Engaging European Local Communities in Biodiversity Genomics Research: A Five-Step Framework for Scientists

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Abstract

Societally relevant applications of genomic science to understanding biodiversity depend on sustained and equitable engagement with Local Communities that supports ethical practice, builds a richer knowledge base, and guides sustainable conservation decisions. Pairing genomic sequencing data with long-held local ecological knowledge offers unique opportunities to gain insights into species biology within lived landscapes. However, meaningful participation of Local Communities and integration of community-held knowledge in genomics-informed research practices remains limited, likely hindered by inadequate engagement training and a lack of researcher incentives. Establishing an engagement framework is therefore essential to align collaboration norms, embed a two-way dialogue, and safeguard fair benefit-sharing between scientists and community representatives. Here, we outline participatory principles throughout the biodiversity genomics project lifecycle from a European perspective, from early sampling design to data interpretation, dissemination, and subsequent policy dialogue. Based on this we develop an engagement framework, adoption of which will strengthen data interpretability, elevate scientific and social legitimacy, while empowering communities to co-design management strategies grounded in both contemporary genomics and generational lived experience. By synthesising engagement drivers, pinpointing obstacles, and distilling lessons from a practical example, we present a five-step framework adaptable to varied cultural and ecological settings. We call on researchers, funders, and community leaders to take up and refine this framework, ensuring local voices shape and benefit from the accumulating genomic knowledge that will direct future conservation actions.

Keywords

biodiversity conservation, community engagement, equitable research, knowledge co-creation, local ecological knowledge, participatory genomics, stakeholder communities

Introduction

Bringing together diverse knowledge holders is increasingly recognised as an ethical responsibility and practical necessity to increase the scope and societal relevance of science (Norström et al., 2020; O'Brien et al., 2025). The rationale for engaging Local Communities as knowledge holders with important contextual expertise comes from evidence that participatory models enhance research legitimacy and outcomes (Satterthwaite et al., 2024; Snapp et al., 2023; Tengö et al., 2017; Wedemeyer-Strombel et al., 2019). Such Local Communities traditionally interact and/or work with and/or live in close association with nature, often maintaining intergenerational connections to a place. Examples could comprise members of fishing, farming, or forestry communities, as well as nature appreciation groups such as hiking, hunting, or bird-watching associations. Others might be less formally organised, connected through the value they hold of a locality such as residents of the neighbourhood surrounding a city park. As a result of their relationships with natural environments, Local Communities accumulate Local Ecological Knowledge (LEK) that is extremely valuable for interpreting species ecology and ecosystem change (Charnley et al., 2007; Emard et al., 2024). Yet, knowledge co-production remains patchy and rare, and many researchers still approach Local Communities as peripheral participants rather than co-creators, citing limited time, lack of training, or inadequate institutional incentives as constraints (Käyhkö et al., 2025).

This disconnect may be exaggerated when technologies used by scientists are complex, rapidly advancing, and not well-understood beyond the research environment, a prime example being applications of genomic sequencing in biodiversity research (for a glossary of terms please see the Supplementary Materials). These technologies are increasingly important given how the use of genomic data is transforming understanding of genetic variation in natural populations (Allendorf et al., 2010). DNA sequencing allows scientists to scan thousands to millions of single-nucleotide polymorphisms (SNPs) and other variants across an organism's entire genome, thereby revealing a detailed portrait of population history and dynamics (Supple and Shapiro, 2018). Long-read technologies facilitate the production of complete, high-quality genome assemblies (Li and Durbin, 2024), which are increasingly available through initiatives such as the European Reference Genome Atlas (ERGA) (Mazzoni et al., 2023) and the Earth BioGenome Project (EBP) (Blaxter et al., 2025). Genomics-enabled research projects typically follow a series of steps, from sample collection to DNA extraction and sequencing followed by bioinformatic processing and downstream analyses (Figure 1). Genome-wide analyses can measure genetic diversity, population structure, and gene flow, and can detect inbreeding, genomic erosion, and signals of local adaptation (Shafer et al., 2015; Supple and Shapiro, 2018; van Oosterhout et al., 2025). The metrics can inform management actions across recurrent application domains: (i) delineating conservation and management units to prioritise lineages for protection, e.g. (Funk et al., 2012; Waples and Lindley, 2018); (ii) assessing climate-related adaptive potential and resilience, e.g. (Razgour et al., 2019); (iii) guiding sustainable use and restoration, e.g. (Andersson et al., 2024; Bernatchez et al., 2017); and (iv) biosecurity and invasive species control through tracing sources and spread, e.g. (McGaughran et al., 2024; Sherpa and Després, 2021). Genomics-based evidence can therefore inform biodiversity management by revealing resilience patterns that guide intervention strategies, for example, showing whether a threatened population harbours sufficient genetic variation, or identifying lineages that merit special protection.

For Local Communities with cultural, livelihood, or place-based connections to the study species and the ecosystems they inhabit, genomics therefore offers a powerful ally, adding a layer of DNA-based evidence that complements long-held LEK. Yet, meaningful community participation in genomics-based projects, from sample collection to data interpretation, has remained limited. Community partners are too often relegated to providing specimens for sequencing or excluded entirely, while the added value their LEK can offer in contextualising and interpreting genetic patterns and informing local policy is frequently overlooked (Albuquerque et al., 2019). When researchers embrace insights and knowledge from Local Communities, LEK can guide sampling strategies, (meta)data collections, frame research questions, and facilitate the translation of genomic findings into actionable and impactful measures (Sheppard et al., 2024). In this context, we examine engagement motivations and mechanisms for weaving place-based knowledge held by Local Communities into biodiversity genomics research in Europe. We use “Local Communities” to refer to groups of people who live in, work with, and care for specific localities, maintaining cultural, economic, and ecological ties to a place. For instance, for research associated with the European Union (EU) Mission “Restore our Ocean and Waters by 2030” (European Commission, 2025a), communities with ties to the oceans, seas, and freshwater courses and bodies are actively engaged through participatory approaches as knowledge partners essential to achieving transformative change. We distinguish Local Communities from Indigenous Peoples, whose status as rights-holders is recognised under international law (United Nations, 2007), noting that Europe’s Indigenous Peoples include the Sámi of the Sápmi region and the Inuit of Kalaallit Nunaat. This distinction avoids conflation that can obscure rights and ensures that place-based communities across Europe are not sidelined. Following critiques that the generic term “stakeholder” can mask positional asymmetries and reproduce exclusionary narratives, we avoid that label here and focus instead on Local Communities as knowledge holders and partners in participatory research (Reed, 2008). Our assessment starts by summarising the types of biodiversity genomics research that can benefit from working with Local Communities, leading to the proposal of a five-step framework to help researchers engage effectively with Local Communities. As community involvement in science grows, such engagement guidance is becoming indispensable (Grill, 2021; Taylor et al., 2017), as is the need to partner with social-science experts (Bennett et al., 2017). Rooted in ethical principles, the proposed framework seeks to strengthen Europe’s biocultural heritage while enhancing the scientific rigour and societal relevance of biodiversity genomics through capacity building, equitable benefit-sharing, and long-term partnerships.

