: both systems now preclude farmers’ ability to save and reproduce protected seeds, even criminalizing the practice. These IPR enclosures also work in concert with marketing rules, biosafety policies, and international trade regimes and investment agreements (e.g. World Trade Organization (WTO), TTP and TTIP), rapidly extending corporate reach in both developed and developing country contexts (GRAIN and LVC 2015). Control of the biological seed, some argue, has become a linchpin in control of the entire agricultural system. The ‘provider of this input’, notes Lewontin, is in ‘a unique position to valorize other inputs’ (Lewontin 2000, 98).

It might at first seem odd to cast such changes to seed systems as primitive accumulation, defined by Marx as ‘nothing less than the historical process of divorcing the producer from the means of production’ (Marx 1977, 875). Marx illustrates this process as immediate and complete, with the effect of instantaneously establishing both a labor pool and market in one transformation. The case of seeds is different: farmers are neither manifestly separated from their land, nor ‘freed’ to sell anything but their own labor. Yet even farmers who retain nominal control of their resources can be brought ‘gradually but effectively into capitalist commodity production’ (Kloppenburg 2004, 25). Indeed, primitive accumulation can be identified in myriad creeping disposessions: where appropriations and accumulations are separated in time and space (Kelly 2011), and in which the everyday articulations between dominant (capitalist) and non-dominant modes of production continuously extend the commodity relation into new spheres. In this sense, the majority of US family farms and increasingly many smallholdings worldwide are already deeply enclosed. Farmers may retain nominal control of land, yet are often trapped in monopolistic factor markets, chronic indebtedness and contract systems that reduce them from autonomous

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2In the software industry, distributors commonly require purchasers to agree to express licensing restrictions printed on software packaging (often called ‘shrink wrap’ licenses). Seed corporations have mimicked this practice with ‘bag tags’ on packages of seed that serve as license agreements for patented products. Farmers need not actually sign a contract, but by tearing open the tag, they effectively agree to terms of limited licensed use. A typical Monsanto bag tag forbids replanting of seed, resale of seed or supply of saved seed to anyone (Janis and Kesan 2002).
farmers to ‘disguised wage workers’ or ‘propertied labor’ (Kautsky 1899; Davis 1980; Mooney 1983; Goodman, Sorj, and Wilkinson 1987).

Science and technology have been instrumental to commodifying seed resources, not only through direct means like hybrid seed, but insofar as they have eliminated barriers to capital in agriculture more generally. In the US, wartime science led the way, first with WWI increases in manufacturing heavy equipment, and second with WWII advances in nitrogen fixation for bomb production. At land grant universities and extension stations, breeding science responded by designing machine-compatible crops, adapting hybrid lines to heavy fertilizer inputs, and – when it became apparent that genetic uniformity and dense cropping engendered great susceptibility to pests and disease – creating seed varieties compatible with high quantities of insecticides, fungicides and herbicides. Green Revolution interventions subsequently ‘diffused’ these technological innovations to the global south, dramatically extending the accumulative scope of transnational chemical, fertilizer, feed and seed industries. Since the 1990s, the science of genetic modification, entwined with patent protections, has continued in much the same vein, contributing to a rise of ‘gene giants’ now emblematic of the concentration of power in modern agri-food supply chains (Howard 2009). The past 150 years have demonstrated amply that agricultural research can itself be understood ‘as the incorporation of science into the historical processes of primitive accumulation and commodification’ (Kloppenburg 2004, 10).

Scholarship to date has drawn critical attention to the myriad ways that dispossession of crop genetic resources is imposed – and how peasants, actors, local people resist (and persist) in ways that are forceful, intentional, organized and quotidian. Domesticated seeds, however, have commanded most of this attention. Despite the fact that Darwin himself noted their under-recognized status,3 wild relatives have remained neglected, many researchers argue, compared with food crops (Davies 1991; Maxted and Kell 2009; Ramírez-Villegas et al. 2010; Hunter et al. 2012; McCouch et al. 2013; Bioversity 2015a). Enclosures of CWRs reach back at least to the mid nineteenth century, when naturalists and gentleman plant hunters collected plant specimens for storage in seed banks and botanical gardens. Russian agronomist Nikolai Vavilov first recognized the breeding value of wild species, and he crisscrossed the globe – more than 115 expeditions in his lifetime – gathering wild relatives in hopes of ‘improving’ disease-prone Russian cultivars (Nabhan 2009). Insofar as primitive accumulation consists of appropriation and accumulation, however, conservation of plants and seeds awaited the breeding science that could valorize these genes. Not until the 1930s were breeders regularly accomplishing the ‘wide’ interspecies crosses capable of mobilizing wild traits into domesticated varieties that could be bought or sold. There is little food market value, after all, in a wild seed that, by definition, people do not cultivate and usually cannot eat. But slowly, imperceptibly by most accounts, wild relatives crossed the boundary into agriculture, achieving a nascent foothold in the commodity form.

Today, a nexus of forces has converged to change the disregard Darwin spoke of. Discourses of climate change, food insecurity and the ongoing challenge of ‘sustainable development’ are helping drive interest in conserving and utilizing CWR genes, just as advances in biotechnology and information systems are expanding scientific capacity to do so. Re-commodification of current crops, infused with climate-hardy traits, is therefore one dimension of the enclosure frontier. But the potential sweep is much larger and

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3 Darwin (1868) observed: ‘it appears strange to me that so many of our cultivated plants should still be unknown or only doubtfully known in the wild state’.
variegated. In situ conservation calls for genetic reserves, opening up the issue of land enclosure. Traditional and local knowledge is bound up in the biology of wild relatives, whether or not intentional management occurs. The potential for industry to propertize this knowledge through IPR is thus a salient epistemic enclosure. In turn, human and ecological knowledge is increasingly being collected, centralized and parsed in a data-fied idiom by conservation and breeding scientists in the vanguard of their research fields. These innovations entail risks of enclosures with restricted access to such data.

CWRs offer an entrée into this complex terrain: some appropriations are occurring ‘upstream’ as part of science and technology (S&T) developments. Others are occurring ‘downstream’ in the field of implementation and use, where breeding with CWR will occur, and where seeds will be banked and land-based genetic reserves will be established. Here, science will have ‘policy-relevant’ say in locating, managing and regulating access to ex situ and in situ sites and their resources. Prior research has suggested how science practices and discourses can facilitate primitive accumulation. In the context of green-grabbing, Fairhead, Leach, and Scoones (2012, 239) consider the rapid assemblage of players – scientists, park managers, state and conservation organizations, the tourist industry – that are ‘more deeply embedded in capitalist networks, and operating across scales, with profound implications for resource control and access’. Extending this approach, I look more closely at the production of S&T knowledge in the conservation and use of wild relatives. I focus on two ‘upstream’ sites of scientific discourses and practices: (1) systematic CWR conservation planning: the conservation science that, in a complementary system, precedes downstream ex situ or in situ implementation (i.e. the design and thinking upstream from gene banking and managing land reserves4); (2) breeding and biotechnology, where traits from wild relatives are identified and used to develop a new array of crops to join the agri-food system.

To investigate how science and technology research is enabling enclosures now and in future, I conducted largely documentary analysis of the technical and policy literature on CWR. Using electronic database searches, I surveyed the scientific literature on conservation science, breeding science and biotechnology relating to CWR for the last 30 years. In particular, I identified a number of significant review articles and edited books that define the state of the field. There is a fairly small community of conservation scientists focused on CWR, so their work over time can be traced. I studied the policy documents (e.g. reports and statements) news briefings and webpages that international institutions and NGOs – such as FAO, Bioversity, the Global Crop Diversity Trust, and CGIAR – have issued on conservation and use of crop relatives over that time. I also reviewed journalism and media coverage of emerging biotechnologies, as well as the popular writings of leading scientists working with wild relatives. (It is increasingly common for agrobiodiversity scientists, particularly at the international level, to express their opinions through blogs, social media and other informal communications). I coded the discourses visible in this technical and popular literature, and analyzed the kinds of practices being developed in conservation planning and plant breeding. To understand the history and politics of germplasm flows, I looked at international plant genetics resource treaties and their histories and secondary analysis. Finally, I sampled extant business and biotechnology industry news to determine whether companies are beginning to exploit CWR resources.

4I did not cover land in this paper, specifically the many issues of land access, use and rights that in-situ conservation raises. This terrain is premature for CWR specifically, though the land-grabbing literature suggests that such appropriations for wild relatives are likely to occur.
The intention of my study, then, was to go beyond a simple political economy of dispossession/enclosure to scrutinize how such moves are discursively constructed and generated in practice through processes of elite science and policy. Wild relatives offer something rare: a concrete opportunity to take the ‘primitive accumulation’ concept and ask how it pertains not only to genetic resources, but to enclosures that assemble around it – to information, land, knowledge and the possibilities of agrobiodiversity renewal.

My look at the upstream scientific discourses and practices is a conceptual contribution, rubbing together the two bricks of agrarian political economy and STS/political ecology. I hope the friction sparks a means to better understand enclosures effectively, in seeds and beyond.

Wild relatives gather recognition

The Asilomar Conference Center in Pacific Grove, California, has an illustrious history. In 1975, more than 140 biologists, lawyers and physicians gathered there to discuss the potential biohazards of genetic recombination, and how to regulate the rapidly advancing sphere of biotechnology. Less than 40 years on, in 2013, Asilomar hosted a meeting of the world’s top plant genomicists. Representing land grant universities, plant science institutes and the seed industry, the attendees convened to discuss the value and potential of breeding with CWRs. The broad consensus amongst participants was reflected in an essay published months later in the journal *Nature*. In it, lead author Susan McCouch expressed both concern and optimism. The bad news: modern agriculture has shed much of the genetic diversity found not only in farmer-bred landraces but also in the ancestral progenitors of cultivated crops. The good news: much germplasm is stored in gene banks around the world – some 1750 by last count. More bad news: this vast stock was merely sitting there, untapped, because the global community had not invested the time, resources or technical acumen necessary to make use of it. ‘How’, McCouch and her co-authors asked, ‘should we begin to mine biodiversity for food security?’ (McCouch et al. 2013, 24).

Such scientific enthusiasm for wild relatives is nothing new. Indeed, both De Candolle (1855) and Darwin (1868) discussed the origin of cultivated plants and recommended the study of related CWR species. In the 1920s, Russian agronomist Vavilov championed their collection and conservation; species of wild *Aegilops*, *Secale*, *Haynaldia* and *Agropyron*, he believed, were promising plants for improving Russian wheat. By the 1940s and 1950s, breeding with CWR had become a routine affair, and successes with introducing wild traits accelerated through the 1960s and 1970s (Meilleur and Hodgkin 2004). A 1988 booklet published by the International Board for Plant Genetic Resources to increase public awareness of CWR describes their little-known contribution to a very familiar fruit: ‘The tomato could simply not exist without the genes from its wild relatives, which have helped it resist a long line of viruses, moulds, wilt, nematodes, and other pests’ (Hoyt 1988, 15). In Asia, the pamphlet suggests, combating rice disease has been one of wild

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5It is sometimes thought that ‘ancestral’ means the wild species has gone extinct, or transformed entirely into the cultivated form. But domestication generally involved only a subset (a population) of any given species. Thus, many wild ancestral lines continue living and evolving alongside their crop kin today. Wild emmer, for example, still grows in the wild in the fertile crescent of the Near East.

6Established by CGIAR in 1974, the International Board for Plant Genetic Resources became the International Plant Genetic Resources Institute (IPGRI) in 1991. IPGRI joined with a network for banana improvement and, in 2006, the two organizations formed Bioversity International.
relatives’ greatest successes. When brown planthopper threatened to devastate rice fields in the 1970s, genes from three wild *O. nivara* plants found in a water-logged field in Uttar Pradesh were bred into IR36 – and are still found in every high-yielding cultivar of rice grown in tropical Asia.

More recent surveys of crop improvement programs (Hajjar and Hodgkin 2007; Maxted and Kell 2009) indicate that wild relatives have been tapped for a wide array of attributes: to confer resistance to pests and diseases, to tolerate extreme temperatures, to withstand drought and flooding, and to enhance nutrition, color, texture, flavor and handling qualities. They have made their way into numerous crops from banana to tomato and from lettuce to chickpea. ‘Nearly all modern crops contain some genes derived from CWR’, write Maxted and Kell (2009). Over the years, efforts have been made to tally the commercial value of this bounty. Prescott-Allen and Prescott-Allen (1986) calculated that yield and quality contributions to US-grown or -imported crops were over USD 350 million per year. Most famously, a Cornell research team estimated that CWR genetic resources contribute approximately USD 20 billion to increased crop yields in the US, and roughly USD 115–120 billion worldwide every year (Pimentel et al. 1997; Bioversity 2015b).

