



Access and Benefit Sharing Considerations for Ancient eDNA and Crop Genomes

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Report for FREYJA: Fostering Reciprocity in Environmental DNA science through Yielded stewardship, Just benefit, and Accountability

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Executive Summary

Ancient environmental DNA and crop genomics can reconstruct past environments, trace crop histories, and recover genetic variation relevant to contemporary environmental and agricultural challenges. These possibilities also raise questions about who may authorize access, whose histories and stewardship are represented in genomic data, and how benefits should be shared. This report examines those questions through access and benefit sharing (ABS), Indigenous Data Sovereignty, and Indigenous data governance.

The central argument is that responsible research requires governance throughout the full research lifecycle. Initial access agreements and eventual benefit sharing leave a “missing middle” in which samples become sequence data, analyses produce interpretations, and outputs enter repositories, breeding programmes, or commercial applications. Consent, mutually agreed terms, provenance, data governance, attribution, and accountability must remain active through these stages and into subsequent reuse.

Neither the age of a sample nor its environmental character removes its relationships to living peoples. Soil, water, permafrost, archaeological materials, and historical specimens may remain connected to Indigenous territories, ancestors, cultural practices, and continuing systems of responsibility. Human genetic bycatch creates additional concerns about privacy and consent. Describing materials as ancient should therefore prompt attention to their histories and relationships rather than presume that they are culturally unclaimed.

The discussion of *kalo* demonstrates why globally circulating crops can retain specific genealogical and cultural significance. A layered approach to benefit sharing distinguishes direct responsibilities to project partners, enduring responsibilities to wider communities of stewardship, and broader responsibilities when genomic value circulates through international research and commercial systems. These layers also inform research on barley, rice, and wheat, whose useful diversity reflects long histories of cultivation, exchange, and farmer innovation.

For ancient eDNA and crop genome research, the practical task is to establish continuing community authority, clear conditions for materials and data, and benefits defined with the people whose lands, knowledge, and stewardship make the work possible. Genomic interventions should be assessed in relation to equitable governance, farmer and community autonomy, ecological responsibility, and the restoration of relationships disrupted by extractive research and industrial agriculture.

Introduction

Advances in ancient environmental DNA and crop genomics are expanding what scientists can recover from sediments, archaeological materials, museum specimens, and historical crop remains (Ruppert et al. 2019). These technologies offer powerful ways to reconstruct past environments, trace crop domestication and movement, and identify genetic variants that may support resilience to drought, disease, and other pressures (Di Donato et al. 2018). Yet the scientific ability to recover and reuse ancient genetic information does not resolve the legal and ethical questions surrounding that information (Astolfi et al. 2025). Rather, it creates new questions about who may authorize access, whose histories and labor are represented in genomic data, how benefits should be distributed, and what responsibilities continue as samples and data move through research infrastructures (Hudson et al. 2019; Hutchins et al. 2025; Carroll et al. 2020).

This report examines those questions through the framework of Access and Benefit Sharing (ABS), while also considering the limitations of conventional ABS approaches for ancient eDNA and crop genome research. Access is often treated as the moment when a permit is issued, or a sample is obtained, while benefit sharing is imagined as a return delivered after the research is complete (Secretariat of the Convention on Biological Diversity 2010, 3). Genomic research, however, creates value throughout the full research lifecycle: as samples become sequence data, data are combined with metadata and knowledge, analyses generate interpretations, and those outputs are deposited, reused, and potentially translated into commercial or agricultural applications (Mc Cartney et al. 2023). The space between initial access and eventual benefit, what we are calling the “missing middle”, is therefore a central site of governance. It is where decisions are made about storage, analysis, interpretation, publication, reuse, intellectual property, and the continuing circulation of genetic information.

The report further argues that neither “ancientness” nor the environmental character of a sample should be used to presume that genetic material is disconnected from living peoples. Ancient sediments, water, soil, permafrost, and crop remains may remain connected to Indigenous territories, ancestors, food systems, cultural practices, and generations of stewardship (Kowal et al. 2023). Ancient crop genomes, in particular, are not archives of biological variation untouched by humans. Instead, they are often records of domestication, exchange, and selection (Mueller 2026). Therefore, responsible research must move beyond narrow questions of legal access to consider Indigenous Data Sovereignty, continuing relationships to place, layered forms of benefit sharing, and whether technological interventions strengthen or circumvent the social and agricultural systems through which biological diversity was created and maintained.

What is Access and Benefit Sharing

Access and Benefit Sharing (ABS) refers to the set of principles, legal frameworks, and ethical practices that govern how genetic resources and associated traditional knowledge are accessed, and how benefits arising from their use are shared. “Access” concerns the conditions under which researchers can obtain biological materials, such as plant tissues or environmental

DNA samples, as well as the data derived from them. This often involves Free, Prior, and Informed Consent (FPIC) from the country or community of origin, and mutually agreed terms (MAT) that define how materials can be used. “Benefit sharing,” in turn, encompasses both monetary and non-monetary returns generated from research and innovation, including co-authorship, data sharing, technology transfer, capacity building, and financial compensation where appropriate.

Historically, ABS frameworks emerged to address imbalances in how biodiversity-rich regions, which are often in the Global South, contributed genetic resources to scientific and commercial endeavors without equitable returns (Morgera and Tsoumani 2010). The Convention on Biological Diversity (CBD) and its Nagoya Protocol formalized expectations that access should be regulated by national sovereignty and that benefits should be shared fairly and equitably (see Figure 1 for timeline). While originally focused on physical genetic resources, ABS discussions have increasingly expanded to include Digital Sequence Information (DSI) (Figure 1), raising complex questions about how open science practices intersect with equity and sovereignty (Bond and Scott 2020).

Evolution of Indigenous Rights, ABS, and DSI Governance

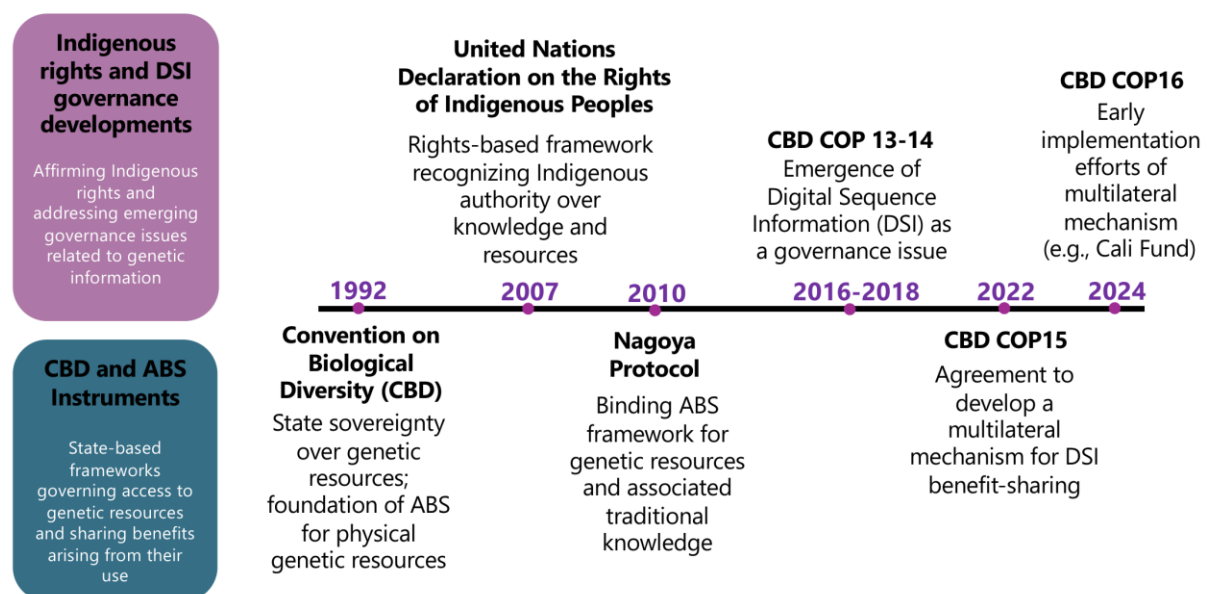


Figure 1. Key developments in international access and benefit-sharing, Indigenous rights, and digital sequence information governance. The Convention on Biological Diversity and Nagoya Protocol established state-based systems governing access to genetic resources and associated traditional knowledge, while the United Nations Declaration on the Rights of Indigenous Peoples articulated broader rights to self-determination, lands, resources, knowledge, and decision-making. DSI emerged as a distinct CBD governance issue beginning in 2016. COP15 established a multilateral mechanism for sharing benefits from the use of DSI, and COP16 operationalized that mechanism and named its financial component the Cali Fund. The parallel positioning of these developments illustrates that Indigenous-rights frameworks and biodiversity-governance mechanisms are related but have not always been institutionally integrated.