Key motivations for engaging Local Communities in biodiversity genomics

Preservation of biodiversity

According to the Convention on Biological Diversity (CBD), and explicitly in the Kunming–Montreal Global Biodiversity Framework, safeguarding biodiversity requires maintaining not only species and ecosystem diversity, but also the genetic variation underpinning resilience to environmental change (CBD COP-15 Decision 15/4, 2022; United Nations, 1992). Genome-wide genomic data allow us to go beyond previous approaches, enabling identification of cryptic lineages, estimation of inbreeding and effective population size, pinpointing adaptive SNPs, or guiding targeted conservation actions (Buzan et al., 2025; Hogg, 2024). Despite the large amount of information that can be derived from the DNA of a single individual, LEK uniquely provides the essential complementary details about habitat history, including traditional land use, and demographic fluctuations (Colloca et al., 2020; Huntington, 2000). When genomic data are integrated with LEK, managers can prioritise genetically distinct populations, design ecological corridors that respect cultural landscapes, and co-develop locally legitimate restoration actions. Moreover, shared interpretation, where scientists present variant maps alongside LEK, can democratise decision-making and embed conservation goals in place-based narratives, increasing the probability of success (Rayne et al., 2022).

Natural resource management

While conservation emphasises protection, natural resource management focuses on the sustainable use of species and habitats for economic or cultural benefit (Fromentin et al., 2022; Obura et al., 2023). Genomic studies can uncover hidden genetic structure in livestock and wild species, diagnose genetic bottlenecks, and quantify demographic impacts of harvesting or habitat alteration (Hohenlohe et al., 2021). Partnerships with Local Communities supply knowledge about, among others, the seasonality and migration routes of species, and practices that shape exploitation patterns. Tensions emerge when conservation targets appear to threaten traditions or livelihoods. For example, across Europe, the recovery of grey wolves reignited conflicts with farmers who may bear the costs of predation or protecting their flocks. Genomic analyses allow researchers to identify gene-flow corridors, enabling managers to deploy targeted deterrents in high-risk zones for coexistence, while maintaining viable predator populations (Laikre et al., 2016). Transparent, inclusive decision-making that recognises LEK can reduce such tensions and produce more durable outcomes (Hansen et al., 2022). Co-designing monitoring protocols can improve trust and compliance with mitigation measures, developing among farmers and decision makers a sense of ownership and support for the process (EU Large Carnivore Platform, 2025; Ostermann-Miyashita et al., 2025; Salvatori et al., 2023, 2021).

Disease prevention

Pathogen outbreaks can disrupt conservation efforts and destabilise local economies. Hence, disease surveillance is a natural meeting ground for genomics and LEK. The *One Health* framework, linking environmental, animal, and human well-being (OHHLEP et al., 2022), places communities on the front line of early detection and control. For example, sequencing allows researchers to characterise pathogens *in situ* (Gardy and Loman, 2018; Latorre-Pérez et al., 2020; Quick et al., 2016), reconstruct transmission routes and introduction events (Gutiérrez-López et al., 2025), and flag genotypes associated with susceptibility or resistance (Lundregan et al., 2020). A European wildlife example comes from African swine fever virus (ASFV) in wild boar, where hunters' associations, farmers, and local forest services co-designed surveillance measures. Whole-genome sequencing of ASFV then traced introduction pathways and transmission chains. Combined with place-based knowledge of boar movements and habitat use, this enabled authorities to delineate control zones, prioritise carcass-removal corridors, and adjust fencing to limit spread (Garigliany et al., 2019; Gilliaux et al., 2019; Sauter-Louis et al., 2021). Because the same community members who discovered carcasses also helped interpret genomic results, trust and adherence to biosecurity measures improved and compliance with access restrictions increased. Participatory evaluations with hunters and farming cooperatives further indicate that engaging their networks strengthens understanding and willingness to support DNA-based surveillance and biosecurity (Stončiūtė et al., 2022; Urner et al., 2021).

Alien species management

Invasive alien species (IAS) remain one of the foremost pressures on global biodiversity (Roy et al., 2024b). Agriculture and public health suffers when invaders are pathogen vectors, and accelerated climate change is shifting range boundaries so rapidly that native–non-native interactions are being redefined within a single generation (Diagne et al., 2021; Roy et al., 2024a). Metagenomics provides solid evidence for the introduction of a new alien species. Subsequently, genomics-based population-wide SNPs reveal the number and origin of introduction events, while scanning for outliers exposes alleles that may confer invasion-facilitating traits (Lawson Handley et al., 2011; Rius et al., 2015). Yet molecular insights can only reach their full potential when paired with input from communities who know the habitat or ecosystem intimately. Coastal fishers in the western Mediterranean, for instance, logged the first sightings of lionfish, enabling researchers to combine photographs and mitochondrial haplotypes to demonstrate a single Suez Canal entry point and design targeted removal dives before populations established (Côté and Smith, 2018). Likewise, farmers in Central Europe have used a smartphone application to map the spread of the *Ambrosia artemisiifolia* weed, supplying real-time distribution data that guides genomic surveys of resistance alleles (Dirr et al., 2023; Loubet et al., 2021). Co-production ensures that control methods respect local cultural values while remaining scientifically reliable. A combination of high-resolution SNPs and local observations can turn IAS management into a proactive, community-endorsed safeguard for ecosystem integrity.