Few people outside of traditional/indigenous farmers know what CWRs are, let alone that they are ubiquitous in the modern food supply. Within PGRFA circles, however, it is evident that CWRs have long been recognized as vital for food security and economic stability (Prescott-Allen and Prescott-Allen 1986; Hajjar and Hodgkin 2007; Kell et al. 2015). If the Asilomar conference is any indication, they remain scientifically beguiling, and a potentially lucrative resource.

For the genetic potential of wild relatives to be realized, however, CWR must not be vanishing under pavement, industrial plows and pressures of climate change. For breeding and biotech to have any purchase on the ‘use’ end of a germplasm pipeline, conservation upstream becomes vital (Vincent et al. 2013). Hence, the imperative of wild relative conservation has emerged prominently in the discourse of mainstream PGRFA institutions, including the CGIAR, FAO, the Millennium Seed Bank and the Global Crop Diversity Trust. Although these institutions have been involved in germplasm collection for many years, they now speak of ‘systematic’ efforts at local, national and global scales, both in- and ex situ.

The Global Crop Diversity Trust, spearheading ex situ efforts described further below, speaks of ‘the most systematic and comprehensive ever bid to conserve the world’s crop wild relatives on a global scale’. Bioversity International, a central hub for organizing in situ strategies, maintains a research platform dedicated to CWRs, and recently helped launch the Global Crop Wild Relative Portal. Their websites declare ‘Crop wild relatives – a key asset for sustainable agriculture’ (GCDT 2015) and ‘Importance of Crop Wild Relatives – Genes with immense value’ (Bioversity 2015c). Wild relatives have also become a key priority activity for FAO, which notes: ‘Natural ecosystems contain important PGRFA, including rare, endemic and threatened CWR and wild food plants. These species are becoming increasingly important as sources of new traits for plant breeding’ (FAO 2011, 33–34). Such narratives herald the institutionalization of CWR in these ‘global’ organizations as well as across the constellation of research and policy bodies with whom they partner.

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7These impressive figures must be an underestimate, as they do not reflect the historical and ongoing intermixing of wild and domesticated genes in traditional agroecosystems, or the role of farmers in promoting such mixing.
Ex situ and in situ: from competing to complementary

The combining of land-based and bank-based strategies in ‘complementary’ designs reflects decades of frictions and evolutions in the natural and social sciences associated with conservation. Despite early calls by researchers such as Frankel (1970) and Jain (1975) for in situ strategies, for many years, the dominant trend in CWR conservation mirrored that for plant genetic resources in general. Ex situ approaches received (and continue to receive) the majority of funding, institutional support, technological advance and policy directives (Cohen et al. 1991). For nearly a quarter century, wild and weedy species were swept up in a general treatment of PGRFA as museum material: best saved through the strategy of ‘collect, stock and freeze’. It became evident, however, that ex situ strategies were not succeeding as expected in safeguarding acceptable levels of wild relative diversity – just as they had struggled to conserve domesticated diversity (Hoyt 1988; Davies 1991; FAO 1996a). Simultaneously, in situ functions of wild relatives rose to prominence, as field-based researchers began to uncover the numerous ecological roles that CWRs play (Harlan 1992).

By the early 1990s, in situ conservation of CWR had joined ex situ conservation as ‘a key element of the integrated tool kit most agricultural scientists feel is needed’ to conserve plant genetic resources (Meilleur and Hodgkin 2004). The new paradigm of ‘complementarity’, a win–win combining both approaches, was detailed in the writings of anthropologist Brush (1991) and endorsed by the national program leader for germplasm at the USDA – who expressed his opinion that the complementarity of ex situ and in situ approaches was already accepted by a majority of agricultural scientists (Shands 1991). Complementarity became more specific to wild relatives when in situ protection for CWR broke into world policy circles. The Convention on Biological Diversity (CBD 1992) and the FAO Global Plan of Action for Plant Genetic Resources (FAO 1996b) began to recognize the importance of CWR in their natural habitats – not as an alternative to ex situ collection, but as complementary to it. Today, updates to the FAO global plan (FAO 2011), the CBD Strategic Plan (Aichi Targets), and the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA 2004) all buttress a regime of in situ–ex situ complementarity.

Within the past six years, ambitious programs have been launched on both fronts. A global ex situ initiative, ‘Adapting Agriculture to Climate Change’ (AACC), was announced by the Global Crop Diversity Trust in 2013. The Crop Trust is managing the 10-year, USD 50 million project, in partnership with the Millennium Seed Bank of the Royal Botanic Gardens at Kew and funded by the Norwegian government. Described as an effort ‘to identify and fill gaps’ in existing collections (Dempewolf et al. 2014), AACC focuses on wild relatives in the gene pools of 29 crops considered important to global food security – all included in Annex 1 of the International Plant Treaty. The first phase of the project, explored below, focused on constructing inventories of CWRs and conducting research to determine species and geographical areas for collection. This research phase was implemented with partners at the International Center for Tropical Agriculture (CIAT) and the University of Birmingham, UK.

In parallel, plans and methods for systematic in situ CWR conservation are underway. Led primarily by researchers at the University of Birmingham in connection with Bioversity International, methods for systematic CWR conservation planning have been developing rapidly in recent years. Following the first-ever continent-wide inventory of CWRs (‘European PGR Forum’, Kell et al. 2005), progress has been made on national strategies in Europe, the Middle East and the Americas, with momentum now shifting to southern
Africa and Central America (Kell et al. 2015). At the global level, the FAO Commission on Plant Genetic Resources for Food and Agriculture commissioned Birmingham researchers to conduct a background study on the establishment of a global network for in situ conservation of CWR. This study, published in 2009, aims to provide sufficient scientific baseline information for individual countries to set up conservation areas for CWR, towards a ‘systematic effort to build up national, regional or global networks of these areas’ (Maxted and Kell 2009). In 2013, the FAO held a special workshop geared to developing an in situ conservation network within a broader context of PGRFA – including modern crops, landraces and wild relatives (FAO 2013).

Framing the climate and food security challenge

Yet formal recognition does not translate fluidly into practical strategies. A common refrain expressed by CWR researchers is that wild relatives fall into an institutional gap between the agricultural and conservation agendas. ‘Agriculture looks at tended lands, conservation does not focus on agricultural resources’ (Bioversity 2015a). Recently, however, the many stakeholders with interest in CWR – from Bioversity to the Crop Diversity Trust, from the USDA to Birmingham scientists – have received a strong wind at their backs: a confluence of crises that make conserving and using wild relatives seem not only beneficial, but imperative. They have also developed poignant narratives that propagate this belief. The literature on CWR conservation shows the active production of a crisis/salvation discourse, in which wild relatives are both threatened by climate change and vital for world food security (see Figure 1). These storylines help justify the activities of conservation science, while also legitimizing potential enclosures through the authority of a scientific lens.

The agriculture literature today is replete with data on the current and impending effects of climate change. In the Fifth Assessment report of the Intergovernmental Panel on Climate Change (IPCC), authors suggest that climate change will reduce agricultural production by 2 percent every decade until 2050. Over that time span, yields of major crops will face an average decline of 8 percent for Africa and South Asia (IPCC 2014). A study on the impacts of recent warming, meanwhile, found that major staple grains have already experienced significant climate-related yield losses – some 40 million tons per year from 1981 to 2002 (Lobell et al. 2008). Many studies on long-term climate trends do not even take into account the risk of extreme climate events: spiking temperature increases, hurricanes or rainfall-induced flooding. Up to 40 percent of the world’s land surface may develop novel climates with new pest and weed complexes (Williams, Jackson, and Kutzbach 2007).

With climate change set to transform growth conditions and arable zones worldwide, climate-hardy wild relatives have never appeared so valuable. Paradoxically, the ecosystems inhabited by wild relatives are also being destabilized by global warming. By 2080, Thuiller et al. (2005) predict, climate change will result in the loss of 27–42 percent of all European plant species in such places, and the immigration or emigration of 45–63 percent of species per 50 km². The greatest changes are expected in transition between the Mediterranean and Euro-Siberian zones – the precise region, say Maxted and Kell (2009), containing the highest proportion of agronomically important taxa. Climate change only adds to the other pervasive threats confronting wild plants: deforestation, urban expansion, invasive species, habitat fragmentation and, not least, the intensification of agriculture.

A survey of the CWR literature reveals many forms of this crisis narrative, both apocalyptic and matter of fact. Endorsing the Global Crop Diversity Trust’s ex situ project,
Figure 1. Why care about crop wild relatives (CWR)? Bioversity’s infographic illustrates the organization’s efforts in promoting CWR research, conservation and public awareness. What are CWR? What threats do they face? Why are they important? According to researchers, CWR contribute USD 115–120 billion per year to improving food production worldwide (Image credit: Bioversity 2015b).
Dempewolf et al. (2014, 370) rekindle a familiar Malthusianism: ‘The world’s human population is predicted to reach over 9.3 billion by the year 2050 … placing ever more pressure on agricultural systems to increase production’. Meanwhile, they continue, climate change models indicate possible yield losses of 6–10 percent per 1°C of warming in a growing season: ‘This means the world could see significant production losses in the future’ (370). Ultimately, they suggest, ‘it will be crucial to adapt agriculture to the increasingly challenging environmental conditions by breeding new crop varieties’ (370). In similar strokes, an influential essay in Nature Climate (Guarino and Lobell 2011, 374), frames a logic of scarcity with burgeoning population, rising temperatures and collapsing yield: ‘With potentially less food to feed more people, we have no choice but to adapt agriculture to the new conditions’.

Remarkably, in situ narratives often follow similar contours. A very recent report on China’s CWRs (Kell et al. 2015, 138) begins:

> The potentially devastating impacts of climate change on crop production and food security are now widely acknowledged. An important component of efforts to mitigate these impacts is the production of new varieties of crops which will be able to thrive in more extreme and changeable environmental conditions.

While in situ narratives tend to be less overtly utilitarian than their ex situ counterparts, a parallel extractive mentality pervades. Wild relatives may be conserved ‘in place’, but their value is likely to be realized externally: ‘Unique and particularly diverse populations of these genetic resources require effective in situ maintenance if they are to continue to meet exploitation needs of current and future stakeholders, and via them, global goods’ (Maxted and Kell 2009, 7).

These examples provide a glimpse of the discourse seen across a swathe of systematic CWR literature: in which food security is generally diminished to an issue of production, and production is configured around a narrow set of variables: the crop, the trait or simply ‘germplasm’. Crop improvement, in turn, is collapsed down to a particular knowledge domain (technical, grounded in a Eurocentric tradition), belonging to a select community of experts (conservation scientists, PGRFA policymakers, public and private breeders), and populating a few key institutions and donor agencies (most prominently, the CGIAR, the FAO, the Global Crop Diversity Trust, and a cluster of agricultural and plant research universities).

It is not altogether surprising that mainstream PGRFA organizations – many of which have been characterized as part of the ‘neoliberal food regime’ (Holt Giménez and Shattuck 2011) – would extend their productivist discourse to absorb wild relatives. More surprising, perhaps, is the degree of self-awareness reflected in many mainstream accounts. Many researchers working in PGRFA readily acknowledge the irony of agricultural intensification as a leading cause of wild relative loss. For example, in a study of the Red List status of CWR in Europe, Kell, Maxted, and Bilz (2012) highlight the role of unsustainable farming practices, such as severe overgrazing, conversion of land to monocultures and the heavy application of fertilizers, herbicides and pesticides. Pollution from pesticide drift, habitat fragmentation from plantation-style agriculture, and the introgression of GMO genes into surrounding natural habitats have all been recognized as drivers of wild relative endangerment (Hoyt 1988; FAO 1996a, 2010, 2011; Friedman 2015).

It is similarly no mystery to these scientists that Green Revolution-style ‘crop improvement’ has eroded the genetic basis of the crop supply. Several decades of high-yield breeding have accelerated genetic erosion within domesticated species. Roughly 75 percent of
crop genetic diversity, according to FAO estimates, has been lost since 1900. Just three crops – rice, wheat and maize – provide more than 50 percent of the world’s plant-derived calories. Within these crops, a few species dominate the food supply, and within those, a few homogenous varieties prevail.

Ironically, it is in the context of this crop genetic erosion that the most seductive CWR story yet is now proposed: to rewind the domestication bottleneck, and reclaim the diversity that our farmer ancestors left aside.