Within biodiversity genomics, ABS takes on new dimensions due to the scale and speed of research (Hutchins et al. 2025). Projects routinely generate large genomic datasets that are shared and reused across international platforms (Porter and Hajibabaei 2018), creating tension between open-access scientific norms and the rights of provider countries or communities (Boeckhout et al. 2018). For scientists, ABS is no longer limited to obtaining permits for sample

collection, but also involves navigating data governance expectations, respecting restrictions on downstream use, and ensuring that collaborations meaningfully include partners from source regions.

In the context of ancient environmental DNA (ancient eDNA), ABS considerations are particularly nuanced. Ancient eDNA is often derived from sediments, ice cores, or archaeological materials, which may originate from territories with deep cultural and historical significance. Even when no living organism is directly sampled, questions of ownership and consent remain relevant. Researchers must consider whether ancient genetic signals are linked to present-day communities, and how findings might impact cultural heritage narratives or land rights discussions. This makes early engagement, transparency, and inclusive collaboration essential components of ethical access.

Similarly, crop genome research, especially involving landraces or wild relatives, sits at the intersection of ABS and global food systems. Many crop genetic resources are governed by additional frameworks such as the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA), which promotes facilitated access alongside multilateral benefit sharing (Frison et al. 2011). However, genomic analyses of these crops, including sequencing and trait discovery, can still raise ABS concerns, particularly when data are used for breeding, commercialization, or intellectual property claims. Ensuring that benefits flow back to farming communities and countries of origin is central to responsible practice.

Part 1 Considerations for Access and Benefit Sharing

Access Considerations

The following access and subsequent benefit sharing considerations are summarized from the **Secretariat of the Convention on Biological Diversity. 2010. *Introduction to Access and Benefit-Sharing*. Montreal: Secretariat of the Convention on Biological Diversity**, in addition to their related online educational resources.

Access and benefit sharing begins with FPIC and mutually agreed terms (MAT), which together define whether genetic resources may be accessed and on what conditions. FPIC is the authorization step: before a researcher collects or uses a genetic resource, the provider country's competent authority, and sometimes other relevant stakeholders, depending on national law, must be provided with sufficient information to make a genuine decision on whether to allow access. MAT is the negotiation step that follows that permission, setting the specific rules for use, transfer, reporting, and benefit sharing. In practice, FPIC establishes legitimacy, while MAT turns that legitimacy into an enforceable set of research conditions. Therefore, for scientists working with biodiversity genomics, ancient eDNA, and crop genomes, access is not merely about obtaining a sample; It also covers the downstream use of sequence data, the circulation of metadata, and the possibility that the work may generate new lines of research, publications, or applications beyond the original project. A well-designed access process begins before sampling or data transfer, with a clear determination of whether the material is covered by ABS rules, who the provider is, and what access measures exist in the relevant jurisdiction. Researchers should not treat access as complete once the sample is in hand. Instead, they should think of it as an ongoing compliance relationship that continues throughout the project.

A practical MAT for genomic research should include a focused set of clauses (Greiber 2012). The first is a scope clause, which defines exactly what is covered: the physical sample, extracted DNA, sequence reads, metadata, and any associated documents or traditional knowledge. The second is a permitted-use clause, which states whether the material may be used only for non-commercial research or also for development, breeding, or other downstream purposes. The third is a data-governance clause, which addresses where data may be stored, whether they may be deposited in public databases, whether access must be controlled, and whether secondary users must accept the same terms. These clauses are especially important in genomics because the research value often lies in the data as much as in the original specimen (see Figure 2 for workflow).

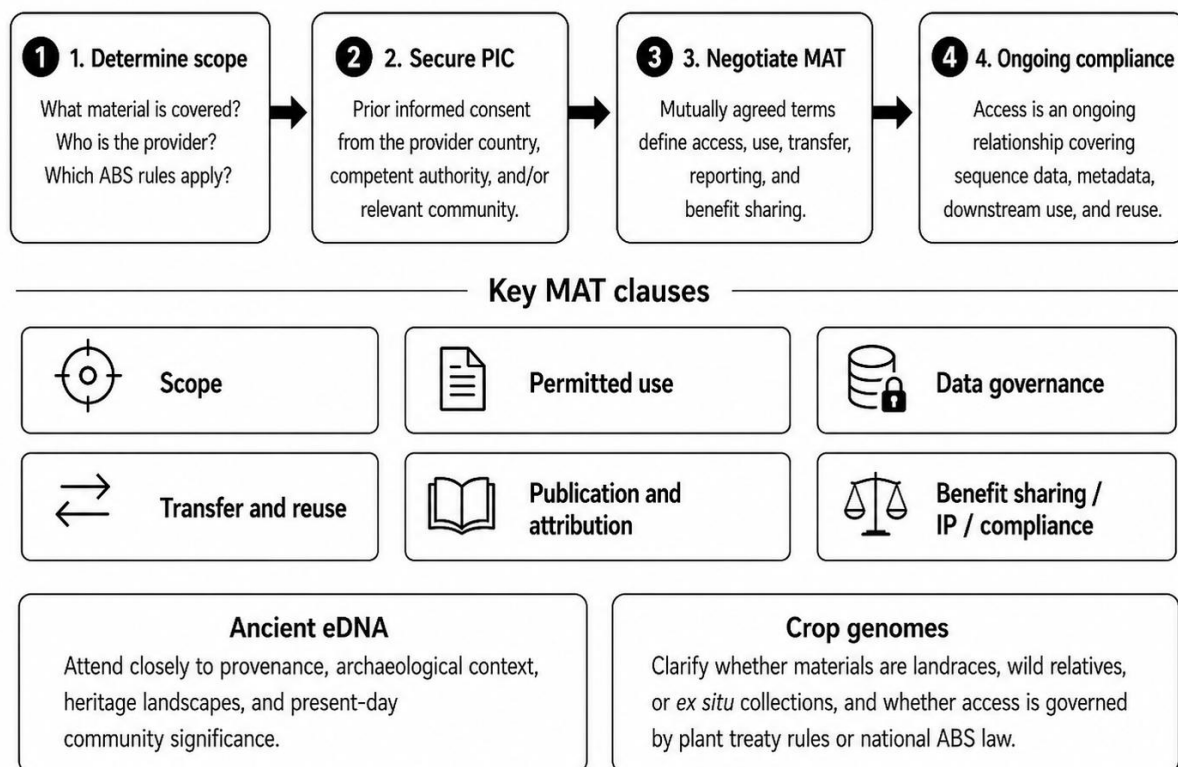


Figure 2. Access considerations for ancient eDNA and crop genomic research. Responsible access begins by determining the legal and material scope of a project, identifying the appropriate provider and governing ABS framework, securing Free Prior and Informed Consent (FPIC), and negotiating mutually agreed terms (MAT). MAT should address permitted uses, data governance, transfer and reuse, publication and attribution, benefit sharing, intellectual property, and compliance. These obligations continue after samples are collected and reused. Ancient eDNA projects require particular attention to provenance, archaeological and heritage contexts, and present-day community relationships, while crop genome projects must clarify whether materials are landraces, wild relatives, or ex situ collections and which national or international access rules apply.