Policy contribution

When genome-wide evidence is examined alongside Local Community knowledge, policy becomes clearer and more defensible. For example, along Norwegian and Icelandic coasts, fishers have long distinguished stationary “coastal” cod from migratory “skrei”. Population genomics later revealed large chromosomal inversions and ecotype-linked divergence, supporting the treatment of multiple management units (Berg et al., 2016; Kirubakaran et al., 2016). Co-developed real-time genetic stock identification now limits bycatch of depleted Norwegian coastal cod while allowing sustainable harvesting of Northeast Arctic cod, a tool implemented with active input from local fishing organisations (Johansen et al., 2018). Operational follow-ups demonstrated how “real-time” genetics can guide area openings/closures and quota decisions in mixed-stock fisheries. A complementary European case reflects observations from fishing communities that greater argentine (greater silver smelt) caught in different areas differ in their traits; low-density SNP surveys have since uncovered population structure and recommended revising the International Council for the Exploration of the Sea (ICES) stock boundaries, providing a clearer mandate for place-sensitive science based regulation (Quintela et al., 2024). Future genome-wide SNP analyses may resolve additional fine-scale population structures in the species. If confirmed, this could warrant revisiting ICES stock boundaries and quotas, and would need to be implemented through participatory transitions with fishing organisations so that new biological insights do not destabilise existing relationships among fleets, ports, and markets.

Weaving Local Community knowledge into biodiversity genomics research: a five-step framework

Biodiversity genomics research can be transformed into a richer and more equitable discipline when LEK is integrated. When researchers ground their work on principles of inclusion, cultural humility, and reciprocal learning, community members move from bystanders to genuine collaborators. From the first outlines of study designs to the final exploitation and dissemination of results, researchers should integrate recognition, respect, and trust into every step. Meaningful collaboration also demands inclusive management: community members should be involved in decision-making, allowing for reflection and a diversity of perspectives. Fair benefit sharing, whether financial, educational, cultural, informational, or infrastructural, should be agreed upon at the co-design stage and re-evaluated during the project lifetime, alongside ethical protections for data privacy and sovereignty. Two-way expertise exchange between researchers and communities further strengthens local capacity, and what starts as a short-term project could develop into a lasting partnership. Clear explanations of how data will be collected and used, how findings might shape policy and management, and how community contributions will be acknowledged help maintain confidence in the research process, preventing the perception of “helicopter science” and “parachute science” (De Vos and Schwartz, 2022). To help translate these principles into practice, the following five-step framework offers a guide for biodiversity genomics research projects (Figure 2). Each step can be adapted to the questions of a given study, reflecting different species, ecology, cultural settings, and logistical and economic constraints, while maintaining the overarching goal of research that advances science and community well-being in tandem.

Step 1: Identify the community and build relationships early

Successful engagement follows two entry paths. In the ideal Plan A (community-led), researchers approach a Local Community first to ask what research questions and outcomes they wish to pursue and agendas, methods, and benefits are co-defined from the outset. Where this is not feasible given mandates, expertise, or timelines, Plan B (researcher-led with early collaboration) begins with the research team’s focal question. Researchers identify community collaborators whose place-based knowledge intersects with the species, habitats, or decisions at stake, and invite them into the discussion as early as possible to test relevance, adapt aims, and share roles (Michener et al., 2012). Examples include fishers’ cooperatives and river associations, farmer and pastoral collectives and foresters, hunting clubs, wildlife-rehabilitation networks, invasive-species watch networks, coastal or urban-park neighbourhood associations, as well as conservation volunteers and land stewards for protected areas. While this guide sets out practical steps for Plan B, it is designed to build toward Plan A as trust and capacity grow, enabling future work to be co-led or community-led. Early establishment of links with community representatives via relevant local structures such as municipal offices/town halls, local non-governmental organisations (NGOs), schools, special-interest or user groups, and, where feasible, appointing community co-researchers, grounds the questions in locally defined needs and signals a commitment to shared responsibility (European Commission, 2025b; Gold, 2022; Reed, 2008; Shirk et al., 2012). Where culturally appropriate and consistent with institutional and funder policies, researchers should inform early that Local Community contributions will be recognised and, where desired, compensated. The specific arrangements, such as remuneration, reimbursement of direct costs, or in-kind alternatives, should be co-designed with collaborators in Step 3. Genuine relationship building, however, hinges on understanding context. Prior training, ideally collaborating with social scientists, on participatory methodologies may be required, to be able to ensure neutrality, minimise possible ethical, economic and political impact of research methods on different parts of the community, and/or anticipate privacy, communication needs and capabilities (language, level of technological literacy, etc.). Spending time on site, attending community gatherings, and talking with cultural brokers will reveal everyday customs, personal dynamics, expectations, and the community's past experiences with researchers (Fortuna, 2019). An open dialogue will then help teams keep collaborations respectful and responsive as values and circumstances evolve (Ansell and Gash, 2008). From the outset, the project will treat LEK as a line of evidence in its own right, recorded in decision logs alongside genomic and ecological data.

Step 2: Value, learn, and respect community etiquette, local context, and knowledge.