**Rewinding the domestication bottleneck**

Roughly 10,000–12,000 years ago, nomadic hunter–gatherers transitioned to life in agrarian societies. Central to this transition was seed selection. Inadvertently at first, later intentionally, our ancestors began identifying and reproducing a small number of favorable traits that were readily recognizable in crops, such as seed size, plant vigor and yield. Darwin himself marveled at the meld of natural selection and ‘artificial’ (human) selection at play in domestication. An important wrinkle for natural selection within agriculture, of course, is that the farm environment is profoundly shaped by human hands: by removing competitor plants (‘weeds’), offering water when there is otherwise none, and enhancing soil fertility. Just by manipulating environments in a certain way, Murphy (2007) suggests, the earliest forms of grain agriculture likely guided the initial genetic changes that were the prerequisites to successful cultivation of those plants as crops. In the wild, for example, most seeds would be shed from reproductive structures, an adaptive trait in the conditions in which plants evolved. But in a tilled field, such seeds would fall to the ground, and not likely be saved for replanting. Thus, the shattering seed head has largely been lost in our domesticated crops. Other such ‘lost traits’ include wild relatives’ gangly growth habits and delayed seed germination (Tanksley and McCouch 1997). Compact plants that sprouted quickly from the earth would have been favored by early agriculturalists.

For millennia, most domesticated plants grew in close proximity to their wild and weedy relatives, enabling a dynamic gene flow. This was especially true in and around Vavilov centers of origin and diversity, where crops are surrounded by their close genetic kin and where complex agroecosystems encouraged mixing, both ‘natural’ and intentional. Mexican subsistence farmers, for example, would intentionally plant their maize on farm borders near wild relatives to raise the likelihood of cross-fertilization and crop enhancement (Hoyt 1988). Swidden cultivation – with ever-changing interfaces of domesticated and wild habitats – brought another potent form of genetic intermixing in African cereals, and is likely to have done the same in other places (Hutchinson 1974). Where geographic proximity, landscape complexity and farmer practices aligned, CWR introgression with crops has been almost continuous, not only casting new light on the once-upon-a-time concept of domestication, but making for agroecosystem resilience.

However, agriculture has been thoroughly re-spatialized, especially following the Columbian Exchange. European explorers, traders and plunderers brought Old World crops to New World frontiers, transplanted germplasm across tropical colonial holdings and shepherded New World seed back to European fields. With this geographic distancing of many food crops away from their wild relatives, the potential for natural (and facilitated) cross-fertilization has grown increasingly slim. Destruction of natural habitat by monoculture production systems has further reduced opportunities for gene flow. Meanwhile, those cultivated crops are having diversity systematically bred out of them. As Tanksley and McCouch (1997, 1063) put it, ‘Because new varieties are usually derived from crosses
among genetically related modern varieties, genetically more variable, but less productive, primitive ancestors are excluded’. Ironically, they note, ‘it is the plant-breeding process itself that threatens the genetic base on which breeding depends’.

This contemporary fix, created by both domestication and modern breeding, has spurred papers with titillating titles such as: ‘Unlocking genetic potential from the wild’ (Tanksley and McCouch 1997) and ‘Taking a walk on the wild side’ (Guarino and Lobell 2011). Retracing the domestication bottleneck, Guarino and Lobell explain, will provide access to ‘lost’ resources – to the ‘reservoir of diversity our Neolithic ancestors left behind’ (2011, 374). Traits from CWRs have already been used to breed crops with adaptations to abiotic stresses such as salt, water and heat extremes. The more common successes have been in the biotic sphere: providing host plants with resistance to insect, fungal and viral pathogens. These stressors may seem tangential to climate change, but as plant pathogens are predicted to shift their ranges, many farmers will experience unprecedented disease pressures. The promise of rewilding the crop gene pool, then, has never looked so auspicious or necessary. As Guarino and Lobell note, ‘If there was ever a time to go back and reclaim this diversity, that time is now’ (2011, 374).

The foregoing analysis of framings and narratives in mainstream CWR discourse hints at strong epistemic similarities across in situ and ex situ researchers and institutions. Under a productivist organizing principle, in situ activities appear aligned with – even subordinated to – the purposes of ex situ extraction and use. Narratives of loss and primitiveness, as I have argued elsewhere (Montenegro de Wit 2015), work to invisibilize peoples for whom wild relatives are very much not lost. Hardly confined to pre-history, these contemporary communities not only use CWR in breeding, they also cook, eat and market wild plants for extra nutrition and income. By framing what exists/persists as lost and unknown, these narratives work to appropriate agency and expertise; they imply that scientist–experts will be needed to regain lost diversity. More subtly, they also shift the burden of genetic diversity loss onto Neolithic farmers, rather than onto their more proximate nemeses: principally industrial agriculture. The discursive ground, then, is well prepared for scientific solutions that foreground systematic/technical planning without unduly disturbing the underlying productivist logic.

But narratives only provide a partial window into important enclosure processes in play. In the following section, I investigate material scientific practices: defining wild relatives, ranking conservation priorities, bringing inventories, mapping and making databases to construct policy-relevant science. Conservation science is seldom recognized as a site of enclosure itself. As with other S&T developments, its internal workings are generally ‘black-boxed’ from critical scrutiny (Latour 1999). By probing the practices, particularly of elite science institutions, we get a glimpse of how primitive accumulation germinates through knowledge production – long before it assembles as visible conservation on the ground.

**Systematic CWR conservation science**

More than 15 years ago, *Genes in the field*, a volume dedicated to in situ conservation, distinguished between two types of in situ. The first type, ‘de facto’ persistence of genetic resources in their natural habitats, refers to areas where ‘everyday practices of farmers retain genetic diversity on their farms’. The second type refers to specific projects and programs ‘to support and promote the maintenance of crop diversity, sponsored by national governments, international programs, and private organizations’ (Brush 2000, 4). Systematic conservation for CWR falls firmly into the latter camp, consisting of scientifically informed protocols for designing and implementing conservation – both in situ and ex situ.
There are many potential approaches to the systematic planning method, and the steps are by no means sacrosanct. Maxted et al. (2007) and Heywood et al. (2007) suggest a model for developing such strategies, at the national and global levels (see Figure 2). This model has since been taken up by studies supporting national and global networks for CWR conservation.

As can be seen in Figure 1, the protocol contains a fork, with pathways diverging to support in situ and ex situ strategies. When it comes to wild relatives, off-site strategies are comparable to those for crop plants: maintenance of germplasm in gene banks, botanical gardens and field-based reserves (Hoyt 1988). In situ strategies, however, diverge significantly from crop conservation – in fact, the latter is sometimes dubbed ‘on-farm’ conservation to distinguish it from the ‘in situ’ of wild relatives, which can range from forests to roadsides.

In situ conservation proposes the maintenance of wild relatives in their natural habitats, either by identifying wild relatives within existing protected areas and highlighting their priority management, or by establishing new protected areas. Maxted and Kell (2009) envision

![Figure 2. Model for the development of systematic national and global crop wild relative (CWR) strategies (adapted from Maxted et al. 2007 and Heywood et al. 2007).](image-url)
a strategy that ultimately creates overlapping national and global networks of such ‘genetic reserves’, which would enlist individual overseers of protected areas, national land management and conservation agencies, and international bodies such as the FAO and International Plant Treaty to devise a worldwide in situ system backed up by ex situ collections. As I illustrate below, the planning for such on-the-ground work begins far upstream, in defining, counting and prioritizing wild relatives.

What is a wild relative?

Before any practical work can take shape, researchers must decide which plants constitute ‘CWR’. A typical definition indicates that wild relatives are not only the progenitors of crops – often a wild plant of the same species – but also species ‘more or less closely related’ to them (Heywood et al. 2007, 245). Exactly how closely related, however, can mean the difference between identifying a few dozen species or thousands of wild and weedy kin. This definitional matter also means a great deal for crop breeding, since, biotechnology notwithstanding, genetic proximity remains a good proxy for ease in breeding.

One simple and intuitively straightforward way to define wild relatives is at the genus level. A CWR would be any taxon belonging to the same genus as a crop. Sweet potato wild relatives, for example, would include all the species and subspecies in the genus Ipomoea. A genus-wide definition was adopted by the European PGR forum (Kell et al. 2005), and has the advantage of easy application. The downside can be its breadth. Analyzing Mediterranean and European floras, researchers found that some 80 percent of these plant species qualified as CWRs (Kell et al. 2008). ‘Gene pools’ are another way of bounding wild relatives. Originally proposed by Harlan and de Wet (1971), the gene pool concept puts close relatives in the primary gene pool (GP1), more remote ones in the secondary gene pool (GP2) and very remote ones in the tertiary gene pool (GP3). Adhering to the primary gene pool generally includes taxa close enough to interbreed viably. But data about interbreeding and genetic diversity are lacking for many candidate species.

For this reason, Maxted et al. (2006) proposed an alternate strategy to supplement the gene pool concept. Based on standard taxonomic classifications, this strategy assigns different ‘Taxon Group’ categories beginning with the crop (Taxon Group 1a), wild relatives of the same species as the crop (Taxon Group 1b), and extending to all wild plants in the same genus as the crop (Taxon Group 4). These taxon groups, they suggest, can be used to establish the degree of relationship between a CWR and the crop when researchers have little information about reproductive compatibility.

Based on these arguments, they propose the following as a working definition of CWR:

A crop wild relative is a wild plant taxon that has an indirect use derived from its relatively close genetic relationship to a crop; this relationship is defined in terms of the CWR belonging to Gene Pools 1 or 2, or taxon groups 1 to 4 of the crop. (Maxted et al. 2006, 2680)

Many authors have since taken up this definition, indicating its value as the best ‘pragmatic’ means available for delimiting CWR. For example, Heywood et al. (2007, 247) argue that casting a genus-wide net is not very helpful when it comes to identifying wild relatives with agronomic potential: ‘There is a need to estimate the degree of CWRs relatedness to enable limited conservation resources to focus on priority species, i.e. those from which desired traits may be most easily transferred to the crop’. Similarly, Maxted and Kell (2009, 9) underscore that ‘conservationists [are] competing for limited resources’, making it vital to apply an accurate definition of the relationship between a crop and its relatives.
Evident in these conceptions of CWR is both a perceived condition of scarcity – in which decision-makers must economize their resource use – and a functional view of conservation, in which ex situ extraction is the presumed objective of in situ work. In a world of numerous competing demands, they imply, rigorous metrics will provide a scientific basis for guiding rational decisions. Defining a wild relative, then, becomes imbricated in a particular strategy of appeal: to policymakers, funding organizations and governments to increase their support for wild relative research.

Yet such appeals cannot help but reshape the science itself, which develops according to foreseen policy relevant criteria. Moreover, ‘accurate’ definitions help streamline conservation priorities through a bottleneck that they themselves create: in which wild relatives come to be defined by their genetic proximity to crops – and, therefore, their potential for breeding purposes. Increasingly, the literature proposes that utility for crop improvement is intrinsic to the very identity of a wild relative species: ‘CWR are species closely related to crops, including crop progenitors, and are defined by their potential ability to contribute beneficial traits to crops such as pest or disease resistance, yield improvement or stability’ (Maxted and Kell 2009, 51, emphasis added by author). These discursive practices are evidence of a new accumulation frontier: where bounding nature according to its production value defines some organisms as valuable, and hitches conservation to those extractive identities.

**Inventory**

An initial step in systematic CWR conservation is constructing an inventory. These can be local, national, regional or global, with different methods applying to each. For example, countries in Europe and the Mediterranean can use the PGR Forum Catalogue – an inventory of this region – as the foundation for their own national inventories. For most countries, however, inventories must be built from botanical scratch. Most countries do not have databases of CWR, per se, but almost all have national checklists of their floristic diversity. These lists include all plant diversity, including cultivated and non-cultivated species.

Researchers, meanwhile, have at their disposal global lists of crops – notably, Mansfield’s World Database of Agricultural and Horticultural Crops – from which genus names can be extracted (Hanelt and Gatersleben 2001). These genus names can then be matched against the national botanical checklist to identify all genera containing cultivated plants. Assuming a genus-wide definition of CWR, all taxa (species, subspecies, etc.) within these genera can be ‘extracted’ as the national CWR inventory (Maxted and Kell 2009). With the ascendancy of digital biodiversity management, much of this work becomes a matter of database comparison, matching and identity extraction.

But using a genus-wide definition also tends to cull a very large set of species in the initial inventory – tens of thousands, in the case of China’s wild relatives (Kell et al. 2015). For this reason, and as I explore below, researchers apply various means of whittling down the candidate conservation pool. In a process I describe as ‘filtering’, these steps of selection and prioritizing CWR further shape the contours of policy prescriptions and imperatives. The use of such filters also explains an apparent contradiction: using a genus-wide definition, when researchers have devoted so much attention to precisely defining what constitutes a CWR. Various filters can also embed definitions, as we will see, moving the architecture of systematic conservation into alignment with specific norms for crop improvement.
Prioritizing

Given that the number of potential CWRs that might be conserved far exceeds institutional capacity – no matter what definition of CWR is applied – systematic conservation plans include several possible means of prioritizing. As Heywood et al. (2007) describe, priority setting may involve some form of threat assessment (e.g. based on IUCN Red List data) and consideration of the economic value of the related crops. Priorities can also take into account cultural importance for local people, the wild relatives’ ecological role, and the presence of the CWR – or lack thereof – in existing protected areas. In addition, ethical and aesthetic considerations, legislation and financial costs can all be factors used to ascribe ‘value’ (Maxted et al. 1997b; Kell, Maxted, and Bilz 2012).