Other MAT clauses should cover transfer and reuse, publication and attribution, benefit sharing, intellectual property, confidentiality, compliance reporting, and termination or destruction. Transfer clauses should require that third parties receive the same restrictions and documentation, while reuse clauses should specify whether future projects require new permission. Publication and attribution clauses should require acknowledgment of the provider country, institution, and collaborators, and in some cases co-authorship or formal review before release. Benefit-sharing clauses should define non-monetary returns such as training, capacity building, equipment, shared methods, data return, or research collaboration, while IP clauses should clarify whether patents or proprietary claims are allowed and under what conditions.

A concise checklist for the access section can be framed as follows (also see Figure 2). First, confirm whether the material falls within the scope of the Nagoya Protocol or another applicable legal regime. Second, identify the provider country, its ABS focal point, and any national access measures. Third, determine whether FPIC is required, and if so, secure the correct authorization before utilization begins. Fourth, negotiate MAT that define permitted use, data sharing, transfer, benefit sharing, and publication rules. Fifth, document permits and retain due diligence records, including any certificate or equivalent reference, for the required period. Sixth, ensure that any downstream transfer or reuse remains within the original terms, or seek amended authorization before proceeding.

For ancient eDNA projects, this access section should be especially careful about provenance and cultural context, because samples may come from archaeological settings, heritage landscapes, or places with present-day community significance. For crop genome studies, the same section should note whether the materials come from landraces, wild relatives, or ex situ collections, and whether access is governed by a plant treaty or by national ABS rules. In both settings, the key message is that access is not a one-time administrative hurdle; it is the legal and ethical entry point for responsible genomic research. It is the legal and ethical entry point for responsible genomic research.

Benefit Sharing Considerations

Benefit sharing is the part of ABS that asks what the providers of genetic resources, local communities, and source countries receive in return for allowing research and use. In the broadest sense, it is meant to make the gains from biodiversity research fairer and more equitable, especially where the original resource, knowledge, or ecosystem came from places that have historically been undercompensated (Grimm et al. 2026). Under the Nagoya framework, benefits can be monetary or non-monetary, and the main idea is that the form of benefit should match the nature of the project, the value created, and the priorities of the provider side.

The benefit-sharing landscape has expanded far beyond simple royalty payments. Monetary benefits can include access fees, up-front payments, milestone payments, royalties, license fees, research funding, joint ventures, and even joint ownership of intellectual property rights (Scholz et al. 2022). These mechanisms are most visible when research leads to commercial products, but they can also appear earlier in the pipeline as part of negotiated support for collection, sequencing, or capacity development. The Cali Fund, a multilateral mechanism for benefit sharing of DSI, is emerging as a principal monetary pathway sponsored by COP, the UN, and UNDP (Orozco and Scholz 2025). In practice, though, many ABS agreements rely more heavily on non-monetary benefits because most genomic projects do not produce immediate commercial returns.

Non-monetary benefit sharing has become the most common and often the most meaningful form of return in biodiversity genomics (Galluzzi et al., n.d.). These benefits include sharing research results, collaboration in research and development, participation in product development, education and training, transfer of knowledge and technology, access to scientific information, and strengthening the capacities of institutions and personnel in provider countries. The Nagoya Protocol also explicitly recognizes institutional capacity-building, human and material resources for administration and enforcement, and access to scientific information as legitimate benefits. For scientists, capacity building is often the most practical and durable benefit. It can include training in field methods, genomics workflows, bioinformatics, curation, and manuscript development; it can also include equipment, reagents, software access, shared datasets, and opportunities for students and early-career researchers (Harden-Davies and Gjerde 2019). In many collaborations, these benefits matter more than cash because they build long-term scientific independence and help ensure that source-country partners are not merely sample providers but full research collaborators (Yua et al. 2022).

In ancient eDNA research, benefit sharing can be more nuanced because the work may involve sediments, archaeological sites, or heritage materials rather than living organisms. Here, benefits may take the form of co-designed research questions, local analytical capacity, training in sampling and sequencing, return of results to museums or heritage institutions, and respectful engagement with communities connected to the site. Where findings have cultural or historical significance, benefit sharing may also include consultation, public communication, and agreements about how results are interpreted and shared. Alternatively, in crop genome research, benefit sharing often connects directly to food security and agricultural resilience. Benefits can include improved breeding materials, shared germplasm information, training for breeders and curators, local participation in trait discovery, and access to tools that support conservation and sustainable use. When research involves landraces, traditional varieties, or farmer-managed diversity, it is especially important that benefit sharing reaches the communities and institutions that have maintained those resources over time.

A useful way to think about the current landscape is that benefit sharing now operates on several levels at once (see layered benefit sharing model below in **“Kalo as an Ancient Crop Genome Case Study”**). There are direct project-level returns, such as payments, training, and shared authorship; institutional returns, such as equipment and infrastructure; and system-level returns, such as conservation funding, policy support, and stronger scientific networks. The best agreements combine several forms rather than relying on a single one, because genomic research often creates value across the full research pipeline rather than at the moment of sample collection. In this sense, benefit sharing is not a discrete endpoint but a continuous process of accountability, requiring researcher involvement from project design through data generation, interpretation, reuse, and long-term stewardship.

The Missing Middle

Benefit sharing is often described as the return that follows access, but in practice it should be understood as an ongoing relationship rather than a one-time payoff. In many biodiversity genomics and ancient eDNA projects, the problem is not only whether benefits are promised, but whether researchers remain engaged long enough for those benefits to be shaped and delivered in ways that matter to provider communities. When benefit sharing is treated as something that happens only after sampling or only after publication, it becomes easy for the relationship to narrow to a transactional exchange rather than a sustained collaboration, which is why the timing of researcher involvement matters. If researchers are present only at the beginning, benefit sharing may be reduced to consultation during project design, with little accountability once samples leave the field or data enter repositories. If they reappear only at the end, the project may have already generated its core value through analysis, modeling, and interpretation, leaving communities with little ability to influence how knowledge was produced or how the benefits are distributed. A more responsible model keeps researchers engaged across the full arc of the project, including sampling, metadata creation, analysis, interpretation, dissemination, and post-project follow-up (Figure 3; Table 1). This model closes the “Missing Middle” gap.