Once an initial mutual understanding has been secured, researchers should cultivate a setting in which information flows in both directions. Brief, regular updates on objectives, timelines, and anticipated outcomes allow partners to monitor progress and raise concerns in real time. Co-design workshops can be used to refine questions and methods so that LEK stands alongside scientific expertise rather than being treated as an anecdotal add-on (Reed, 2008; Shirk et al., 2012). These can be used to specify how LEK contributions are cited, versioned, and, where needed, embargoed, so knowledge remains visible without being subsumed. Equally important is recognising boundaries. Some LEK will not be shared, and some may be shared only on the condition that it is not made public. Treat consent as an ongoing process rather than a one-off form. To support two-way capacity-building, provide primers in locally preferred formats and languages such as glossaries, visual walkthroughs of sampling and analysis, LEK protocol notes, so researchers and community collaborators can navigate each other's methods. Offer granular consent for different uses (e.g., internal interpretation vs. public dissemination), document "do-not-share" elements, and agree how sensitive content will be handled (e.g., aggregation, generalisation, delayed release) (ALLEA, 2023; ESRC, 2025; EU, 2016). In biodiversity contexts, adopt an explicit "sensitivity" protocol for place-based knowledge whose disclosure could cause harm, drawing on best practice in sensitive-species data governance (Chapman, 2020; SRA, 2021). Because many European researchers have personal ties to the places where they work, positionality dynamics must be made explicit. Disclose local affiliation, avoid implicit pressure to participate, create routes for confidential feedback, and, where dual roles risk inappropriate influence, consider an independent facilitator for consultations. Reflexive practice (e.g., positionality statements, field notes, team debriefs) helps surface assumptions and supports ethical judgement in situ (ALLEA, 2023; Dirr et al., 2023; ESRC, 2025). Finally, codify these arrangements in the project's data management and engagement plans, with clear points of contact, languages to be used, meeting calendars, and agreed channels for sharing interim and final results. This anchors reciprocity and transparency, reinforces trust, and, consistent with the chosen entry path, either enables immediate co-design (Plan A) or lays the groundwork for proportionate co-creation in step 3 (Plan B), with roles and scope aligned to community interest and capacity (Israel et al., 1998; Shirk et al., 2012; Wallerstein and Duran, 2010).

Step 3: Co-create the research process by sharing authority and roles

Once a relationship is established, the research team should invite community collaborators to act as co-creators (Plan A) or proportionate collaborators (Plan B) rather than passive informants or sample collectors. Jointly refining aims and methods with those who live with the outcomes, in Plan A, co-designing from the outset. In Plan B, making targeted adjustments to align the study with local context and priorities lays firm foundations for equitable and impactful science (Michener et al., 2012). Genuine participation, situated near the summit of Arnstein's ladder of citizen power (Arnstein, 1969), can include jointly framing questions, recruiting and training local residents as 'citizen scientists', and agreeing on an opt-in spectrum of roles such as advisor, co-researcher, co-lead, so no one is pressured beyond their comfort or capacity. Creating clear avenues for community input and, where appropriate, shared oversight of research protocols, data stewardship, and benefit-sharing further reaffirms relationships. Plan B may involve local collaborators assisting with sampling design/implementation or interpreting the results side-by-side with researchers, helping uncover ecological patterns scientists could overlook and affirming LEK as part of the evidence base. Some collaborators may value recognition, purpose, or new skills over remuneration. Where grants are proposed, the budget should have a meaningful share of community priorities where feasible (stipends or honoraria when desired, equipment, training, materials, and operational costs). The research team should be trained on unconscious bias as well as equality, diversity, and inclusion considerations throughout the research process. Role-specific training commitments, for community collaborators (e.g., sampling, data walkthroughs) and for researchers (e.g., facilitation, LEK protocols), should be agreed proportionate to Plan A or Plan B. This will empower them to detect interaction imbalances and adapt participatory strategies accordingly. Decisions about sampling, data ownership, and dissemination should be informed by community input and, where feasible, taken collaboratively so that the work remains focused on local priorities and increases the likelihood that findings are embraced and sustained by the community.

Step 4: Ensure mutual benefit and transparency

Research partnerships succeed when communities can draw a clear line from their contributions to tangible returns knowing that not all research yields immediate or material outcomes. Researchers therefore have a responsibility to set realistic expectations, stating clearly what the project can and cannot deliver. They should also state the uncertainties and timelines involved, and that plans may change. Enduring trust-based relationships and mutual learning are meaningful outcomes and indicators of success. Accordingly, teams should agree on terms that specify a data management plan, sharing of protocols, intellectual-property rights, and details on if, when, and how benefits will flow back to the Local Community. Create a simple benefit register that lists community-defined benefits, the evidence that will demonstrate delivery, timelines, and responsible roles and review it at agreed intervals. Such benefits may range from capacity-building workshops, co-authorship, and acknowledgement, to grant funding budgeted for community priorities, infrastructure support, and informational/cultural outputs (e.g., plain-language summaries, public talks, school activities, posters in local venues) (Gold, 2022; Kegamba et al., 2022). At the same time, researchers should be clear that ecological benefits are often a long-term outcome and may not be immediately visible, so transparency about timelines and limits of impact is essential. To maintain trust, agree on communication routines and document where data go and why, and create public-facing data-management notes to build understanding and confidence (Thuermer et al., 2023; Wilkinson et al., 2016). As projects evolve, involve community representatives in adjustments rather than making unilateral changes, and include a straightforward dispute-resolution clause (who decides what, how to escalate, and when to review) so disagreements can be handled respectfully and in line with the community's agreed governance terms (MacQueen et al., 2015; Wallerstein and Duran, 2010). Partnerships become more ethical and resilient when transparent processes are implemented, increasing the likelihood that findings will be accepted and translated into lasting benefits for the Local Community (Michener et al., 2012).