One example of how scientists apply priorities comes from a recent global inventory of CWR. Originally developed for the Global Crop Diversity Trust (principal partner in the global ex situ project), the ‘Prioritized Crop Wild Relative Inventory’ (Vincent et al. 2013) was designed to inform both ex- and in situ efforts. It specifies two key priority concerns: (1) socio-economic importance of the related crop; (2) potential use for crop improvement. The first filter works in an exclusive sense, by removing all CWR not considered important according to their relatedness to crops listed in the International Plant Treaty (Annex 1 crops) and a world reference of major and minor food crops (Groombridge and Jenkins 2002). The second filter works to rank CWR within these priority crop genera according to breeding value; here, researchers use a combination of gene pools and taxonomic groups to estimate breeding potential, alongside published records of successful and potential use. The global inventory concluded by identifying some 1667 taxa (1392 species and 299 subspeciﬁc taxa) of critical importance for economic and food security.

Analyzing these priority-setting steps, however, reveals the subtle (and not so subtle) ways in which systematic CWR planning could perpetuate enclosures. First is the growing reliance on only a few prioritization criteria to the neglect of myriad others. Increasingly, the literature reﬂects an opinion that only three priorities are ‘of greatest relevance when assigning priorities to CWR species in the context of conservation planning’ (Kell et al. 2015, 142; see also Vincent et al. 2013): socio-economic importance of the related crop, breeding utility and threat status. As an example, a recent national inventory of China’s CWRs began by tallying human food crops that were cultivated in China over the period 2002–2011. Crops with an annual production value over USD 500 million were identiﬁed and the native wild relatives of these crops became the foundational list of important CWR (Kell et al. 2015). The assumption is that wild relatives will be used to develop valuable crops, such that commodity revenues and trait value come to justify conservation of the wild species. Meanwhile, what gets ﬁltered out and de-prioritized are values intrinsic to CWR that may be unrelated to crop improvement: stabilizing agroecosystems in situ, providing ecosystem service beneﬁts (at multiple scales) and contributing to spiritual, agricultural and livelihood practices of local peoples. Throughout Africa, for example, people are known to eat wild cowpea species (Vigna spp.), while in Madagascar, wild yams (Dioscorea spp.) are a rich source of carbohydrates. Both are also sold in local markets, providing additional household income. CWR that do not move through the crop improvement pipeline, or that never enter formal commodity markets, are seen as less important to address – and, thus, less important to protect.

Second is the inherent contradiction in pegging the values of CWR to the socio-economic values of their related crops. The risks herein should be fairly obvious: the crops that are most proﬁtable, ubiquitous and energy yielding today reﬂect the structure and organization of the predominant agri-food system. High-grossing crops are often those
pushing out much agrobiodiversity, wild relatives included. Similarly, industrial staples such as rice, corn and wheat comprise an increasing proportion of the world diet (Khoury et al. 2014), so metrics based on current nutritional provisioning will tend to reinforce the agri-food status quo.

The discourse of CWR science seems to be moving into lockstep with a longer standing synergy between commodity production and scientized nutrition. Mudry (2009) examines how organizations such as the USDA attempt to legislate a healthy diet by mandating quantities of food based on measurable nutrients – calories, vitamins and serving sizes. This quantification has the effect of controlling how people eat, how they believe they should eat and, in turn, consumer demand for certain foods. It occludes the quality of nutrition outside of Western dietetic boundaries – and says little about how food is produced, by whom, or under what social and environmental conditions. Similarly, wild relatives are now assessed through reductive quantities such as dollar value or the caloric value of their related food crop. In the case of the China inventory (Kell et al. 2015), a novel method was employed. Using FAO statistics, researchers calculated global nutrition values for human food crops, according to average annual per capita energy supply. The intention was to consider the transnational value of local wild relatives. As the researchers put it,

although the priority for most countries is to conserve resources that are of greatest potential socio-economic value to the nation, it is important to consider the value of genetic resources in a broader geographic sense since no country is self-sufficient in food supply. (Kell et al. 2015, 7)

Latent in these priority-setting methods, then, is the potential to perpetuate many facets of the current ‘socio-economy’ based on their very starting points. It is through these priorities that we can see the edges of primitive accumulation being forged: signaling to industry, governments, scientists and civil society where genetic resource value is to be found (where it is not to be found) and what sort of value it represents. Wild relatives currently appear to be things we should care about because they will improve crops already central to our industrial food system.

Ecogeographic studies, threat assessment and ‘gap analysis’

After a prioritized inventory has been compiled, researchers conduct ecogeographic studies and threat assessments to further refine the list of priority taxa, followed by ‘gap analysis’ to identify which wild relatives are not adequately conserved in ex situ collections and where genetic reserves could be established in situ (Heywood et al. 2007).

Considered the backbone of CWR conservation, ecogeographic work consists of an epic data trawl: researchers must collate all information available about wild relatives’ ecology, geography and diversity – both taxonomic and genetic. Such information can come from existing literature or from novel field surveys and interviews, with common sources including gene banks, herbaria, museums, government ministries and plant research institutes. The ‘passport information’ associated with accessions in banks and herbaria specimens, for example, describes where CWR were collected, as well as their center of origin and diversity.

Increasingly, digital databases intervene both upstream and downstream of ecogeographic work. As gene banks build massive informatics platforms (DivSeek, InfoSys), much knowledge of PGRFA is coming online, including passport information and genomic, phenotypic and taxonomic data. Germplasm holdings at far-flung museums and universities are now accessible on the web, and an increasing number are being
brought into centralized data management systems. On the input end, these databases have become key to gathering ‘occurrence’ records – information about CWR whereabouts in banks and on land. On the output end, the results of ecogeographic studies are frequently entered into regional and national databases to enable geographic information system (GIS) mapping and analysis.

For ex situ conservation, according to Maxted et al. (2008), the ultimate goal of ecogeographic studies is to identify populations of CWR thought to contain genetic diversity that is not already conserved in off-site collections. ‘Gap analysis’ allows researchers to fill gaps between extant gene bank collections and actual distribution on land. For in situ conservation, the goal is to locate land areas with high concentrations of priority CWR species and work to preserve them. Yet the work does not end here. Once land enters the calculus, ‘threats’ take on a new valence. In addition to considering threats to individual CWR taxa – a common step in creating a prioritized inventory – threats must pertain to in situ territory: to the likelihood of endangerment from habitat fragmentation, over-exploitation, expanded urbanization, unsustainable agriculture and climate change. Structured assessments can then fill the in situ gaps by showing which combinations of land sites contain the ‘optimal or ‘best’ sample of CWR species in the minimum number of genetic reserves.8

Ideally, Maxted and Kell (2009) suggest, it will be possible to locate and establish such genetic reserves within existing protected areas. But creating new protected areas specifically for CWR conservation should not be excluded either, as CWR species are famously cosmopolitan in their tastes, inhabiting roadsides, urban lots and other disturbed habitats that may not have been considered appropriate for protected area status.

Sociopolitical factors: where are the people?

Designers of systematic CWR science widely acknowledge that human dimensions should come into account – whether in negotiating seed collections or establishing genetic reserves. Especially in the latter case, where land is involved, decisions over access and use must involve farmers and indigenous and local communities (see e.g. Maxted 1997a; Hunter and Heywood 2010; Maxted, Magos, and Kell 2013).

These scientific recognitions have followed and informed discourse at the international policy level. The ITPGRFA promotes ‘Farmers Rights’, and the FAO Global Plan of Action on PGRFA (FAO 2011) is replete with statements supporting the role of local peoples in conservation of agrobiodiversity, including CWRs.9 Reflecting such policym-science conjunctures, the South African Development Community – Crops Wild Relatives (SADC-CWR) project,10 launched in 2014, is explicitly pluralistic, aiming to include a

8 ‘Genetic reserves’ are proposed as the preferred model for conservation of CWR in situ. As defined by AEGRO, a European network that promotes in situ and on-farm management of agrobiodiversity, genetic reserves are ‘areas designated for the active, long-term in situ conservation of wild populations where the primary consideration is to preserve its genetic diversity’ (AEGRO 2015).

9 Reflecting the participatory turn in 1990s sustainable development discourse, both the First (1996) and the Second (2011) FAO Global Plans of Action on PGRFA emphasize farmers and indigenous and local peoples. The latter recognizes their role as guardians and stewards of agrobiodiversity on farm and in situ (FAO 2011, 20), calls for policy supports to strengthen local conservation capacity (27) and even underscores farmer/indigenous participation in crop improvement, using ‘participatory, de-centralized, and gender-sensitive approaches’ (58).

10 SADC-CWR aims to address the ‘in situ conservation and use of crop wild relatives’ in countries of the South African Development Community. The three-year project is a partnership of African universities and institutional partners including Bioversity and the University of Birmingham.
broad group of stakeholders as ‘decision-makers’: from national policymakers to actors in agriculture (technical departments, plant breeders), environment agencies, conservation NGOs and farmer organizations (SADC-CWR 2015a): ‘The promotion of indigenous knowledge can also be advantageous to CWR’ (SADC-CWR 2015b).

But it remains unclear to what extent recognition of local knowledge on paper extends to activities on the ground (many of which are very nascent), and whether recognition will translate into authentic social empowerment. Under the scientific leadership of Ehsan Dulloo, the CWR program at Bioversity is poised to become more cognizant of local ecological expertise. In a promotional film, he notes: ‘Farmers tolerate the presence of crop wild relatives on the farm because they recognize the value that these crop wild relatives bring to their cultivated plants’ (Bioversity 2015a). However, at the 2014 Genepool Utilization Conference, Bioversity researchers presented on plans for a ‘Community of Practice’ for CWR. Sketching who would be important in such a community, they named ‘FAO, CBD, UNEP, ITPGRFA, UNESCO, IUCN, CGIAR, NGOs, etc.’, leaving aside explicit mention of peasants, indigenous peoples and public citizens (Dulloo and Drucker 2014). To include a diversity of stakeholders is also potentially misleading, since inclusion says little about the terms of inclusion, or the quality, extent and duration of participatory practice (see e.g. Sperling et al. 2001). Epistemically, different knowledges can be included on highly uneven terms: how is legitimacy granted and shared?

A large scholarship has explored lay–expert divides in environmental governance (e.g. Irwin 1995; Wynne 1996; Fischer 2000; Collins and Evans 2008). In conservation of biodiversity, as with PGRFA, recent years have seen a marked shift towards the inclusion of farmer, local and traditional knowledges. Yet implicit in this participatory turn are unresolved tensions. A strong tradition in dominant PGRFA institutions remains rooted in an ‘information deficit’ model, which assumes a lack of knowledge in the public. Scientists, then, should educate the public for their own good, and the wellbeing of all, in line with sustainability goals. This trend is seen, for example, in the SADC project language:

These CWR species are often neglected and thus threatened in the wild, due to ignorance of their value to agriculture by policy-makers, decision-makers and ecologists. Also breeders and farmers, in particular, are unaware of these resources and often lack the skills to mine the genetic diversity from CWR for use in novel varieties. (SADC-CWR 2015c)

The arguably more dominant model in PGRFA conservation today is not information deficit, but what Delgado (2008) terms ‘knowledge co-production’. Exemplified by the Convention on Biological Diversity, this model recognizes indigenous, local and traditional peoples, whose knowledges are characterized as potentially ‘relevant for the conservation and sustainable use of biological diversity’ (UNEP/CBD 1992, art. 8). Relevant is a key word, as it implies that local knowledge becomes valuable only after it has been assessed from a scientific point of view (Agrawal 1995). Delgado shows how this expert–lay relation unfolds in Brazil, where the Landless Workers’ Movement (MST) is promoting agroecology as its preferred mode of agricultural production. Technicians purport to value and validate farmer lay knowledge, but as Delgado’s research reveals, legitimacy is selective. Parts of local knowledge that conform to agroecology receive ‘distinctive recognition’, while the others are ‘problematized’ and targeted for expert remediation. In other words, the part of local knowledge that does not count as ecological expertise ‘remained invisible or categorized as ignorance’ (Delgado 2008, 571).