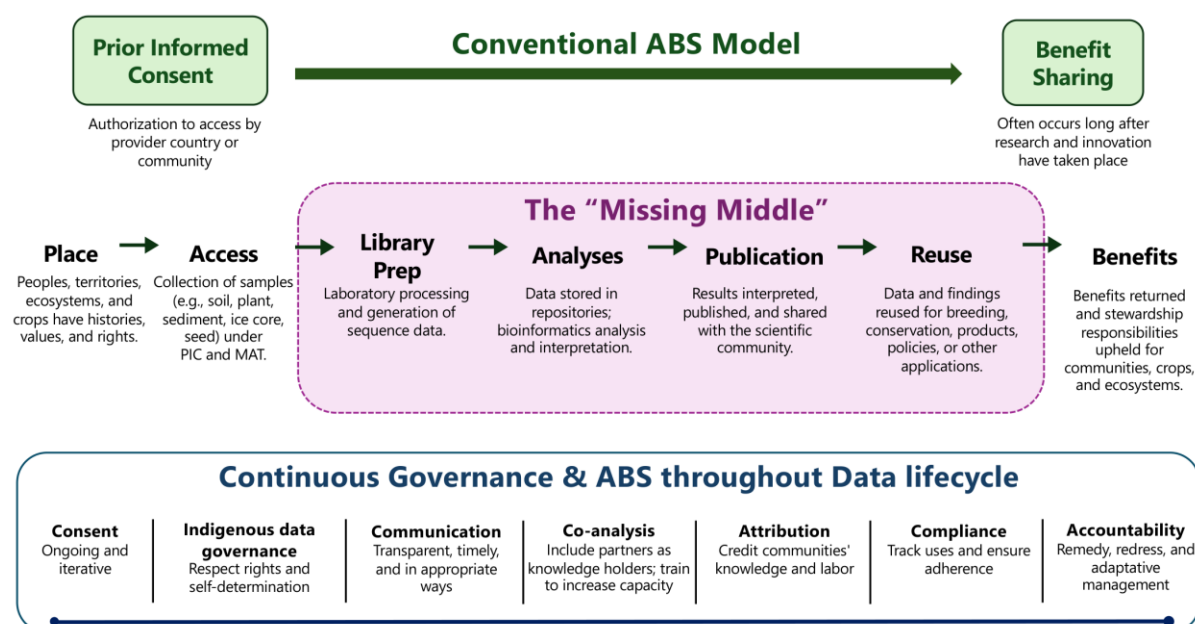


Figure 3. The “missing middle” of access and benefit sharing in genomic research. Conventional ABS models often emphasize Free Prior and Informed Consent (FPIC) at the point of access and benefit sharing at the end of a project. Yet significant scientific and economic value is created between these points as samples are processed, sequence data are generated and analyzed, findings are published, and data are reused. Continuous governance across this lifecycle, including iterative consent, Indigenous data governance, communication, co-analysis, attribution, compliance, and accountability, helps ensure that communities retain meaningful authority and that benefits and stewardship responsibilities are sustained beyond initial access.

Lifecycle step	Typical practice	Governance risk	Better practice
Before sampling	No engagement	Research is framed before community input, turning FPIC into approval of a pre-designed project rather than shared governance.	Relationship-building, Free Prior and Informed Consent (FPIC) as a process
Sampling	Permit or project approval	Consent treated as complete once sampling occurs	Community protocols, sampling plans co-defined
Sequencing	Data generation in lab or service provider	Community loses visibility after material leaves territory	Agreements specify lab handling, storage, destruction/return, and reporting
Metadata	Minimum technical fields	Provenance, people, protocols, and obligations are omitted or flattened	Provenance, cultural authority, Indigenous name & taxonomy, Local Contexts labels/notices, and governance decisions travel with data
Analysis	Researcher-led bioinformatics	Interpretation separated from local knowledge and stewardship	Co-analysis, inclusion of community interests and defined variables, and community review before public claims are made
Repository deposition	Open access default deposition, such as NCBI and BOLD	Unrestricted reuse and loss of traceability	CARE-aligned repositories, controlled access where needed, and community-approved data tiers
Reuse and modeling	Secondary users access data globally	Downstream value is untracked; AI/ML training obscures origin	Persistent identifiers, access logs, benefit-sharing triggers, and post-project monitoring

Table 1. Governance risks and better practices across the genomic data lifecycle. Conventional research practices can narrow community involvement to initial permission and allow authority, provenance, and accountability to weaken as samples become sequence data, metadata, analyses, repository records, and downstream applications. Better practice requires governance to remain active from relationship-building before sampling through reuse and modeling, using iterative FPIC, community-defined protocols, agreements governing material and data handling, culturally meaningful metadata, co-analysis, controlled-access repositories, traceability mechanisms, benefit-sharing triggers, and post-project monitoring.

Part 2 Indigenous Governance and Additional Perspectives

Indigenous Research Data Sovereignty and Governance

The discussion of ABS and whose communities to engage would be incomplete without contextualizing it within Indigenous research and the increasing recognition of Indigenous data sovereignty and governance. Much environmental research is conducted on Indigenous lands and examines the effects of Indigenous management. A good place to start in terms of understanding whose Indigenous lands your work is within is by visiting the following website: <https://native-land.ca/>.

Many Indigenous scholars and community leaders have made clear that research cannot be treated as a neutral act (Smith 2022). Research has often been one of the ways colonial institutions extracted land, biological materials, and knowledge while concentrating authority elsewhere (Tuck & Yang 2014). Reid et al. 2024 argue that ethical ecological research with Indigenous Peoples is not about adding kindness to an extractive model; it requires truth-telling, FPIC, relationships, attention to Indigenous Lands and Waters, and agreements that protect Indigenous intellectual property and authority. Ermine's concept of ethical space is also useful here because ancient eDNA governance requires more than institutional compliance; it requires an agreed space where different legal orders, knowledge systems, and responsibilities can meet without one simply absorbing the other (Ermine 2007). Indigenous research methodologies also push against the assumption that community engagement is just one step in a protocol. Relationships, accountability, consent, and benefit are part of the methodology itself (S. Wilson 2008).

Alongside global and centralized governance interventions, there has been a growing movement of Indigenous Data Sovereignty (IDSov) within Indigenous communities globally to honor and uphold the sovereignty of Indigenous Peoples whose lands, bodies, and relatives are often the source of biological samples and environmental data (Kukutai and Taylor 2016). IDSov is rooted in Indigenous Peoples' inherent rights to self-determination and is concerned with the recognition of Indigenous Peoples' rights and interests in data, including greater control over the collection, ownership, access, use, reuse, and application of data connected to their peoples, territories, lifeways, and resources (Lovett et al. 2019). Indigenous data governance is the set of mechanisms, protocols, and practices through which communities exercise that control and move toward IDSov in practice (Figure 4) (Carroll et al. 2019). In this way, IDSov is not simply about data access or data ownership in a narrow technical sense; it is about authority, responsibility, and the ability of Indigenous communities to govern how data derived from their lands and relations moves through research infrastructures.



Figure 4. Relationship between Indigenous Data Sovereignty and Indigenous data governance. Indigenous Data Sovereignty refers to the inherent right and authority of Indigenous Peoples to govern data connected to their peoples, territories, lifeways, and resources. Indigenous data governance is the set of mechanisms, protocols, institutions, and practices through which communities exercise that authority across the data lifecycle, including decisions about data collection, access, storage, interpretation, sharing, reuse, and application. Governance therefore provides the practical means through which Indigenous Data Sovereignty is enacted, rather than serving as a substitute for the underlying right to self-determination.

IDsov concerns are particularly urgent in biodiversity genomics and ancient eDNA, where data can be generated at large scales from Indigenous lands and waters and then circulated far beyond the original sampling context. Over the past five years, Indigenous scholars and collaborators have increasingly pushed biodiversity genomics and eDNA fields to grapple with IDsov across the data lifecycle. For example, McCartney et al. 2022 argue that Indigenous Peoples and local communities must be treated as partners in global biodiversity sequencing, not simply as sample providers, and that trustworthy partnerships require attention to samples, data, Traditional Knowledge, and community protocols across the lifecycle of biodiversity genomics. Hudson et al. 2023 similarly frame Indigenous Peoples' rights in genomics data as part of broader Indigenous research sovereignty, emphasizing that research systems must support Indigenous control over data and downstream activities. In Hutchins et al. 2025 on arthropod metabarcoding in Hawai'i, this point is especially important because the novelty, scalability, and potential covertness of eDNA and metabarcoding mean that a single environmental or bulk sample can reveal ecological relationships, species presence, and community knowledge that may not have been explicitly consented to as "data".

More recent work on eDNA in Aotearoa pushes this further by moving from principles to infrastructure. Adams et al. 2026 propose an Indigenously designed ecosystem for eDNA research and application that includes culturally appropriate data storage and analysis, Indigenous governance frameworks, and researcher- and institution-level certification for working with Māori communities and eDNA-derived information. This is an important shift because it recognizes that IDsov cannot depend only on individual researcher ethics. It has to be built into repositories, compute environments, consent processes, and institutional training.

For eDNA and biodiversity genomics, IDSov offers a way to govern the “missing middle” between access and benefit sharing.