Step 5: Plan for long-term engagement and knowledge transfer

Engagement of Local Communities should persist beyond the scientific publication of research results. At the project start, map who needs what after the project wrap-up (e.g., municipal officers, cooperatives, schools, NGOs) and co-plan dissemination and uptake pathways, what products will be delivered, in which languages/formats, by whom, and on what timeline (European Commission, 2025b; Michener et al., 2012). Practical outputs include simplified summaries, one-page policy briefs, and community talks or school activities, all designed using behavioural-insight tips so they are short, actionable, and audience-specific (Nagyova and Michie, 2023). To make results easy to find and reuse, deposit sequence data and metadata in verified repositories and publish data/analysis code with persistent identifiers, open licenses, and clear documentation that meets findability, accessibility, interoperability, and reusability (FAIR) guiding principles (Wilkinson et al., 2016). For local use, provide downloadable data collections, a simple online public dashboard or webpage, and contact points for follow-up. Importantly, plan a handover by identifying a local steward (e.g., town office/NGO) and budget a brief "train-the-trainer" so tools can be maintained without an external team (Gold, 2022). Next, schedule post-project follow-ups (e.g., after 6 and 12 months) to review uptake and adjust materials using straightforward indicators (reach, reuse, decisions influenced) aligned with EU knowledge-valorisation guidance (European Commission, 2025b). Finally, recognise contributions visibly, co-authorship when warranted, public acknowledgements, certificates, or hosting results events in community venues, so benefits remain tangible. Using this approach increases the likelihood that genomics-based insights will be implemented rather than simply published, and reinforces the legacy of the project outcomes (Gudek et al., 2025).

European whitefish: An example of the five-step framework in action

To demonstrate the practical applicability of the proposed five-step framework, we include a real-world application involving the European whitefish (*Coregonus lavaretus*) population in Lake Leman (also known as Lake Geneva) (Figure 3). This use-case, detailed in the Supplementary Materials, illustrates how the framework can be effectively applied to address ecological challenges, particularly when different Local Communities and countries are involved. The successful rehabilitation of the European whitefish, known locally as the Corégone or the Féra du Léman, in this lake is a testament to the value of active involvement and sustained engagement with Local Communities to achieve long-term positive ecological outcomes.

Discussion

Community scientists, academic researchers, and public-sector decision-makers should converge on a common standard for ethically rooted knowledge-sharing engagement, which will substantially enhance the credibility, inclusivity, and real-world impact of European biodiversity genomics. The path toward a widely embraced framework must consider three principal axes: i) ethics-grounded participation that recognises LEK as legitimate evidence, ii) two-way capacity-building infrastructure that equips community members to understand the science and supports researchers to navigate community engagement and knowledge co-production methods, and iii) evidence-driven reciprocity that ties research outputs to tangible, transparent, and community-defined benefits. Practical next steps include embedding location-based expertise in sampling design, hypothesis formulation, and data interpretation, as well as institutionalising transparent benefit-sharing protocols that recognise and reward contributors through acknowledgement and co-authorship, targeted training, and measures and activities that promote sustainable local engagement. We extend general guidance on participation and communication (Gold, 2022) to the genomics research domain by specifying sample and data governance, FAIR-aligned sharing of metadata, workflows, and code, and locally meaningful dissemination so that sequencing results and interpretation are usable by non-specialists. In conservation contexts, partnering with social-science expertise, where appropriate, supports co-designed, context-appropriate measures and transparent evaluation of uptake and equity impacts (Bennett et al., 2017), an emphasis our five-step framework makes explicit. As set out above, the steps we propose, spanning early partner identification to post-project knowledge transfer, embrace open science practices, confer methodological robustness and social legitimacy, thereby elevating the scientific impact and civic trust associated with genomics research.

Our five steps operationalise the core principles in established guidance. Norström et al.'s four principles for high-quality knowledge co-production: being context-based, pluralistic, goal-oriented, and interactive (Norström et al., 2020), map onto Steps 1–5 (context scanning, plural knowledge, shared goals, iterative dialogue). The Multiple Evidence Base (MEB) approach (Tengö et al., 2017) clarifies how to mobilise, translate, negotiate, synthesise, and apply diverse knowledge types without subsuming LEK into science. The proposed framework inserts these tasks at explicit project checkpoints. Finally, the International Association for Public Participation (IAP2) Spectrum: inform + consult + involve + collaborate + empower, and Community-based Participatory Research (CBPR) traditions e.g. (Israel et al., 1998) underpin our gradient of roles and shared authority. Together, these anchors position the framework as a practical bridge between theory and day-to-day practice.

The framework allows for decisions that are defensible in both peer-reviewed journals and community decision-making contexts. A co-owned approach can lead to adaptive management that keeps pace with environmental change while respecting cultural identity, provided it is sustained by long-term relationships, resourcing, and shared governance beyond a single project (Armitage et al., 2009; Wallerstein and Duran, 2010). However, widespread uptake remains constrained by compressed funding timelines, limited interdisciplinary training opportunities, and academic reward structures that still privilege rapid publication over relationship building. These issues are substantive and should be addressed systematically. However, they need not stall progress. In the meantime, teams can take proportionate steps that improve outcomes now: set conservative promises and communicate uncertainties; pilot co-design on a limited set of decisions with Local Community collaborators; set aside small budgets for recognition or training; treat consent and positionality as living artefacts; and share plain-language summaries, data, and code so results will travel. Even partial adoption of these practices can increase the legitimacy, equity, and durability of decisions, delivering better outcomes while building the relationships and evidence base needed for full implementation over time. Methodologically, working across knowledge systems still requires careful design choices: when to keep evidence side-by-side within their own validation logics (per the MEB approach), when to negotiate linkages across them, and how to avoid assimilationist framings. Structured reflexivity tools for interdisciplinary teams can help. On impact, evidence syntheses in adjacent fields show positive signals but also uneven evaluation and non-trivial transaction costs, the ‘dark sides’ of co-production, underscoring, as noted above, the case for proportionate, pre-agreed metrics and evaluation of both scientific and community outcomes. Rather than a grand redesign, the invitation is practical: start where you are, use the five-step framework to structure proportionate collaboration, and share what you learn. Small, transparent moves, early conversations with Local Communities, modest co-design on decisions that matter locally, and plain-language products, compound into better science and fairer outcomes. As more teams adapt and report on these steps, a community of practice can grow around comparable methods and lessons, reducing uncertainty for newcomers and raising the standard for everyone. We encourage researchers, community collaborators, and funders to join this effort by trialling the framework, documenting successes and challenges, and contributing case studies so that biodiversity genomics in Europe advances with, and is accountable to, the places it serves.