In CWR conservation, the highly obscure processes of systematic planning – the defining, priority setting and gap analyzing – are especially prone to this subtle invisibilization.
Local knowledge can be, and is, included in systematic planning. But only to the extent that it conforms to pre-existing scientific principles of sustainability and conservation. Enclosure of the material seed, then, begins on this slipstream of knowledge exclusions: both the blatant information-deficit form, and the stealthier co-productive form. Scientists may not intentionally propagate enclosures, but their methodologies anticipate them in the qualified inclusion of community actors.

Conservation science is not alone, however, in making the ground fertile for epistemic and material appropriations. As we have seen, the priorities of conservation, in- and ex situ, are increasingly dictated by breeding value and the prospective caloric or dollar return from CWR-improved crops. The science of how to incorporate wild relative genes into domesticated plants thus becomes the second major hinge in our enclosures story. Plant breeding and biotechnology is initially more obvious as a site of primitive accumulation given its history with biological and legal enclosures. The very name Monsanto is something of a signpost for a dispossessive regime. Less evident (and less explored) is the making of the S&T knowledge upstream of oligopsony control. Wild relatives are not new to breeding science, but they are injecting new energy into the field. By offering the potential to re-commodify current crops with wild genes, they are pulling the frontier of primitive accumulation into a genetic space whose boundaries are pushed by the ambitions and technologies of science, and what gene-tinkerers can do.

**Breeding and biotechnology**

Until the 1980s, the range of CWR breeding ‘successes’ could be counted on one hand. Stories about wild genes preventing devastation by pests and diseases, according to Hajjar and Hodgkin (2007), were dominated by a handful of triumphs. *Oryza nivara* provided resistance to grassy stunt virus in rice; *Solanum demissum* gave potatoes protection against late blight; and *Agropyron elongatum* and *Aegilops umbellulata*, respectively, conferred stem and leaf rust resistance in wheat (Prescott-Allen and Prescott-Allen 1986). In the past 30 years, however, the discovery and use of new resistance genes from the wild have steadily increased in these crops and others. Commercialized tomatoes now derive nearly all of their resistance genes from wild relatives (Rick and Chetelat 1995). In rice, the original *Oryza nivara* genes still fend against grassy stunt virus on millions of hectares across South and Southeast Asia (Barclay 2004), while several different wild species of rice confer resistance to at least six other diseases (Hajjar and Hodgkin 2007). Sweet potato wild relatives have been tapped for traits from protein enhancement to drought tolerance (see Figure 3).

Nonetheless, a common refrain amongst researchers for many years is the longstanding under-exploitation of wild relatives ( Tanksley and McCouch 1997; Maxted and Kell 2009; Guarino and Lobell 2011; McCouch et al. 2013). This perceived under-utilization reflects, in part, the challenge of working with wild species. It is an everyday occurrence for breeders to hybridize two varieties of a crop species; they even cross the species or genus boundary in what is known as a ‘wide cross’. Yet wild relatives, being undomesticated, are less predictable. If the plants are genetically compatible at all, the resulting embryos may not be viable without special ‘rescue’ techniques, and offspring of CWR hybrids are often sterile. In addition, there has been fear of yield collapse: the possibility that introducing wild relatives’ genes will disrupt the high-yielding gene complexes breeders worked so hard to stabilize in the first place. Perhaps unsurprisingly, wild relatives have achieved notoriety amongst breeders for being ‘difficult’ (Stebbins 1958; Zeven, Knott, and Johnson 1983; Sharma et al. 2013). As one breeder tells Guarino and Lobell (2011,
it’s a bit like crossing a house cat with a wildcat. You don’t automatically get a big docile pussycat. What you get is a lot of wildness that you probably don’t want lying on your sofa.

Weeding out this unwanted wildness demands a process known as ‘pre-breeding’, in which modern varieties are crossed with wild relatives, followed by repeated backcrosses to the modern parent. Even then, the result is not plow-ready, but represents an intermediate product: germplasm ‘enhanced’ for public or private-sector use. This added step in the breeding process, in turn, has carved an institutional division of labor. Most crop-breeding programs, according to Guarino and Lobell (2011, 375), are not set up to make full use of species that require lengthy and intensive management: ‘Breeders, particularly in the private sector, are rewarded for releasing new varieties quickly, and wild relatives are viewed as too unwieldy to use with sufficient ease and speed’. The public sector has therefore become the workhorse of wild relative breeding, historically at CGIAR centers.

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11To call the CGIAR a ‘public institution’ is increasingly a stretch. A restructuring process – intended to streamline the funding process and reduce transaction costs – led to the separation of the CGIAR Consortium (the research centers) from the CGIAR Fund in 2010. The latter is administered by the
as the International Center for Wheat and Maize Improvement (CIMMYT) and the International Rice Research Institute (IRRI), though now extending to the International Center for Agricultural Research in the Dry Areas (ICARDA; see Valkoun 2001 for examples of wheat pre-breeding using CWR) and the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT; see Sharma et al. 2013 for legume pre-breeding with CWR). The decline of public sector plant breeding – indeed ‘emasculating’ of the sector as a whole (Kloppenburg 2010) – has meant slow progress in wild relative research.

But the ground is shifting rapidly beneath wild relative breeding, transforming both the motivations for overcoming biological obstacles and the technological capacity to do so. Climate change is at the core of these recent developments: as genetic diversity is increasingly recognized as fundamental to climate-resilience, R&D and commercial attention has turned to consider the vast repository of latent diversity in wild relatives. Conventional breeding seems to retain many advantages over genetic engineering (GE) for dealing with complex traits such as drought tolerance – and crossbreeding with CWR offers one such conventional approach. Yet neither breeding nor biotechnology is a stable regime, and molecular science is rapidly transforming both. Calls to unleash the ‘tremendous genetic potential locked up in seed banks’ ( Tanksley and McCouch 1997, 1063) have pulled CWR to the center of a molecular revolution: in which wild relatives are targeted for genome-wide methods of more efficient, yet ‘traditional’, plant breeding, alongside GE techniques touted as organic ‘rewilding’. Perhaps unsurprisingly, the conjunctures of climate, science and technology, and agricultural sustainability have put wild relatives on a path with heady promise, curious contradictions and important repercussions for how, where and by whom value is created and captured. Below, I consider these elements in further detail.

World Bank, as Trustee, and governed by a Fund Council. Between 2010 and 2014, top Fund contributors have been the US, the UK, the World Bank, and the Bill and Melinda Gates Foundation (BMGF). Roughly USD 175 million from BMGF (out of USD 180 million) have been window 3 gifts – i.e. targeted to specific CGIAR centers and not considered by CGIAR to be ‘untied aid’ (CGIAR Fund 2015). The increasing hold of philanthropy capital and private–public partnerships on the CGIAR has been criticized, but is also seen as a public system vying to retain relevance at a time of private-sector dominance in agricultural and agbiotech research.

12 ‘Conventional breeding’ is a broad term depicting methods that introduce new variety to plants without reliance on genetic engineering. Conventional breeding includes ‘classical’ techniques – known to farmers since ancient times – of interbreeding closely or distantly related individuals to produce new crop varieties or lines with desirable properties. After WWII, ‘modern’ techniques added to the conventional toolkit included induced mutagenesis (chemical and irradiation) and plant tissue culture. Increasingly, conventional breeding makes use of molecular tools such as genomic sequencing, bioinformatics and marker-assisted selection.

13 Biological technology, or biotechnology, is an ambiguous and politically loaded term. Broadly, any deliberate manipulation of biological material or systems is a kind of biotechnology, including seed hybridization using classical crossbreeding (Goodman, Sorj, and Wilkinson 1987; Kloppenburg [1988] 2004). For the purposes of this paper, I use agricultural biotechnology in the more commonly understood sense: ‘as the use of DNA-based technologies for crop improvement’ (Murphy 2007, 157). In turn, GE is a sub-class of agricultural biotechnology, described most simply as ‘in vitro techniques for manipulating nucleic acids and introducing or reintroducing it into plants’ (D. Gurian-Sherman, pers. comm.).

14 A note on nomenclature: Many plant biologists use ‘traditional’ interchangeably with ‘conventional’ to describe a broad set of non-genetic engineering methods (see also note 12). I use ‘conventional’ throughout this paper, but it is important to note the discursive power of ‘traditional’ breeding, which carries a slate of rooted, habitual, natural and customary connotations.
Returning ‘lost’ diversity to the domesticated gene pool has never looked so vital, as climate change both demands such re-diversification and threatens to eradicate many wild species. A heavily politicized debate surrounds climate adaptation: on one side, agronomic and agroecological approaches target soil, water, plants, animals and other elements of the farm ecology; on the other side, breeding focuses on adapting one plant – the crop – to the changing environs. In turn, crop-centric communities are divided over conventional breeding and biotechnology. Industry pursues both tracks but is increasingly trained on the latter, in hopes of genetically engineering more ‘crop per drop’.

Mounting research suggests, however, that conventional breeding techniques may still eke out an advantage when it comes to complex multi-genic traits such as drought resistance and nitrogen-use efficiency. Monsanto’s GE Droughtguard corn seeds have been shown to provide only about 6 percent yield increase in the US, and only under moderate drought conditions (Gurian-Sherman 2012). By contrast, non-GE methods are being used to develop drought-resistant corn varieties in at least 13 African countries. In field trials, these varieties are matching or exceeding yields from nonresistant crops under good rainfall – and yielding up to 30 percent more under drought conditions (Gilbert 2014). Conventional breeding has also made important drought-resistance inroads with staple crops that are popular in the developing world such as sorghum, millet, cassava, rice and wheat.

Wild relatives enter into these crop improvement debates in a curious way, creating cross-hatching patterns of public/private, industrial/organic and traditional/modern across growers, research institutions and agri-food corporate interests. In the context of climate adaptation, industry appears to be reappraising the value of conventional plant breeding techniques, within whose reach wild species lie. Seed companies have an incentive to expand their conventional breeding pipeline to make use of wild relatives, while avoiding the taint of ‘GMO’. Conventional breeding with wild relatives is also an auspicious gain for public plant breeders in the organic community, who have long focused on breeding techniques that are less capital intensive than knowledge and skill intensive (OSA 2011). At the same time, some scientists argue that new biotechnologies offer a means of GE with wild relatives in ways that could bypass GMO regulation and still qualify as ‘organic’.

The conventional method of transferring genes from wild plants to crop plants is known as ‘introgression breeding’. It involves crossing the crop plant with a wild relative, creating a hybrid plant, followed by multiple generations of backcrossing the hybrid to the original crop. This method, the standard in pre-breeding described above, results in a genetic background that is mostly crop, with a few ‘introgressed’ CWR traits. Introgression breeding can expand – and already has expanded – the available gene pool in crops, and increase overall genetic diversity (Sanchez, Wing, and Brar 2014; Warschefsky et al. 2014). It also has the distinct advantage that the genes responsible for the desired traits need not be known in advance. But there are also drawbacks of working with a ‘wildcat’. A considerable amount of time – up to 10 years – can be expended in the pre-breeding stages of backcrossing to remove undesirable genes. Unwanted genes located near sought-after genes can be especially difficult to eradicate (a phenomenon known as ‘linkage drag’). Finally, the

15Speaking at the University of Nebraska’s Water for Food Summit in 2010, Monsanto President Robert Fraley said: ‘The widespread adoption of improved agronomic practices, advances in breeding and improvements and adoption of biotechnology will help farmers squeeze more from every ounce of water to meet the demands of a hungry, growing world … increasing the “crop per drop” is vital’ (Monsanto 2010).
method has long been considered unviable for complex traits such as yield and tolerance to cold, salt and drought (Andersen et al. 2015).

Some of these obstacles have abated with the molecular advances that introgression breeding has undergone in recent years. Still within the conventional breeding (non-GMO) realm, researchers commonly use a plant’s genetic make-up to predict its agronomic potential and traits. Genetic markers, for example, can identify individual plants carrying specific genes for disease or stress tolerance, without ever exposing the plants to the relevant agents. Using such genome-wide approaches, McCouch et al. (2013, 24) suggest, breeders can ‘eliminate 70–80% of individuals in any generation without having to invest in laborious multi-environment field testing’.

Even the meddlesome problem of yield has begun to give way. For obvious reasons, CWR are not generally high yielding: ‘productivity’ is largely a quality resulting from the process of plant domestication. Like drought tolerance, yield is also a complex trait, unlike most of the single-gene traits for pest and disease resistance. But in a much-cited paper published in 1997, Tanksley and McCouch suggested that yield potential is very likely lurking in wild relatives. The problem, they wrote, is that breeders were blinded by their own methods of search. They were looking for beneficial traits associated with wild relatives, instead of looking for beneficial genes. The standard approach to utilizing wild germplasm entails screening entries from a gene bank for a clearly defined trait, recognizable in the physical appearance (the phenotype). But while effective for single-gene traits, Tanksley and McCouch (1997, 1064) argued, ‘only a small proportion of the genetic variation inherent in exotic germplasm will ever be exploited for crop improvement as a result of this strategy’.