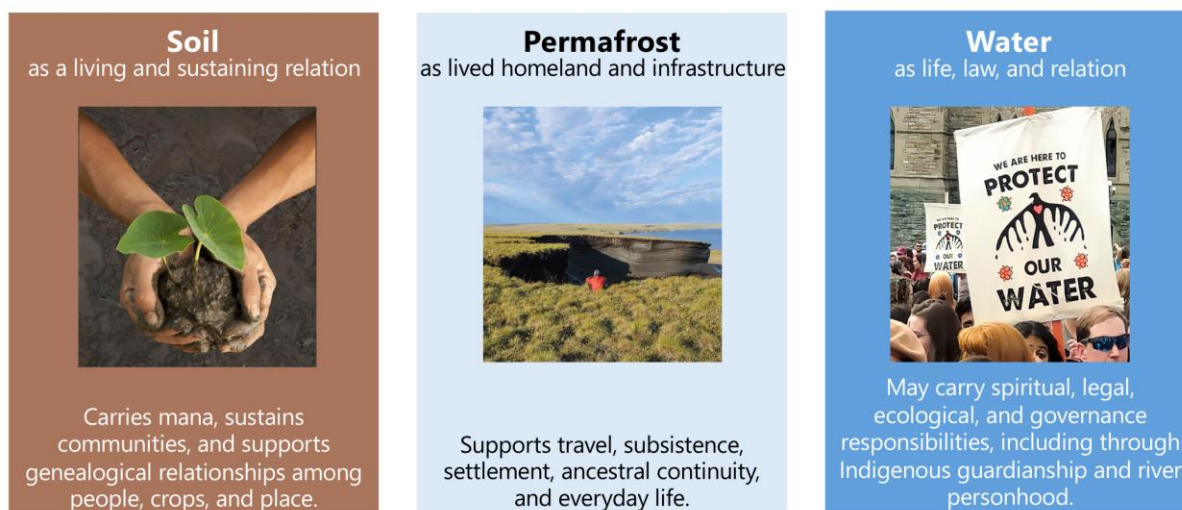
More than Just Substrate

One of the primary components of honoring Indigenous data sovereignty is understanding the biocultural context of the landscape and specific organisms or substrates in which you are working (Mc Cartney et al. 2023). In Indigenous studies, the concept of “two-eyed seeing” can apply here, where you understand an object, a landscape, or an environmental process through Indigenous and Western sciences and epistemologies (Wright et al. 2019). Indigenous science is the transmission of environmental knowledge through generations in Indigenous communities (Kimmerer 2002). Western science is a system of knowledge based on the scientific method, originating in Western Europe (Ramos 2018). Here, I provide an Indigenous epistemological view on ancient eDNA and the common ancient eDNA substrates used in the field.

Ancient eDNA is often described as a minimally invasive method, and therefore culturally sensitive, because it can detect organisms from soil, water, and other environmental media without trapping, collecting, or killing them (Ramos 2018). However, from an Indigenous perspective, “minimally invasive” cannot only mean less physical disturbance. A cup of water, a scoop of soil, or a permafrost core can still carry information about relatives, homelands, food systems, medicines, ancestors, and places governed by community protocols, which is why ancient eDNA has a double-edged cultural significance. On one hand, it can support Indigenous stewardship by helping communities monitor waters, track invasive organisms, document ecosystem change, and care for places in ways that align with community priorities. On the other hand, it can extract sensitive ecological and cultural knowledge without the same direct encounter that would normally trigger consent or protocol (Adams et al. 2026). Therefore, environmental samples should not just be treated as empty substrates; they are part of living homelands and collecting them means entering relationships that already have histories, obligations, and caretakers.

The relationality of ancient eDNA is clear in soil-based examples. In Aotearoa New Zealand, the idea that humans originate from and return to the earth reflects whakapapa, or genealogical connection between people and the living world (Henare 2015). In Hawai‘i and Aotearoa, soil is also understood as having mauri and wairua, and therefore its own mana that must be guarded through stewardship rather than extraction (Henare 2015; Handy 1940). These framings resist the reduction of soil to a neutral substrate and instead place it within a moral and relational order (Figure 5).

Permafrost raises similar concerns. In the Mackenzie Delta and other Arctic regions, Indigenous knowledge holders describe permafrost not simply as frozen ground, but as critical and alimentary infrastructure: a web of relations that supports mobility, subsistence, and cultural continuity (Figure 5) (Datta et al. 2026). From that perspective, thaw is not only a biophysical process but also a disruption of the relations that sustain communities, food systems, travel routes, and responsibilities to place (Gartler and Crate 2025).



Embedded within broader systems of kinship, story, spirituality, and responsibility

Figure 5. Environmental materials sampled for ancient eDNA are not neutral substrates but are embedded within distinct Indigenous homelands, relationships, and systems of responsibility. In Hawai‘i, Kānaka ‘Ōiwi relationships with soil and ‘āina emphasize nourishment, mana (power), genealogy, cultivation, and reciprocal care among people and place. In the Mackenzie Delta and other Arctic Indigenous homelands, permafrost is understood not only as frozen ground but as lived and alimentary infrastructure that supports travel, subsistence, settlement, ancestral continuity, and everyday life. In Indigenous water-governance contexts, including Māori relationships with the Whanganui River in Aotearoa and the responsibilities of Indigenous nations within the Klamath Basin, water may be understood as a living relation carrying spiritual, ecological, legal, and governance obligations. These examples illustrate how ancient eDNA sampling can enter existing systems of kinship, law, and spirituality that extend beyond conventional scientific permitting. They are place-specific and should not be interpreted as representing a single or universal Indigenous understanding of land and water.

Water creates another set of obligations, especially where rivers are treated as rights-bearing or personhood-bearing entities. Examples such as the Whanganui, Atrato, Magpie, and Klamath show that rivers may have guardians, legal standing, or Indigenous governance structures that require more than standard permitting (Kramm 2020). In those settings, ancient eDNA sampling can capture culturally significant species, invasive species, endangered species, pathogens, and other sensitive ecological relations. Governance may therefore need to include consent, sampling locations, data storage, sequence reuse, database deposition, geolocation masking, benefit sharing, and return of results, all shaped by the relevant legal and Indigenous authorities. Canadian water governance offers a similar lesson. Recent water management agreements in the North explicitly incorporate Indigenous and local knowledge into monitoring and decision-making (Milián-García et al. 2026). First Nations perspectives also emphasize water as a living relation with spirit, responsibility, and law, rather than as an object of extraction (Figure 5) (N. J. Wilson and Inkster 2018). Applied to ancient eDNA, this means that water sampling is never only technical; it is part of a broader relationship of stewardship, accountability, and shared responsibility to place.

Human Bycatch

Ancient eDNA research also raises concerns about human bycatch, or the incidental capture of human genetic material in samples collected for biodiversity monitoring (Whitmore et al. 2023). Water, soil, air, and surface samples can contain traces of human DNA shed through skin, hair, saliva, wastewater, or other bodily materials. Therefore, studies designed to detect fish, insects, plants, or microbes may also collect information from the people who live, work, harvest, or conduct ceremony in those places. This is especially important in Indigenous territories, where ancient eDNA sampling can unintentionally transform lands and waters into sources of human biological data without consent. Human bycatch therefore expands the ethical stakes of ancient eDNA beyond species detection: it raises questions about privacy and consent, and whether environmental samples should be treated as containing potentially sensitive human and community data (De Groot 2023). In practice, that means researchers need to think carefully about how samples are processed, what kinds of human traces might be retained in sequencing outputs, and whether those traces could be linked back to identifiable people, families, or communities. It also means that data management plans should address whether human-derived information will be filtered, masked, destroyed, or governed under additional restrictions before any release or reuse (Bartholomeeusen et al. 2026).

Complicating Ancientness

With the report's focus on ancient eDNA, it is pertinent to be clear about the totality of what "ancient" means, especially across scientific fields and even within Indigenous epistemologies. The context provides a nuanced understanding of the timelines in which ancient eDNA research is conducted, whose timeline is being centered, and ways to navigate the layers of ancientness.