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Author Contributions

Conceptualisation: CdG, CJM, AMo, AMi, LO, JP, EB, RMW; Methodology: CdG; Investigation: CdG, EB; Resources: CdG; Writing - Original Draft: CdG, CB, KL, LLB, AMo, MM-N, AMi, LO, JP, MJR-L, EB; Writing - Review & Editing: CdG, CB, LSM, TC, CRDP, SK, JAL, KL, LLB, CJM, AMM, S-OM, AMo, MM-N, AMi, LO, JP, MJR-L, TES, OZ, EB, RMW; Visualisation: CdG, LSM; Supervision: CdG, CJM, RMW; Project Administration: CdG, CJM, EB, RMW; Funding Acquisition: CJM, EB, RMW.

Supplementary Material

The supplementary materials are provided as a PDF with three sections: (1) an explanatory glossary of terms used in the manuscript; (2) the detailed presentation of the European whitefish example of the five-step framework in action; and (3) supplementary references.

Figures and Figure Legends

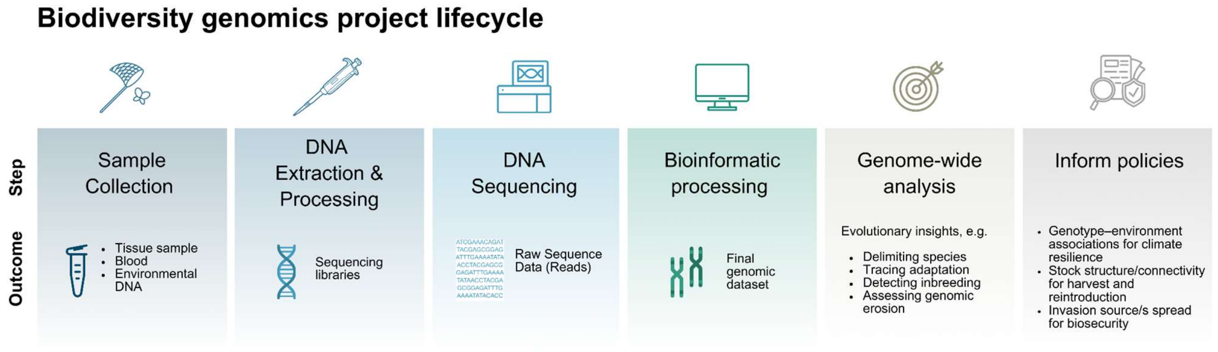


Figure 1. Key steps and outcomes comprising a typical biodiversity genomics research project. In the lifecycle of a biodiversity genomics research project, samples such as tissue, blood, hair, saliva, feces, or scats are collected and processed through DNA extractions and library generation in the laboratory. Subsequently, next-generation sequencing machines are able to deliver millions of DNA fragments (reads), and bioinformatic pipelines can then process these reads into genome assemblies or population genomic datasets for downstream analyses. Depending on the question – species delimitation, signatures of adaptation, estimates of inbreeding, etc. – different genome-wide analyses can then be applied, the results of which can then be used as a source of evidence for informing policy and species/habitat management decisions. Importantly, genomic data allows reanalyses for new questions in the future provided associated metadata is readily available (Forsdick et al., 2025).

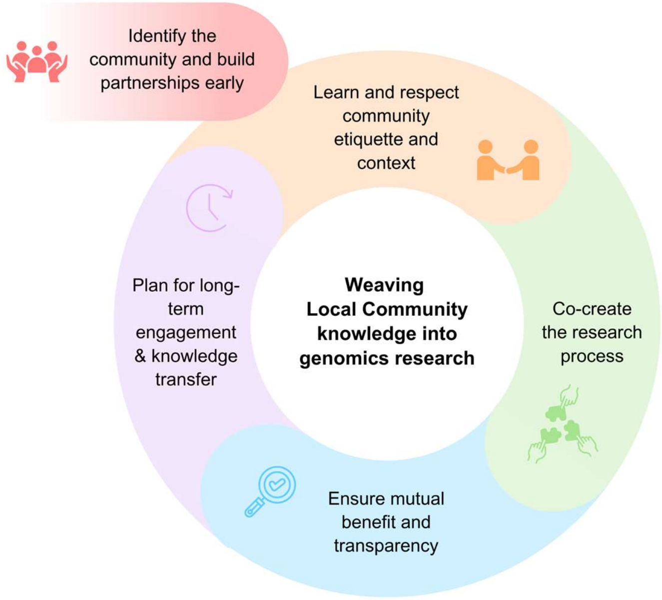
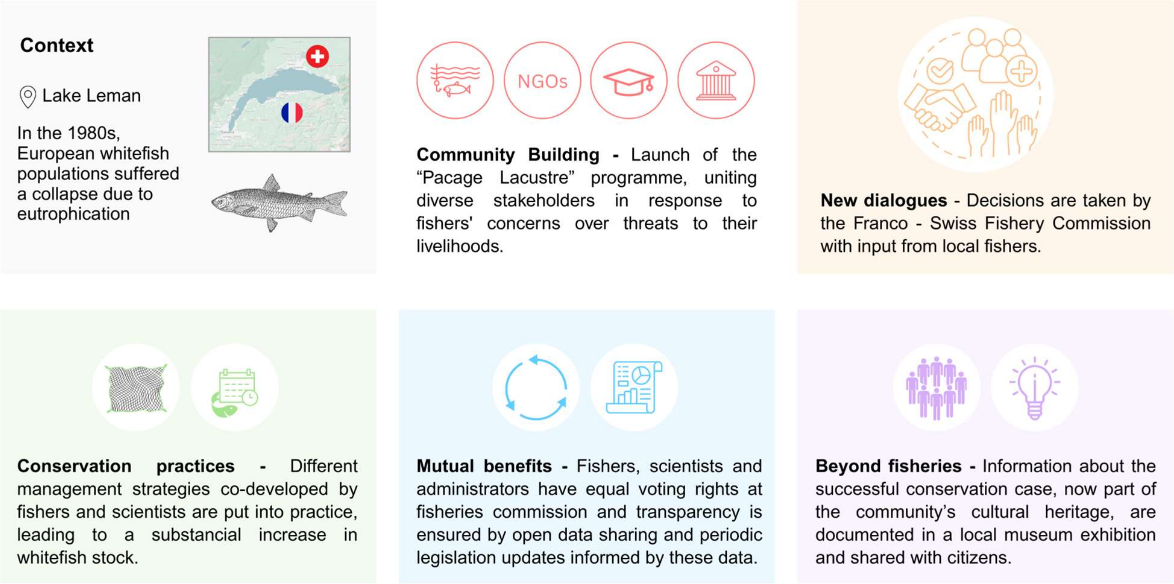