Today, breeders widely appreciate this lesson. Many plants’ traits are ‘quantitatively inherited’ – sprinkled across the plant genome, amongst many genes that collectively contribute to the characteristic. It means that complex traits such as yield or drought cannot not be enhanced by targeting a single ‘locus’ in a genome, as these traits result from many loci that create the behavior. Quantitative traits have now been identified in numerous CWR species, according to Hajjar and Hodgkin (2007), and ‘the potential to exploit them as a breeding resource using new molecular technologies has yet to be fully realized’ (Mawser and Kell 2009).

Some scientists, however, believe the future of CWR lies less with conventional breeding than with GE. They have many potential ways to introduce wild relative DNA into crop genomes. ‘Transgenic’ technology, usually mediated by Agrobacterium, is the most familiar of such approaches. Here, researchers harness the bacterium’s natural gene-transfer apparatus to insert foreign DNA at a random insertion point in the host plant. A closely related method, called ‘cis genesis’, involves transferring genes between organisms that could otherwise be conventionally bred. Wild relatives are therefore ripe territory for cis-genesis, given their mating compatibility with crops. But the technique likely to shake up wild relative biotech – as it has shaken the field of GE on the whole – is a powerful genomic editing tool known as CRISPR.16 It will carry ramifications not only for how CWR genes are transferred, but also for the pool of distant wild traits that are potentially exploitable, and, therefore, for what is defined as a CWR.

16Genomic editing is a class of biotechnology that dates back roughly a decade. Techniques include zinc-finger nucleases (ZFNs) and transcription activator-like effector nucleases (TALENs) in addition to the newer CRISPR-Cas9 system (CRISPR is short for clustered regulatory interspaced short palindromic repeats). They all enable a broad range of genetic modifications by inducing DNA double-strand breaks that stimulate distinctive pathways of gene repair.
CRISPR has risen to prominence since 2012, when researchers first started using it in animals and plants, and has achieved blockbuster status amongst GE scientists, praised for its relative simplicity, speed and precision. ‘In the past, it was a student’s entire PhD thesis to change one gene’, Bruce Conklin, a geneticist at the Gladstone Institutes in San Francisco, told the *New York Times.* ‘Crispr just knocked that out of the park’ (Kahn 2015). More properly called CRISPR-Cas9, this ‘new’ technology piggybacks on a natural feature of the microbiological world: by storing snippets of viral DNA within a part of their own genomes called CRISPR, the bacteria can mobilize an enzyme called Cas9 to cut viral DNA with the same sequence.

Harnessing this adaptive immune system, researchers have created an artificial ‘guide RNA’ into which they can insert a few sequences corresponding to the host gene they wish to modify. They can now send the Cas9 enzyme to precise locations, in any organism of choice, directing it to snip and stitch raw DNA ends back together. ‘It really opens up the genome of virtually every organism that’s been sequenced to be edited and engineered’, Jill Wildonger of the University of Wisconsin–Madison told a reporter for the *Proceedings of the National Academy of Sciences.*

Less commonly emphasized in stories to date on CRISPR is a new/old double edge (Montenegro de Wit 2016). In one of its many functions, it can control genes in crops without introducing any foreign DNA – for example, inserting or deleting single base pairs to ‘knock out’ gene activity. Such knockouts in crops can eliminate genes that affect food quality, divert energy away from valuable end products, and confer susceptibility to diseases (Bortesi and Fischer 2015). But CRISPR also rapidly scales up the ability to insert genetic material – and, thus, the potential to make the more familiar GMOs. Donor DNA can range from synthetic oligonucleotides to genes of fish, fungi or CWRs.

In fact, a team of Copenhagen scientists has recently proposed using CRISPR to rewild crops using CWR genes. In a high-profile study published in *Plant Cell,* they explore the feasibility of genomic editing (which they call ‘precision breeding’) with wild relatives: ‘The most efficient methods of rewilding are based on modern biotechnology techniques’ (Andersen et al. 2015, 426). “…cisgenesis and precision breeding offer precise alternatives to introgression breeding that are much faster, because they are not based on crosses’ (429). No rewilded crops have yet been created. But, in principle, CRISPR could offer more control and speed for rewilding as well as a route around the quagmire of complex traits. Standard GE methods generally manipulate only one or a few genes at a time, making multi-genic traits such as drought tolerance tough to engineer (Goodman 2014). Harvard researchers have already used CRISPR to simultaneously alter 62 genes in pig embryos. The same capability is almost sure to hold true in plants, given CRISPR’s agility across hosts.

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17Gene insertion with CRISPR-Cas9 can happen in two main ways. Very occasionally, the Cas9 enzyme leaves ‘sticky end’ overhangs when cutting DNA, allowing researchers to introduce a gene of interest. More frequently, Cas9 generates blunt-end cuts. By providing a donor template, researchers can facilitate a process of ‘homology-directed repair’, in which the new gene insert is effectively copied into the host sequence (Bortesi and Fischer 2015).

18Some individual genes can affect genetically complex traits. Transcription factors are one such class of genes, now commonly targeted by researchers seeking drought resistance. However, studies suggest that genetic approaches, whether breeding or engineering, are unlikely to substantially mitigate losses from drought in the real world, where droughts vary in time and duration, and target genes unexpectedly alter more than one trait, producing undesirable (pleiotropic) effects on crop growth (Gurian-Sherman 2012).
Yet not everyone is so certain that genomic editing will offer a significant advantage over traditional cross-breeding when it comes to wild relatives. Researcher Chuck Benbrook has expressed concern over ‘the precision part of precision breeding’: unexpected effects on other genes can occur when a new gene is added, or when an existing one is silenced (Kolata 2015). Geneticists call this phenomenon ‘pleiotropy’. In addition, even CRISPR rubs up against the old problem of agroecological diversity. Genes associated with more complex traits often perform differently in different crop types (the ‘genetic background’ effect) and under varying environmental conditions (the ‘gene X environment’ effect) (Dekkers and Hospital 2002; Cattivelli et al. 2008).

While popular discourse may pit conventional and genetic approaches against one another, contemporary scientific practice reveals considerable cross-traffic between the two approaches – involving both the industrial and organic agricultural communities. Interestingly, the pairings of mode and practice are not what we might think. At CIMMYT, the institutional cradle of Green Revolution research, scientists using conventional breeding have developed several promising varieties of wheat that provide higher yields in drought conditions, some already in distribution. A few of these are crosses between modern lines and wild relatives of wheat from the Middle East, where wheat originated. These lines, Marris (2008) reports, change their root architecture in drought conditions, going deeper. Meanwhile, the Copenhagen research team proposes that using CRISPR to rewild crops is an elegant marriage of organic and biotech. Rewilding has yet to be embraced by the organic movement, they argue, but the method could be used to scale up productivity in organic systems that have struggled to achieve yields comparable to those of industrial systems. Thus, while industrialized agriculture institutions employ ‘old-fashioned’ breeding to exploit wild relatives, some researchers in organic systems are touting GE as a way to close the ‘yield gap’ in organic farming.

In both cases, wild relatives are proving adept at morphing the configurations of R&D in the context of a perceived ‘ancestral’ or ‘natural’ advantage over GMO. Whether due to public skepticism over genetically engineered food, regulatory scrutiny of biotech or increasing societal concern about ownership and patenting of GMOs, wild relatives appear to offer a more natural way of doing business.

Curiously, discourses of ‘nature’ can usher in applications of CWR contrary to environmental sustainability. Wild relatives have already been used to confer resistance to herbicides such as the popular weedkillers imidazolinone and sulfonylurea. Wild relatives have also been mined for ‘cytoplasmic male sterility’ (CMS) traits that increase the efficiency of producing F1 hybrids – that is, the biologically enclosed seeds that cannot be replanted by farmers (Berlan and Lewontin 1986). The USDA is now extending this commodity-farming motif in a project focused on sunflower wild relatives. After crossing the US states to collect wild plants related to cultivated Helianthus, they have begun exploring cytoplasmic male sterility and herbicide tolerance, in addition to resistance to major pests and pathogens. Long-term objectives include breeding sunflower with high yield and high oil content, and ‘increasing the oil per acre yield of sunflower’. The weedkiller sunflower, marketed as Clearfield, is already estimated to be ‘worth millions of dollars globally’ (Hajjar and Hodgkin 2007). Who will capture this market for the future breadbasket of rewilded crops?

Part of the fate of CWR, in this respect, is bound up in regulatory policy for GMOs. In the US, any food classed as non-GMO is prohibited from containing ‘unnatural’ genes – that is, genes that could not have occurred in nature within that plant (no fish genes in corn, in other words). But adding a gene from a wild relative of the same plant using genomic editing would be allowed, according to the Copenhagen scientists. US rules
focus on product, and the product of such ‘rewilding’ is genetically indistinguishable from a crop interbred with CWR through conventional means. The rules are different in Europe, where GMO is defined not by the product but by the process. As long as the method involves some form of GE (transgenic, cisgenic, genomic editing), no resulting food can pass as non-GMO. Thus, a rewilded product would likely pass muster as non-GMO in the US, but not in Europe. Contingent upon their embrace by organic consumers and organic farmers, crops genetically engineered with wild relatives could pry open a large market for organic seed in the US (where 90 percent of seed for organic systems is still industrially bred). It could, of course, also foster resistance and public backlash, as Benbrook cautions, given the well-documented sociopolitical and ecological corrosions of GE. This is not to suggest that chemical agribusiness is not also poised to win big if rewilded crops manage to sidestep GMO regulations. Markets in Europe and Africa could be opened up for crops that are not GMO but are also hardly organic – herbicide-tolerant varieties of sunflower, for example.\footnote{Agbiotech companies are already using CRISPR to develop crops, livestock, biofuels, industrial enzymes and new strains of fermentation microbes – all potentially sidestepping regulations on engineered crops (Kahn 2014; Pollack 2014). CWR could add to the crop and biofuel development pipeline.}

Until recently, the biological demands of mating two plants together have configured the definition of CWR – in terms of genetic proximity and therefore breeding utility. However, as demonstrated above, molecular advances are transforming the speed and scope of conventional breeding, while engineering tools like CRISPR are bringing the genomes of more distant wild relatives (the secondary and tertiary gene pools) into new reach. With these changes, the very identity of a ‘wild relative’ has been destabilized: as biotechnology shears usability away from genetic proximity, what constitutes a CWR will have to expand to reflect the wider spheres of genes newly pregnable and useful. For commercial interests, there is explicit value in reaching into foreign parts of the plant gene pool. But there are countervailing dynamics too. As more ‘foreign’ species become beguiling candidates for appropriation, there continues to be much material and affective value in being not so foreign – that is, in the close genetic kinship that is signature of being a wild relative. The terrain of CWR today is therefore shot through with both unexpected alignments and new takes on old divisions of labor: industry availing itself of ‘traditional’ (though increasingly molecular and capital intensive) breeding, organic researchers touting ‘natural’ GE, and the public sector doing the slow work of pre-breeding the foreignness out of privately exploitable genes. It is also increasingly a world in which high-tech genomic editing, digitized information databases and probabilistic modeling create the material possibilities of using CWR, while idioms of ancestry and nature shape public perception, regulatory policy and valorization in the market.

Establishing enclosures: complementarity, gene governance and big data

We have begun to see how the discourses and practices of conservation science and breeding science are reinforcing one another in engendering new values for CWRs. Plant breeders and engineers cannot mobilize value without effective conservation, and conservation gathers credibility for its activities by offering utilitarian CWR value: germplasm that might be useful for improving crops deemed valuable according to certain metrics. Conservation plans, genetic reserves, pre-breeding, CRISPR and crisis narratives are co-evolving, in ways both diffuse and readily identifiable. In itself, each discursive object (cf. Escobar
2011[1996]) is unlikely to facilitate primitive accumulation. But when these S&T elements move into synchrony with developments in information technology, legal architectures and industry moves, it becomes very likely that enclosures will occur. Knowledge production never occurs in a vacuum, and CWR science is no different. The existence and potential of its discursive and material enclosures is always coproduced in historical context, with practices/processes in other knowledge domains. In the following section, I explore the following as interrelated sites of primitive accumulation:

- Institutional conservation and use policy – ‘complementarity’ between in situ and ex situ;
- Commodification and historical trends in appropriation;
- Legal architectures for genetic governance;
- Information technology – the assembly of ‘big data’.