Ancientness is relational rather than absolute. In molecular biology, a century-old museum specimen may be ancient because its DNA is fragmented, chemically modified, and contamination-prone. In paleogenomics, "ancient" often refers to archaeological or paleontological remains thousands to hundreds of thousands of years old, with rare exceptional DNA records extending into million-year timescales under cold, stable conditions (Dalén et al. 2023). In paleoproteomics and biomarker studies, the temporal horizon can extend much further because some proteins and lipids persist beyond the practical survival window of DNA (Cappellini et al. 2018). As the accompanying table shows (Table 2), what counts as ancient depends on the target molecule, the sampled material, the preservation environment, and the conventions of the research community.

The meaning of ancient also shifts according to what evidence researchers hope to recover. DNA generally provides relatively fine-grained genomic information, but it has a limited survival horizon and becomes increasingly fragmented over time. Proteins, particularly those preserved in enamel, may survive for millions of years, although they typically provide less genomic and taxonomic resolution. Lipids and other biomarkers may persist even longer and can reveal broad information about organisms, environments, diets, or ecological processes without preserving an intact genome (Summons et al. 2022). Fossils, pollen, spores, phytoliths, and other morphological traces can extend the record further still, but they represent different

forms of biological evidence and support different kinds of inference (Zargar et al. 2025). “Ancient,” then, does not describe a single archive. It names a collection of partially overlapping molecular, material, and disciplinary archives, each with different temporal limits and interpretive possibilities.

The concept of ancientness may also operate differently within Indigenous knowledge systems, although no single Indigenous understanding of time should be presumed. Western scientific classifications often position the ancient past as a distant period separated from the present by chronological time. Many Indigenous temporalities, by contrast, emphasize continuity among ancestors, present-day communities, lands, other-than-human relations, and future generations (Killsback 2013). The past may remain present through genealogy, oral histories, place-based knowledge, ceremony, cultivation, and continuing responsibilities. For example, within Kānaka ‘Ōiwi (Native Hawaiian) scholarship, *ka wā mamua* describes the past as “the time in front”: that which is known and can guide movement into a future that cannot yet be seen (Wilson-Hokowhitu 2019). Mo‘okū‘auhau (genealogy) similarly connects people, places, events, and kin across time rather than consigning ancestors to a completed historical period. Within these frameworks, temporal depth may strengthen rather than weaken a relationship.

From these perspectives, describing something as ancient does not necessarily mean that it is inert or no longer governed by living relationships. Ancestors and ancestral practices may continue to participate in contemporary life, while present generations understand themselves as carrying responsibilities inherited from those who came before and owed to those who will follow. Indigenous oral traditions may also function as intergenerational records of history, ecological change, and relationships to place rather than simply as stories about a vanished past. Scientific language that places materials in “prehistory” or “deep time” can therefore create a form of temporal distancing, making Indigenous peoples appear external to their own histories or suggesting that old materials have become culturally unclaimed. Indigenous approaches to deep histories instead emphasize the ongoing, intimate, and living relationships that communities may maintain with ancient places, beings, materials, and events.

These differences in how temporal relationships are understood also have ethical and governance consequences. Labels such as “ancient,” “archaeological,” or “prehistoric” can create the impression that sampled materials belong to a remote and socially disconnected past. Yet old sediments, crop remains, animal bones, or environmental traces may remain connected to living peoples, territories, food systems, ancestors, and cultural histories. Temporal distance does not dissolve these relationships and, within some Indigenous frameworks, may deepen the responsibilities attached to them. A centuries-old museum specimen may have been collected from Indigenous lands under colonial conditions, while a millennia-old crop genome may reveal histories of selection, movement, and stewardship that continue to matter to present-day farming communities. The report’s broader concern with access, benefit sharing, and Indigenous data governance therefore cannot begin only after researchers decide that a sample is sufficiently recent to have identifiable stakeholders.

FIELD / SAMPLE COMMUNITY	APPROXIMATE AGE RANGES	MAIN REASON THE LIMIT DIFFERS
Fresh-Tissue Molecular Biology	ANCIENT: Days to years if mishandled; decades if archived USEFUL: Fresh to about 10 years; longer if frozen EXTREME: Decades in ultracold or well-preserved archives	The baseline is high-quality DNA/RNA. “Ancient” often means degraded relative to fresh, high-molecular-weight material.
Museum Genomics / Museomics: Animals, Insects, Birds, Mammals	ANCIENT: About 50–200+ years USEFUL: 19th- and 20th-century specimens EXTREME: A few hundred years, sometimes older	Drying, heat, formalin, fumigants, and storage histories can fragment or chemically damage DNA. A century-old pinned insect can behave like ancient DNA.
Herbarium / Plant Museum Specimens	ANCIENT: About 50–250+ years USEFUL: 100–300 years EXTREME: Several centuries in some cases	Drying can help preservation, but heat drying, chemicals, and storage matter. Plant secondary compounds can also complicate extraction.
Fungal Collections / Mycological Specimens	ANCIENT: Decades to centuries USEFUL: 50–200 years EXTREME: Several hundred years for dried fruiting bodies or preserved collections	Fungal tissues can degrade quickly and may be colonized by other microbes. Spores, sclerotia, and dried specimens may preserve differently from soft tissues.
Palaeomycology / Ancient Fungal DNA From Sediments	ANCIENT: Hundreds to thousands of years USEFUL: 1,000–50,000 years EXTREME: Tens of thousands of years, especially lake sediments or permafrost	Sediments can preserve short fungal DNA fragments. Signals are mixed-community and context-dependent.
Archaeological Plant, Animal, And Microbial DNA	ANCIENT: Hundreds to thousands of years USEFUL: 1,000–50,000 years EXTREME: 100,000+ years in cold, dry, or stable contexts	Archaeological DNA is usually low-copy and fragmented. Wet, warm, acidic, or charred contexts are much harder.
Human Ancient DNA	ANCIENT: Usually more than 100–500 years, but context-dependent USEFUL: 1,000–50,000 years EXTREME: Hundreds of thousands of years in exceptional material	Teeth and petrous bones often preserve better than other tissues. Ethical and governance issues strongly shape what should be sampled.
Non-Human Ancient DNA: Bones, Teeth, Permafrost Animals	ANCIENT: Thousands of years USEFUL: 10,000–100,000 years EXTREME: 1 million+ years in very cold settings	Cold, dry, stable environments slow DNA degradation. Warm and wet environments sharply reduce survival.
Sedimentary Ancient DNA / Ancient eDNA	ANCIENT: Hundreds to thousands of years USEFUL: 1,000–100,000 years EXTREME: Up to million-year scales in exceptional sediments	DNA can bind to minerals and persist as short fragments. Interpretation is harder because eDNA is mixed, mobile, and contamination-prone.

FIELD / SAMPLE COMMUNITY	APPROXIMATE AGE RANGES	MAIN REASON THE LIMIT DIFFERS
Pollen, Spores, Phytoliths, Starch Grains	ANCIENT: Hundreds to thousands of years USEFUL: 1,000–100,000+ years EXTREME: Hundreds of thousands to millions of years for morphology	These records often preserve structures rather than recoverable DNA. They can outlast DNA but usually provide broader taxonomic resolution.
Ancient Proteins / Paleoproteomics	ANCIENT: Thousands to millions of years USEFUL: 10,000–1 million years EXTREME: 10–20+ million years for enamel proteins in exceptional cases	Proteins, especially enamel proteins, can survive longer than DNA, though taxonomic and genomic resolution differs.
Lipids / Biomarkers / Ancient Organic Molecules	ANCIENT: Thousands to millions of years USEFUL: 1,000–100,000+ years EXTREME: Millions of years, sometimes older	Some lipids and biomarkers are chemically more stable than DNA. They often provide ecological or broad taxonomic signals rather than whole genomes.
Paleontology / Fossils Without Biomolecules	ANCIENT: Thousands to millions of years USEFUL: 10,000 to 100+ million years EXTREME: Hundreds of millions to billions of years	Paleontological ancientness often means mineralized remains, traces, or morphology, not recoverable DNA.