Figure 2. Summary of the five proposed steps for weaving Local Community knowledge into biodiversity genomics research. Local partnerships should be established before the project starts, and engagement should continue after publication of scientific results. This framework spans the full research cycle: (1) identifying the community and building partnerships early, either approaching local communities first to ask what research questions and outcomes they wish to pursue or bringing the research team's question to the local community early to discuss context, test relevance, adapt aims, and share roles; (2) learning and respecting community etiquette and context to cultivate a setting in which information flows in both directions; (3) co-creating the research process, which can include jointly framing questions, recruiting and training local residents as 'citizen scientists', and agreeing on an opt-in spectrum of roles such as advisor, co-researcher, co-lead, so no one is pressured beyond their comfort or capacity; (4) ensuring mutual benefit and transparency, e.g. by agreeing at the outset on terms that specify a data management plan, sharing of protocols, intellectual-property rights, and details on if, when, and how benefits will flow back to the Local Community; and (5) planning for long-term engagement and knowledge transfer can involve mapping who needs what after the project wrap-up and co-planning dissemination and uptake pathways, such as what products will be delivered, in which languages/formats, by whom, and on what timeline.



In the 1980s, European whitefish populations suffered a collapse due to eutrophication

Community Building - Launch of the "Pacage Lacustre" programme, uniting diverse stakeholders in response to fishers' concerns over threats to their livelihoods.

New dialogues - Decisions are taken by the Franco - Swiss Fishery Commission with input from local fishers.

Conservation practices - Different management strategies co-developed by fishers and scientists are put into practice, leading to a substancial increase in whitefish stock.

Mutual benefits - Fishers, scientists and administrators have equal voting rights at fisheries commission and transparency is ensured by open data sharing and periodic legislation updates informed by these data.

Beyond fisheries - Information about the successful conservation case, now part of the community's cultural heritage, are documented in a local museum exhibition and shared with citizens.

Figure 3. Summary of the five proposed steps for a real-world application involving the European whitefish (*Coregonus lavaretus*) in Lake Leman. Following the collapse of populations in the 1980s, (1) community building through the Pacage Lacustre programme united diverse stakeholders, (2) new dialogues were established via the Franco–Swiss Fishery Commission with input from local fishers, (3) conservation practices were co-developed and implemented by fishers and scientists, (4) mutual benefits were ensured through equal voting rights, open data sharing, and transparent

legislation, and (5) outcomes extended beyond fisheries, with the recovery becoming part of local cultural heritage and shared in museum exhibitions.

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Supplementary Materials

Engaging European Local Communities in Biodiversity Genomics Research: A Five-Step Framework for Scientists

1. Glossary

Adaptive genetic traits: traits (or phenotypes or characteristics) encoded in an organism's DNA that enhance its survival and reproductive success in a specific environment.

Benefit-sharing: the fair and equitable sharing between stakeholders of monetary (e.g., royalties from the creation of commercial products derived from resources) and non-monetary (e.g., research skills and knowledge) benefits that may result from the use of genetic resources ("Nagoya Protocol on access to genetic resources and the fair and equitable sharing of benefits arising from their utilization to the convention on biological diversity," 2011).

Biodiversity genomics: the application of genomic data and analyses to the understanding of all eukaryotic organisms (Theissinger et al., 2023).

Data stewardship: research practices designed to optimise data management in alignment with the FAIR Guiding Principles (findability, accessibility, interoperability, reusability) to enhance data reusability for the benefit of the scientific community and the public (including local communities).

Earth BioGenome Project (EBP): an international initiative that aims to coordinate global efforts to sequence, catalogue, and characterise reference-quality genomes of all of Earth's eukaryotic biodiversity (Blaxter et al., 2025; Lewin et al., 2022).

European Reference Genome Atlas (ERGA): a pan-European scientific community of experts in genome sequencing and analysis that aims to coordinate the generation of reference-quality genomes for all eukaryotic species in Europe (Mazzoni et al., 2023).

Gene flow: the transfer of genetic material between populations of the same species through migration, mating, or dispersal of individuals or gametes.

Genetic bottleneck: the abrupt reduction in the size of a population due to environmental events (e.g., natural disasters, disease, or human activities) and/or other pressures. A genetic bottleneck results in a significant reduction of genetic variation.

Genetic variation: the differences in DNA sequences or the diversity of genes within and among individuals and populations of a species.

Genome assembly: a computational representation of a genome sequence. A genome assembly can be of varying quality (contiguity, completeness, correctness) based on the sequencing technologies used.

Genomic data: data that includes a high density of genetic markers, such as single-nucleotide polymorphisms (SNPs), typically numbering in the thousands or millions, distributed across an entire DNA sequence.

Genomic erosion: the progressive loss of genome-wide diversity over time in small, isolated populations (van Oosterhout et al., 2025).

Genomics: a branch of molecular biology focused on the study of an organism's complete DNA (the genome), including all of its genes, their functions, and structure. Genomics refers to both individuals, populations, and species.

Helicopter science: also known as parachute science, refers to the practice where scientists from the Global North (typically High Income Countries) conduct studies in the Global South (typically Low to Middle-Income Countries) with little to no involvement from–or benefit to–local scientists and Local Communities (De Vos and Schwartz, 2022).

Inbreeding: the mating between closely related individuals, which increases the chance of offspring inheriting identical genetic variants from both parents, thereby reducing genetic diversity.