As reviewed above, since the early 1990s, ‘complementarity’ has been widely recognized by international researchers and policymakers, suggesting that we can indeed have both in situ and ex situ strategies, coexisting and non-competing. My claim is that complementarity, enshrined now in many international policy instruments, is likely to contribute to wild relative enclosure because the character of complementarity remains highly ‘ex situ-centric’. As Graddy-Lovelace (2015) describes it, the notion of ‘centricity’ enables us to get beyond the mere existence of in situ or ex situ. On one hand, ex situ-centric conservation values in situ cultivation insofar as it serves ex situ collections. On the other hand, in situ-centric conservation values ex situ institutions insofar as they repopulate and foster in situ renewal. Thus, ex situ-centric does not obviate the need for in situ practices – indeed, it demands them. But it configures a gravitational tug, drawing knowledge and resources into central repositories, towards sites of elite knowledge-making and classification.

The idiom of ‘complementarity’, I argue, has made space for such an ex situ-centric epistemology to take hold within and around in situ projects, programs and studies. As plans unfold to protect natural habitats and ecosystems populated by CWR, the ex situ-centricity tends to mobilize germplasm towards off-site ‘use’ including breeding new crops and appropriating their value. It is this spatial and social patterning of germplasm flow, rather than the existence of ex situ or in situ per se, that should concern us. Ironically, in binding land-based protected habitats to bank-based repositories, ex situ appropriation becomes more ecologically sustainable. By conserving the evolutionary and ecological processes that renew diversity, and creating ‘backups’ in gene banks worldwide, the complementary system becomes more stable – and better able to fuel ongoing accumulation.

Commodification potential is a strong motive force shaping the ex situ-centric flow of resources and knowledge in mainstream complementarity. Wild relative crops promise great returns on investment, for those with the capital and technical acumen to utilize them. According to Bioversity researchers, in the United States, the desirable traits of wild sunflowers (*Helianthus* spp.) are already worth roughly USD 267 million to 384 million annually to the sunflower industry. One wild tomato variety, these experts say, has contributed to ‘a 2.4 percent increase in solids contents worth US$250 million’; and three wild peanuts have provided resistance to the root knot nematode, ‘which cost peanut growers around the world US$100 million each year’ (Hunter and Heywood 2010, 11). In perhaps the most extensive review of CWR in public breeding programs to date, Maxted and Kell (2009) found some 234 studies reporting agronomically useful wild relative traits (for 29 food crops). Although ‘trait value identification’ does not translate neatly into actual use of traits – such data are often considered proprietary – these
evaluations provide the first inkling of value recognition in the R&D pipeline. Here, the trends are clear: since 2000, there has been a significant uptick in ‘the number of attempts to improve quality, husbandry and end product commodities’ (Maxted and Kell 2009). In turn, the so-called gene giants are furthering their pursuits of CWR traits. According to journalistic reports, Monsanto has requested samples of teosinte, a wild relative of maize, from workers at Native Seed/SEARCH, a non-profit organization that works to preserve indigenous agrobiodiversity (Bill McDorman, the former director of Native Seed/SEARCH, politely turned them down).

Historical trends in primitive accumulation, in turn, show that circuits of dispossession are already entrenched in global seed exchanges. In 1977, teosinte was rediscovered in Mexico and brought to the US to be distributed widely to university and private breeders. One economist has estimated the traits derived to be worth about USD 6.8 billion per year (Kloppenburg 2004). Little or none of this wealth, however, has been returned to Mexican coffers. Indeed, the world political economy of genetic resources has long reflected numerous tilted planes: uneven geographic richness of biodiversity, uneven S&T capacity and uneven power relations amongst people, communities and nations. For reasons ecological and geographical, the centers of origin for agrobiodiversity tend to fall in the tropics – mostly in the ‘global south’. Thus, historical collection of germplasm by botanists, diplomats, plant-hunters and Green Revolutionaries configured an asymmetrical, northward flow of genes. With the expansion of commercial seed production from the mid-twentieth century onward, an important stream of germplasm began flowing in the opposite direction. The reversal, however, reflected a sea change in the political economy of seed: ‘Plant genetic resources leave the periphery as the common – and costless – heritage of all mankind, and return as a commodity, private property with exchange value’ (Kloppenburg 2004, 169).

Wild relatives appear likely to deepen these circuits of dispossession yet further. The Global Priority CWR Inventory (Vincent et al. 2013) indicates that the 10 most important countries for further collecting are: China, Mexico, Brazil, USA, Iran, Turkey, Spain, Greece, Indonesia and Guatemala. The country with the most native wild relative species is Peru (at 58) followed by Mexico (39), China (35), Turkey (28) and Bolivia (23). Ford-Lloyd et al. (2011, 563) suggest that: ‘Germplasm, CWR, and the genes that they possess will therefore need to be moved around the world more than ever before in order to facilitate the process of agricultural adaptation as a response to changing climate’. If it is from several of the world’s poorest nations that wild relatives could be extracted, the question is whether reciprocated benefits will be commensurable to the value of what was taken.

The international legal structures governing plant genetic resources will influence greatly who controls and benefits from CWR. Unfortunately, the scientific literature on CWR is scant on access to, and use and benefits of, wild relatives. Meanwhile, legal scholarship on crop genetic resources tends to overlook wild species. What can broadly be surmised, however, is that in situ, wild relatives fall under locally specific jurisdiction, frequently tied to land rights. Terms of access and use are contingent on where wild relatives set their roots: on private lands, public lands, or lands held in internationally protected areas such as those in the UNESCO Man and Biosphere program or the FAO Globally Important Agricultural Heritage sites (GIAHS). Ex situ holdings also vary according to site and scale. Germplasm in national gene banks is generally considered public property of the state, and CGIAR holdings are nominally held in the global public domain. Today, a number of regimes for germplasm governance reflect the overlapping nature of IPR and germplasm access and benefits. These frameworks include the Convention on
Biological Diversity (CBD), the Trade Related Aspects of Intellectual Property (TRIPS) agreement of the WTO, UPOV (1991) and national IPR laws.

Ascending since 2004, the International Plant Treaty attempts to address some of the logjams created by these overlapping regimes. Specifically, it responds to what critics felt were weaknesses in the CBD paradigm of treating germplasm as ‘national sovereign property’ and is designed to articulate fluidly with TRIPS, UPOV and patent laws (Fowler 2013; J. Kloppenburg, pers. comm.). In brief, the Plant Treaty establishes a Multilateral System (MLS) of access-and-benefit sharing for 64 crops considered the ‘world’s most important for food security and interdependence’.20 Invoking a commons approach, the MLS suggests that ‘everyone’ is able to freely access germplasm for these 64 crops, in return for an equitable sharing of research and any commercial proceeds.

In principle, IPR is forbidden on any genetic materials (whole seeds, genetic parts or components) obtained directly from the MLS. ‘Recipients shall not claim any intellectual property or other rights that limit the facilitated access to the plant genetic resources for food and agriculture, or their genetic parts or components, in the form received from the Multilateral System’ (ITPGRFA 2004, Art. 12.3(d), my emphasis). However, derived materials – that is, materials changed beyond the form received – fall outside the ‘commons’ of the MLS. Once germplasm is transfigured by conventional breeding or biotechnology into qualitatively distinct forms, no obstacle exists to patenting or variety protection. Developers of proprietary products pledge to pay benefits back into the Multilateral Fund, but enforcement of this mechanism is weak or non-existent; moreover, the payback represents a fraction of the potential profits that could be gained through seed commoditization.

There are at least three mechanisms by which CWRs become subject to enclosure vis-à-vis the Plant Treaty. First is through the backwards pressure on both in situ and ex situ conservation plans for CWR. As previously noted, the 10-year global ex situ initiative, AACC, was developed around 29 crops considered important to global food security – all included in Annex 1 of the Plant Treaty. The Global Crop Diversity Trust, a leading partner in this initiative, then commissioned a global prioritized inventory of wild relatives (Vincent et al. 2013) to inform both land-based and gene-bank strategies. A first step in the inventory-making process was culling only CWR related to Annex 1 crops and recognized major and minor food crops (Groombridge and Jenkins 2002). In turn, research teams are now using the global inventory to create national inventories for Wales, Spain, Libya and Jordan, and a regional conservation strategy for Europe. With this growing network of inventories based on priorities established by Plant Treaty criteria, the result is a high likelihood that conserved CWR will be related to Annex 1 crops – and will be genetically related to species covered in the MLS. Via breeding or engineering of CWR traits into their related crops, these wild relatives (or at least their gene ‘parts’) are effectively brought into the MLS.

Second, and relatedly, while the Plant Treaty only governs access through the world’s public ex situ repositories,21 it supports the complementarity of in situ and ex situ approaches. CWRs are explicitly included in the Treaty’s call to ‘promote in situ

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20Annex 1 of the Plant Treaty includes 64 food crops and forages covered under the Multilateral System. For the full list, see Annex 1 in ITPGRFA (2004).
21Access to germplasm in the MLS is configured through the world’s gene banks: local repositories (e. g. in university research labs), national seed collections, and international banks, including the vast holdings of the CGIAR. The intent is to share a set of ‘efficient rules of facilitated access’ for all gene banks held in the public domain (ITPGRFA 2015). Germplasm held in the private domain, by corporations and other private agencies and institutions, is excluded from Plant Treaty jurisdiction.
conservation of wild crop relatives and wild plants for food production, including in pro-
tected areas, by supporting, inter alia, the efforts of indigenous and local communities’ (ITPGRFA 2004, Art. 5.1(d), my emphasis). This language, however, veils a strong mandate for collections of CWR ex situ (Moore and Tymowski 2005), as well as an implicit understanding that ‘sustainable use’ of CWR will be achieved through ex situ control. Cooperation is needed ‘to promote an efficient and sustainable system of ex situ conserva-
tion… and promote the development and transfer of appropriate technologies for this purpose with a view to improving the sustainable use of plant genetic resources for food and agriculture’ (ITPGRFA 2004, Art. 5.1(e), my emphasis). The Treaty, then, sutures protected areas and gene banks in an ex situ-centric system, where value potentially accumulates at the downstream end of a ‘use pipeline’: for the benefit of researchers, private breeders and agro-industry.

Third, the Plant Treaty has been lauded for including farmers’ rights, recognizing the historical and ongoing role of farmers and indigenous peoples in creating, renewing and safeguarding biodiversity. But many critics have called the recognition anemic at best, especially when the MLS does little to preclude intellectual property. The Treaty’s invocation of a commons has been called but a ‘trope’ in this regard – accurate, perhaps, in por-
traying how traditional and indigenous peoples relate to their seed, but legitimizing the continued ‘free appropriation’ of resources from communities who would share under terms such terms (Kloppenburg 2004; Aoki 2008; De Schutter 2009). From an epistemic vantage point, it is also evident that the ‘commons’ denotes access by a selective community of experts with ‘technical know-how’. The Multilateral System, the treaty secretariat proposes, ‘sets up opportunities for developed countries with technical know-how to use their laboratories to build on what the farmers in developing countries have accomplished in their fields’ (ITPGRFA 2015).

The practices of IPR governance, conservation science, and breeding science are increasingly intertwined through ‘big data’ and information systems. In the realm of dom-
esticated plants, the ex situ-centric paradigm has been described as emphasizing ‘data-fica-
tion’ (Iles et al. 2016). CWRs are also being data-fied, I suggest, with information technology becoming as central to PGRFA work as the preservation of material seed stocks. Both conservation and breeding have shifted into this data-driven terrain. Producing conservation knowledge about CWR is now part of a highly digitized, statistically intensive project of identifying, mapping and modeling species distributions for ex situ collection and/or in situ conservation. For example, many collection studies begin at gene banks, herbaria and botanical gardens, whose records are increasingly available as digitized databases about CWR in their possession. In turn, technologies now as commonplace as Google Maps can give researchers a quick visualization of these occurrence records (i.e. where CWR exist), while statistical modeling, combined with GIS, goes a step further: to map the potential dis-
tribution of wild relatives on the land. Maps can then be compared with gene bank holdings to identify gaps in current ex situ holdings and prioritize land areas for collection. Online databases such as the Global Atlas of CWRs (http://www.cwrdiversity.org/distribution-
map/) and the Crop Wild Relatives Global Portal (http://www.cropwildrelatives.org/) have become repositories for such information, illustrating new ways that data are being compiled, analyzed, published and rendered searchable (see Figures 4 and 5).

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22In the Treaty secretariat’s interpretation, the modus operandi is giving ‘scientific institutions and private sector plant breeders the opportunity to work with, and potentially to improve, the materials stored in gene banks or even crops growing in fields’ (ITPGRFA 2015).
Figure 4. Where a wild sweet potato lives – and might live. Although sweet potato is a staple food across Asia and Africa, its center of origin and diversity is in the Americas – meaning wild relatives are also concentrated here. To map where crop wild relatives (CWR) exist, scientists look for ‘occurrence’ records in databases kept by herbaria, gene banks and museums. Occurrence of the wild form of sweet potato (wild *Ipomoea batatas*) appears as red dots on the map (black dots in print publication). Using environmental modeling and geographic information systems (GIS), researchers can then determine the full potential range of these CWR based on what is known about species’ adaptations to temperature, elevation, precipitation and soil types. In one study, researchers modeled 27 different input variables to arrive at the potential distribution of each CWR species (Khoury et al. 2015). In this map, the possible range of wild sweet potato is shown in green (gray in print) (Image credit: Crop Wild Relative Global Atlas 2013).