Table 2. How “ancient” varies across fields, materials, and molecular archives. What counts as ancient depends on the research community, the type of biological evidence being studied, and the conditions under which it was preserved. Museum specimens may be treated as ancient after only decades or centuries when DNA is highly degraded, while DNA from cold and stable environments may persist for hundreds of thousands or, in exceptional cases, more than a million years. Proteins, lipids, fossils, pollen, and other material traces can extend the recoverable record further, but support different levels of biological and taxonomic inference. The ranges shown are approximate and illustrate that ancientness is relational rather than a single chronological threshold.

Part 3 Application to Ancient Crop Genomes

With considerations for access and benefit sharing, Indigenous governance and epistemologies, and the concept of ancientness fully explored with ancient eDNA, we will now apply that to the ancient crop genome questions associated with AEGIS. First, we explore how benefit sharing often needs to be layered based on crop type, the crop's biocultural and socio-political context, the type of research being done, and how many communities and stakeholders are a part of the crop's history. We will specifically explore this by investigating taro as a global commodity versus kalo (taro in the Hawaiian language) as a cherished relative and heritage crop in Hawai'i. Second, we will extend this example of taro versus kalo to the common crops in which AEGIS engages: rice, wheat, and barley. Lastly, we briefly discuss the ethics associated with utilizing genome modification to circumvent global agricultural issues.

Kalo as an Ancient Crop Genome Case Study

Benefit sharing becomes more complicated when the crop in question is not rare, localized, or newly discovered, but is instead a commercially circulating resource that already moves through global markets, breeding systems, genomic databases, and supply chains. In those cases, researchers' responsibility cannot be limited to a single host community or project partner because the underlying genetic resource may circulate and generate value across many sites and institutions. Broad benefits may accrue to the particular people, farms, institutions, or communities directly involved in the research, while longer-term benefit sharing may require more distributed mechanisms capable of returning value across the wider systems that contribute to crop conservation, breeding, and use. This is where the logic of multilateral or pooled models becomes important. For example, the Cali Fund creates a global mechanism through which commercial users of digital sequence information can contribute to biodiversity-related benefit sharing, including support for Indigenous Peoples and local communities (Orozco and Scholz 2025). For widely circulating commercial crops, benefit sharing therefore does not have to stop with bilateral arrangements involving one project partner or one provider group. It can also operate through broader mechanisms that recognize that genetic and commercial value is often cumulative, produced through generations of cultivation and stewardship and then further developed through breeding programs, research institutions, and private industry (Greiber 2012).

Taro, however, demonstrates why commercial circulation cannot be treated as the only basis for determining responsibility. Taro is cultivated and sold globally, but in Hawai'i it is known as kalo: a Kānaka 'Ōiwi heritage crop with deep genealogical and cultural significance. In Hawaiian genealogical traditions, kalo is not simply a plant resource but an elder relation (Aikau and Camvel 2016). Its presence in supermarkets, international breeding programs, or genomic databases does not transform it into a culturally unencumbered commodity. Nor does the availability of taro varieties elsewhere erase the particular responsibilities tied to Hawaiian 'ike, stewardship, and the intergenerational relationships through which kalo has been maintained.

The diversity of Hawaiian kalo itself reflects this history of care and innovation. ‘Ōiwi farmers developed around 300 named varieties through generations of selection, cultivation, exchange, and adaptation to particular soils, water systems, and elevations (Kagawa-Viviani et al. 2018). This diversity should not be understood as simply “natural” variation waiting to be discovered by contemporary genomics. It is also the material outcome of Indigenous agricultural knowledge and labor. An ancient kalo genome may therefore contain evidence not only of plant movement and biological adaptation, but also of deliberate human selection and the accumulated innovations of generations of Hawaiian farmers (Jonathan Goldberg-Hiller and Noenoe K. Silva 2015).

With kalo, commercial circulation also cannot be separated from the history of research and institutional power. Discussions of benefit sharing must reckon with past controversies surrounding genetic engineering and claims of ownership over taro varieties at the University of Hawai‘i. Those disputes raised questions about cultural violation, institutional authority over living heritage, and the right of Kānaka ‘Ōiwi communities to determine what kinds of alteration, ownership, or commercialization are appropriate for kalo (Gugganig 2019). In this context, benefit sharing is not only a question of distributing future gains, but also whether the research relationship avoids repeating earlier forms of extraction (Hudson et al. 2019).

For heritage crops such as kalo, benefit sharing should be layered (Figure 6). At the project level, benefits should accrue directly to the growers, communities, cultural practitioners, repositories, or stewardship groups whose materials, lands, knowledge, or labor make the research possible. These benefits might include co-designed research questions, access to results, co-authorship, training, equipment, support for variety conservation, restoration of lo‘i (traditional taro pondfields) and agricultural infrastructure, or other returns defined by the communities themselves. Such benefits should not be treated as compensation for access alone; they should reflect continuing participation in how samples are analyzed, how genomic histories are interpreted, and how findings are communicated and reused.

A second layer concerns the wider community of stewardship (Figure 6). A project may obtain a sample from one farm or collection, but the variety itself may carry the labor of many generations and may remain culturally connected to communities beyond the immediate provider. The institution holding a specimen is not necessarily the sole source of authority over it. Researchers may therefore need to distinguish between the party legally able to provide access and the broader peoples or lineages whose relationships and knowledge are embodied in the crop. This is particularly important for historical and museum specimens, where institutional custody may be the result of earlier collection practices rather than evidence of exclusive ownership.

A third layer concerns the broader commercial and scientific ecosystem (Figure 6). Since taro circulates globally and may generate value through genomic research, breeding, biotechnology, or product development, multilateral benefit-sharing mechanisms may also be appropriate. These broader mechanisms can complement, but should not replace, the direct responsibilities owed to Hawaiian communities. A pooled contribution to biodiversity conservation does not resolve obligations arising from work with a culturally significant

Hawaiian variety, just as a bilateral agreement with one farm does not address all the value that may later be generated through global commercial reuse.

The deeper point is that commercial circulation and cultural significance are not opposites. A crop can be globally traded while remaining a sacred, ancestral, and political relation in a particular place. For that reason, benefit sharing for kalo should not be reduced either to a purely commercial logic or to a narrowly localized one. It must distinguish among immediate responsibilities to project partners, enduring responsibilities to the Hawaiian communities and lineages that have created and maintained kalo diversity, and broader responsibilities arising when genomic resources produce value across international research and commercial systems.