Figure 5. Mapping wild sweet potato collection priorities. Wild relatives of sweet potato are concentrated in Mexico and Central America. But their range is large, stretching from the central United States all the way down to Argentina. To determine priorities for crop wild relative (CWR) collection, researchers can conduct a ‘gap analysis’ that assesses current gene bank holdings for ecological and geographic comprehensiveness. It enables them to see, for example, if a species has a very wide geographic range, covering numerous ecosystems, while only a few samples are held in collections. It can also tell them if the total occurrence data (herbaria, museums, botanical gardens) is very large, but the gene bank holdings are small. Usually written and performed in the programming language ‘R’, the product of such gap analysis can be visualized in map layers. High-priority locales for collection of wild sweet potato, shown in orange (grey in print), include Guatemala, Nicaragua and much of southeastern Mexico. (Image credit: Crop Wild Relative Global Atlas 2013)
On the breeding side, gathering data from gene banks is no longer the equivalent of combing through old library card catalogs. The Germplasm Resources Information Network, operated by the USDA, chronicles its seed accessions in an online genebank information management system that is now being replicated globally as DivSeek. This platform comprises a search engine through which users can access genomic, phenotypic and molecular characterizations of the world’s ex situ stores of agri-food genetic resources, including wild relatives. DivSeek underscores the mobilization of plant genes into valuable food products: ‘to enable breeders and researchers to mobilize a vast range of plant genetic variation to accelerate the rate of crop improvement and furnish food and agricultural products to the growing human population’ (DivSeek 2016). As suggested by attendees of the 2013 Asilomar Conference, such data systems will link conservation data with breeding prospects. When biologists’ genotypes and phenotypes are linked to conservationists’ ecological and geographic field data, researchers will gain the ability to design more targeted ground experiments and to develop predictive models of plant performance. In the DNA fingerprints of banked exotics, the attendees offered, is nothing less than ‘a genomic “parts list”’ that ‘can guide our remodeling of cropping systems for the future’ (McCouch et al. 2013, 44).

The rise of big data, then, is injecting new potential into the respective arenas conserving and utilizing agrobiodiversity. But it is only through becoming connected that conservation and breeding/biotech establish a use pipeline, and assemble the practices of enclosure. Information infrastructures provide this critical interstitial tissue, without which siloed S&T would be mostly stillborn. Intensive data-fication is particularly conducive to primitive accumulation, as it appears to provide unheralded shareability, transparency and public accessibility of information. It enables predictive modeling of landscapes and plant behavior unthinkable in an era prior to high-throughput algorithms. Simultaneously, however, it makes possible the generation and harvesting of more abstract forms of value: where tens of thousands of background data points can produce a shortlist of ‘high priorities’ for policymakers, even if the process is illegible to those outside the data-literate.

With the proliferation of online portals, information systems and databanks, several questions have emerged. Who has access to digital data? What sorts of knowledge does the digitized system include – and exclude? Is information which is ostensibly public and accessible to all enclosed in less noticeable ways? Graddy-Lovelace (2015) has outlined some of these concerns, noting, for example, that agrobiodiversity in DivSeek is classified and standardized as open access in principle. Yet under the terms of the Plant Treaty, derivatives of plant germplasm can be enclosed through imposing patents and other IPR. Lack of internet (or even computers) can also preclude access to information in these systems. A ‘digital divide’ that already separates many low-income farmers and rural communities from their wealthier urban counterparts could well fissure access to PGRFA information, including wild relatives.

Broadband, however, may not be the most important obstacle. With the emphasis on genomic technologies, GIS and statistical modeling, these information systems embed the particular knowledges of the scientists and professionals who created them. Even if DNA fingerprints are publicly available, the question becomes, is ‘genotype’ a language that most people speak? A data-fied cosmos has difficulty capturing the many situated, affective and practical knowledges of people on the ground who have shaped the processes giving rise to CWR diversity. Although international policy regimes such as the CBD and the Plant Treaty affirm traditional ecological knowledge, such place-based wisdom can be recalcitrant to the quantitative categories of digital infrastructures. If brought into a digitized
space, these knowledges are frequently reduced and simplified (from ‘rooted’ to rootless), making them amenable to exploitation and appropriation (Thrupp 1989; Rocheleau 2011; GRAIN and LVC 2015).

Conclusion

In this paper, I have argued that CWRs represent an emerging frontier in biotechnology, conservation, data science and agricultural science along which primitive accumulation may occur. Industry is poised to capture value from beneficial traits embedded in many species that are both proximately and distantly related to crops – with the more distant relatives newly appropriable through advanced GE. The climate change crisis affecting agro-nomic potentials worldwide has brought research, breeding and policymaker interest in wild relatives to a new height because of the climate-hardy characteristics of CWR species. ‘Rewilding’ the current crop gene pool is now proposed as a way to retrace the domestication bottleneck, plumping up the genetic stock of diversity eroded through more than a century of productivist breeding. None of these potentials can be realized, however, if wild relatives themselves disappear, anchoring the extractive, accumulation potential of traits in the conservation capacity of ‘complementary’ ex- and in situ programs.

A rich literature has explored processes of enclosure. From Marx and Luxemburg to Federici and Harvey, primitive accumulation is now recognized as an ongoing and generalized phenomenon, with diverse current manifestations. Written into the fabric of what McMichael (2008) calls the globalization project, and what Hardt and Negri dub ‘Empire’ (2004), enclosures rest upon a central tenet of neoliberalism: ‘the appropriation of that which is shared in the “commons” or the “public domain” and its transformation into an exclusive, commodified form’ (Kloppenburg 2010, 369). What I contend is that knowledge production – especially the production of scientific knowledge – is central to how frontiers of primitive accumulation/dispossession develop. Many ‘ex novo separations’ (cf. De Angelis 2004) will assemble through the material and discursive practices of researchers, technicians and science–educators; they will be structured into science–policy institutions, intellectual property frameworks and governing bodies for genes, data/knowledge and land. In agrobiodiversity alone, S&T developments are rapidly co-evolving and being assembled into an infrastructure of extraction. Multiple interlinked epistemic processes are impelling the appropriation of genetic commons and its transformation into a commodity form.

In this paper, I have attempted to break open the black box of systematic conservation science, scrutinizing the methods, the inclusions and exclusions of data, the metrics, the measures and the assumptions built into how wild relatives are defined and prioritized. Production of conservation value through these S&T processes influences policymaking, providing the scientific legitimation for the protection of certain wild organisms, and certain biodiverse places. Simultaneously, I have probed the technological/knowledge space inside plant breeding and biotech, which are expanding the potential scope and scale of germplasm ‘use’. From conventional breeding boosted by genomics and bioinformatics to the burgeoning world of CRISPR engineering, technologies that produce new combinations of diversity are rapidly overcoming nature’s old obstacles. Biological reproduction between CWR and domesticated crops has always occurred in complex agroecosystems. Pulled into an ex situ-centric use pipeline, however, this interbreeding is poised to become (systematically) commodity driven as it brings wild genes into a domesticated form. With CWR receiving little protection, as of yet, from international PGRFA governance frameworks, the motive forces of political economy, IPR and datafication suggest the
continued appropriation of germplasm along uneven lines. These scientific, legal and data practices and discourses should be recognized as sites of primitive accumulation.

What does this mean, in turn, for impeding dispossession? How does an STS/political economy understanding become useful for thwarting appropriation of wild relative value and enabling repossession?

To close, I will just sketch a few ideas that emerge from the preceding inquiry. First is that interdisciplinary thinking will be essential. Yes, interdisciplinarity is a term much en vogue, as much to extend colonial habits of thought as to overcome them. But I suggest that social scientists with more dexterity in diverse scientific idioms can also be a strong antidote to these trends. By investigating the methods and models in ecology, biotechnology and information sciences, it will be possible to ‘see’ the upstream S&T enclosure processes at work before they manifest on the ground. The constructivist angle, moreover, helps us see that these sciences are not naturally occurring. Many human agents are involved, including researchers of all kinds, policymakers, funders, international agri-food institutions and civil-society organizations. These actors busily frame and construct scientific discourses and practices. So, if we are to counteract the gravitational pull of ex situ-centricity, a promising strategy is finding ways to destabilize and reorient these active knowledge-making activities.

What might this destabilization look like? I suggest we need changes at the foundation of S&T development – that is, democratizing science and removing its scientized underpinnings:

Scientism is when we treat decision making on a new technology as objective, value free, and best based on scientific evidence of quantifiable risks, while avoiding relevant ethical, cultural, and social dimensions. Because of scientization, we tend not to ask ourselves ‘What is the purpose or end goal of this technology?’ or ‘What kind of world or type of agriculture do we want?’ Instead, we want to know, ‘Is there sufficient evidence of biological or ecological harm from this particular agricultural technology?’ (Kinchy, quoted in Teller 2012)

Applied to agrobiodiversity, to disrupt the dominant tenor of S&T developments, we need to integrate science with farmer experiences and social organizing. We need to expand the criteria by which we appraise the rapidly evolving assemblage of conservation science, breeding science and data science. Agroecology provides one such modality. Insistent on the validation of farmer and indigenous knowledge, it seeks a ‘dialogo de saberes’ between Western sciences and other forms of expertise (Leff 2004; Martínez-Torres and Rosset 2014). It is also a normative science, asking at the outset what kind of agriculture we want, and building the S&T architecture from there. How ‘we’ is configured is seldom smooth or uncontested (see Delgado 2008, 2009), but, at its best, agroecology aims for a reflexive, participatory practice that is grounded in a subversive politics: a commitment to disrupt the homogenizing forces of the globalization project with biological and cultural diversity. It offers renewal of such diversity, in situ, instead of its capture in a commodity form.

What agroecologists and others have understood is that the world is already brimming with CWR conservationists.

For millennia, farmers have ‘exploited’ wild relative genetics for crop improvement by intentionally moving variation across species to enhance their cultivated crops. As previously noted, Mexican indigenous farmers are known to have planted their maize on the periphery of farm fields so as to encourage introgression between CWR species and corn (Hoyt 1988). In the 1960s and 1970s, Western researchers began to take note of such
farmer-led gene flow. Especially in areas under traditional agriculture, they discovered, crops are frequently enriched by genetic exchange with wild and weedy relatives – making the farming system more resilient to environmental change (Harlan 1965; de Wet and Harlan 1975; Altieri and Merrick 1987). These findings corroborated wider recognitions in agroecology and ethnobiology: that ‘wilderness’ is auspicious for agriculture (Posey 1984; Oldfield and Alcorn 1987; Toledo 2001; Nabhan 2009; Perfecto, Vandermeer, and Wright 2009; Nazarea, Rhoades, and Andrews-Swann 2013). And rather than threaten biodiversity, some forms of farming – and some farmers – seemed to actually enhance it.

Recent studies have affirmed the interdependency of wild relatives with peasant systems. A Dryland Agrobiodiversity Project in West Asia discovered that many intensively cultivated areas contain significant CWR diversity in field edges, habitat patches and roadsides (Al-Atawneh et al. 2008). In the industrially cultivated Beqaa Valley of Lebanon, rare populations of wild relatives were found inhabiting country lanes. In the Hebron area of Palestine, and in Jabal Al-Druze in Syria, modern orchards revealed very rare species of wild plants related to wheat, barley, lentils and peas (Maxted and Kell 2009). The guardians of agrobiodiversity are also not limited to growers. Local peoples across Africa, Asia, the Americas and Europe collect, cook and eat wild relative species. Wild foods provide sustenance, petty income and many other non-food uses, from medicinal and ritual to fiber and fuel (Nabhan 1989; Meilleur 1994). In their activities, these peoples may not be intensively managing farms or interbreeding crops and CWR. Nonetheless, the ‘wild’ spaces from which they harvest, through which they migrate, and on which they make their livelihoods are deeply imprinted with human knowledge and practice. Saving CWR can be found in their everyday resistances of cultivating foodways and deflecting pressures to deforest, extract and pave over.

In short, we have plenty of empirical evidence that CWRs needn’t be protected, exploited or brought to ‘improve’ crops destined for commoditization and industrial consumption. In situ conservation systems have sprouted up without planned, systematic intervention. Sciences and scientists that can navigate, with humility, through other regimes of knowledge making are well poised to democratize the practices of making and knowing nature. They may well discover that the most potent sciences for resisting enclosure are already underfoot.

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