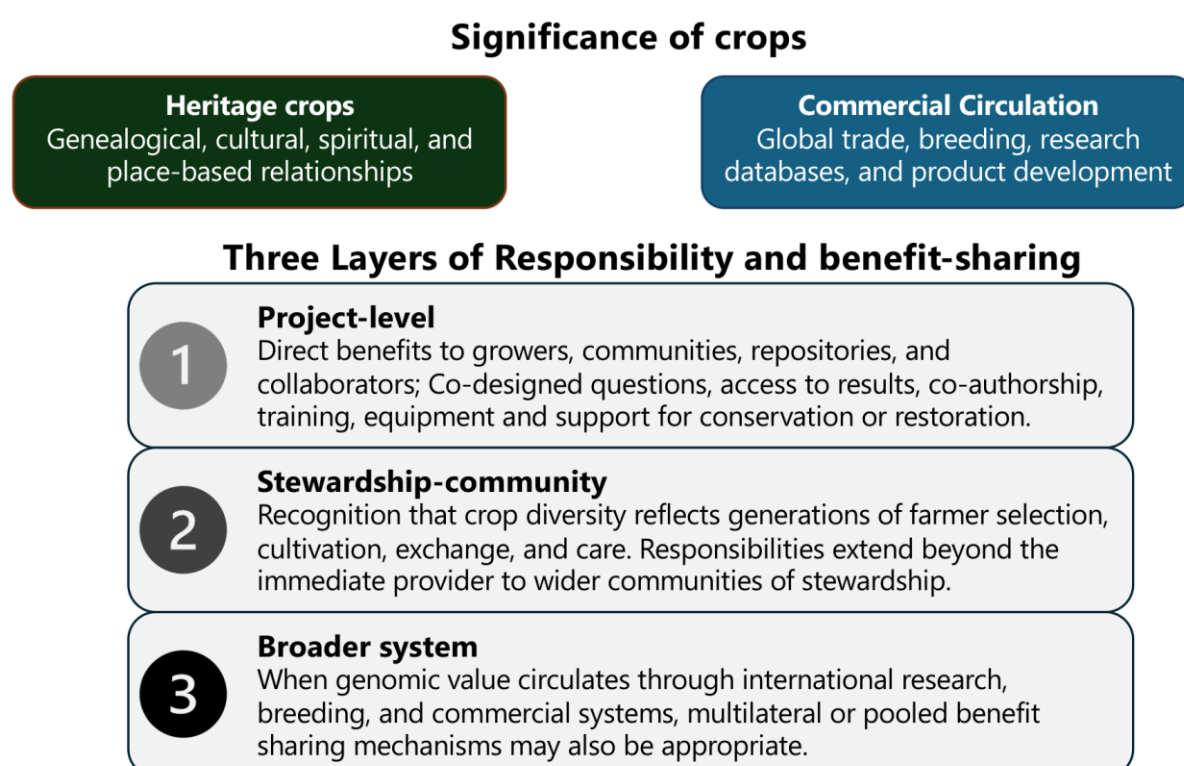


Figure 6. Layered benefit sharing for heritage and commercial crop genomics. Crops such as taro, barley, rice, and wheat may circulate through global markets, breeding programs, research institutions, and genomic databases while also remaining embedded in genealogical, cultural, spiritual, and place-based relationships. Responsible benefit sharing should therefore operate at multiple levels: direct returns to project partners and sample providers; recognition of the wider communities whose generations of selection, cultivation, exchange, and care produced crop diversity; and broader multilateral or pooled mechanisms where genomic value circulates through international scientific and commercial systems. These layers are complementary rather than interchangeable.

Extending the Framework to Barley Rice and Wheat

The same layered approach to benefit sharing applies to the ancient crop genomes that AEGIS is investigating, including barley, wheat, and rice. AEGIS proposes to identify ancient genetic variants and introduce promising variants into modern crops to improve resilience. Yet these crops are not only globally traded commodities or biological resources. Their genomes also contain the accumulated effects of domestication, farmer selection, migration, exchange, and adaptation across thousands of years.

Barley is a particularly useful example because its domestication history appears geographically complex. Its earliest and most widely accepted domestication occurred in the Fertile Crescent approximately 10,000 years ago (Badr et al. 2000), but genomic research has also identified distinctive relationships among cultivated barley and wild barley from the Tibetan Plateau (Saisho and Purugganan 2007). Some studies have interpreted this diversity as evidence that Tibet was an additional domestication center, or that cultivated barley had polyphyletic origins. Other genomic analyses instead conclude that Tibetan hulless barley, or qingke, arrived through eastward dispersal and was subsequently shaped by strong local selection (Zeng et al. 2018).

This disagreement is itself important. Ancient genomics may change which regions and farming communities are understood as contributors to crop domestication and diversification. Even where the Tibetan Plateau is not ultimately classified as an independent center of barley domestication, generations of Tibetan farmers transformed introduced barley into locally adapted hulless forms capable of supporting agriculture under high-altitude, cold, and drought-prone conditions. The relevant contribution is therefore not limited to the initial moment of domestication. It also includes the long processes of selection, cultivation, and knowledge through which crops became adapted to particular cultural and environmental landscapes.

Rice raises similar questions at an even broader geographic scale. Asian rice has a complex domestication history involving divergent japonica and indica populations (Jing et al. 2023), while African rice represents a separate domesticated species with its own history of farmer innovation (Sweeney and McCouch 2007). Scientific debate continues over whether the major Asian rice groups emerged through independent domestication, shared domestication genes moving among populations, or some combination of domestication and later introgression (Choi et al. 2017). Ancient variants recovered from rice should not be treated as placeless genetic solutions. They may be connected to distinct histories of cultivation, irrigation, selection, and stewardship across East, South, and Southeast Asia or Africa.

Wheat likewise originated through domestication processes in the Fertile Crescent beginning roughly 10,000 years ago (Faris 2014), but wheat encompasses multiple species and genomic lineages whose histories include hybridization, farmer selection, and dispersal into new environments. Research increasingly complicates any simple account of a single crop emerging from a single point of origin (Levy and Feldman 2022); for some wheat groups, evidence supports a more geographically distributed and reticulated domestication process within the broader Fertile Crescent (Zeder 2025).

For AEGIS, these histories complicate the identification of the appropriate provider or beneficiary of an ancient genetic variant. The sediment or archaeological material may come from one country, the variant may reflect cultivation across several regions, and its adaptive value may have been produced through generations of farmer selection before entering modern collections or breeding programs. Legal access may be granted by the institution or country holding the sample, but that does not necessarily capture all the communities whose agricultural knowledge and labor contributed to the trait.

Benefit sharing for barley, rice, and wheat should therefore operate at several levels. Direct benefits are owed to the institutions, farmers, and communities participating in sampling and research. Broader regional benefits may be appropriate where a variant is connected to a historically important center of crop diversification or adaptation (Figure 6). Multilateral mechanisms may also be necessary when crops and genomic information have circulated too broadly for their value to be attributed to one provider alone. As with *kalo*, these levels should complement rather than replace one another.

The central question is not only where a crop was first domesticated, but where, how, and by whom its useful diversity was produced. Ancient crop genomes may reveal variants associated with drought, cold, disease resistance, or other desirable traits, but those variants are often the biological record of long-standing agricultural relationships. Recognizing that history shifts the framing from the scientific “discovery” of useful ancient variation toward acknowledgment of the peoples and farming systems that helped create and sustain it.

The Ethics of Circumvention

The recovery and modification of ancient crop genetic variants is often framed as a technological solution to food insecurity and environmental change. Yet many critiques of biotechnology caution that these interventions can leave the underlying causes of the crisis untouched. Contemporary food insecurity is not simply the result of inadequate yields or insufficient genetic diversity. It is also produced through colonization, dispossession, unequal access to land and water, and an agricultural industrial complex that concentrates control over seeds, production, and distribution (Sommerville et al. 2014; Lappé et al. 1998; Patel 2013). A thorough ethical analysis must therefore ask whether ancient crop genome modification addresses the problem or merely temporarily alleviates some of its effects while reproducing the same system that created them. A crop engineered for drought tolerance or higher yield may be useful, but those traits do not by themselves determine who controls the seed, who can afford to grow it, who has access to land, or who receives the resulting food. The central problem may not always be yield, but access, governance, and distribution.

How food is grown also matters. Treating ancient genetic diversity as a technical resource can separate crop resilience from the farming systems, relationships, and Indigenous knowledge through which that diversity was originally developed and maintained (Holt-Giménez and Altieri 2012). Ancient variants should therefore not be understood as standalone fixes. Their value depends on whether they support more equitable access, ecologically responsible cultivation, farmer autonomy, and the restoration of the social and agricultural relationships that industrial food systems have disrupted.

Conclusions

Ancient eDNA and crop genomics make it possible to recover biological information across extraordinary temporal scales, but temporal distance does not eliminate contemporary responsibility. The central challenge is not simply determining whether a sample is legally accessible or identifying a benefit that can be returned at the end of a project. It is building forms of governance that remain active as materials become data, data become scientific and commercial value, and that value circulates through institutions, databases, breeding programs, and industries. This requires layered benefit sharing, sustained researcher accountability, recognition of Indigenous and farmer innovation, and meaningful authority for communities connected to the lands, waters, crops, and histories being studied. For projects seeking ancient variants as solutions to present-day environmental and food-system crises, the ethical question is therefore not only whether those variants can be recovered and used, but whether their use supports equitable governance, farmer and community autonomy, ecological responsibility, and the restoration of relationships that extractive research and industrial agriculture have often disrupted.

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