Invasive alien species (IAS): species that establish themselves in natural or semi-natural ecosystems or habitats that they have never inhabited before. They are often agents of change and threaten native biological diversity (Roy et al., 2024).

Metagenomics: the sampling and sequencing of (partial) genome sequences of a community of organisms inhabiting a common environment.

One Health: an integrated, unifying approach that aims to sustainably balance and optimise the health of people, animals, and ecosystems. It recognises the health of humans, animals (domestic and wild), plants, and the wider environment, as closely linked and interdependent.

Single Nucleotide Polymorphism (SNP): it occurs when one nucleotide (A, T, C, G) is replaced by another one in a DNA sequence, creating a variation at a single DNA base pair in the genome among individuals.

Stakeholder: any person or group of people who directly or indirectly influences or is influenced by the research being conducted. A stakeholder may have an interest in the research and/or can affect its results, whether positively or negatively. A stakeholder is not necessarily a direct user of the research's findings and is not always affected by them (Durham et al., 2014).

Whole-genome sequencing: the sequencing of an individual's entire genome content to identify genetic variation by comparing it to a reference genome.

2. Real-World Application: The salmonids of Lake Leman

Here, the five-step framework is exemplified in the long-running effort to rehabilitate European whitefish (*Coregonus lavaretus*) in Lake Leman (also known as Lake Geneva), a deep peri-Alpine lake shared by France and Switzerland. Intense eutrophication in the 1960s-70s drove annual whitefish catch from ≈100–200 tons (t) to just 30–50 t, setting off alarm among the lake's professional fishing families and recreational angler clubs. In response, these groups joined regional and national authorities and limnologists from the French INRAE research station in Thonon-les-Bains to launch the cross-border **"Pacage Lacustre"** supportive-breeding programme in 1983, formalising a partnership that still anchors stock management today (Rogissart et al., 2024). A Franco-Swiss commission oversees the fishery and mandates shared decision-making. Compulsory catch logbooks introduced in 1986 give fishers direct input into monitoring and evaluation. Recent advances extend from hatchery genetics to non-invasive molecular surveillance to track whitefish and perch (*Perca fluviatilis*) spawning, information that feeds back into adaptive quota setting and season closures. Together, these documented actions offer a concise, real-world canvas on which to map each step of the Local Community engagement framework outlined above.

Step 1 – Identify the community and build partnerships early

The decline in whitefish was threatening the livelihood of dozens of professional fishing families. In response, these fishers, together with recreational-angler associations and local NGOs, petitioned regional and national authorities and reached out to INRAE limnologists at the Thonon-les-Bains research station in France, identifying them as key partners in addressing the crisis. Their joint response was the cross-border "Pacage Lacustre" programme, launched in 1983, which formed a partnership among the fishers, scientists, and both French and Swiss governments (Rogissart et al., 2024).

Step 2 - Learn and respect community etiquette and context

Soon after the *Pacage Lacustre* programme began, scientists entered the decision-making process of the **Franco-Swiss Fishery Commission**, a binational body created by the 1980 bilateral accord that still governs Lake Leman's fisheries and conducts its business (Comité Mixte Franco-Suisse, 1980). During its early sessions, the professional fishing cooperative and angling clubs identified the few gravel shoals where *whitefish* still spawned and made clear that the brood-stock harvest must coincide with their November–January fishing season. The partners also agreed that hatchery production would rely exclusively on gametes stripped from wild Leman spawners, a precaution later validated by early genetic surveys showing the lake's whitefish are genetically distinct from neighbouring stocks (Champigneulle and

Gerdeaux, 1992). The team created a two-way dialogue by incorporating local calendars and ecological knowledge into the programme.

Step 3 - Co-create the research process

Dialogue soon matured into practice. Each winter, professional Leman fishermen harvest fully ripened *whitefish* spawners, stripping gametes before transferring them to the hatchery. This routine preserves the lake's endemic gene pool, giving fishers tangible control over the most sensitive stage of the life cycle. Long-term catch records revealed that the standard 36 mm gill-net mesh captured more than 60% of males and over half the females before ovulation. Acting on fishers' recommendations, managers adopted a 44 mm mesh that releases most sub-adult males yet still retains gravid females, significantly improving egg yield (Champigneulle et al., 2001). Additional practice-driven refinements followed, for instance, non-ovulated females are now held in shore tanks until fully matured, or eggs have to be fertilised within two hours of capture. These small adjustments lifted first-week larval survival above 70 % (Champigneulle et al., 2001, 1983).

Collaboration continues beyond the hatchery phase. Fishers maintain floating nursery cages and, since 1986, maintain log books that document gear, effort, and externally marked fish. This generates a high-resolution data collection for stock assessment. Mark–release–recapture trials, co-designed to fit commercial routines, adopted Alizarin Red S otolith staining as a permanent tag; subsequent analyses showed that released juveniles can return up to 27 kg of harvest per 1000 juveniles, guiding evidence-based decisions on release size and timing (Caudron and Champigneulle, 2009; Champigneulle and Gerdeaux, 1992). Fishers are recognized as genuine co-investigators of the management experiment by embedding local expertise in gear choice as well as post-release monitoring.

Step 4 - Ensure mutual benefit and transparency

Lake Leman's fishery is governed by the 1980 Franco-Swiss Accord. This created a binational commission that still gives professional fishers, scientists, and administrators equal voting rights. The commission's statutes oblige both countries to publish annual stocking quotas, currently 10 million whitefish juveniles. Both countries are also required to review their rules every five years to ensure that gear limits and closed seasons are continually updated. Data flows in the opposite direction (Hofmann and Raymond, 2014). Since 1986, mandated log books have supplied the high-resolution capture statistics that feed directly into the commission's public reports, revealing, for example, a total take of 1241 t across all sectors in 2012 (Hofmann and Raymond, 2014). Most importantly, collaboration benefits are tangible. After sustained lobbying from the fishing syndicate, the French environmental law was amended in 2002 to legalise the sale of broodstock caught during the winter egg fishery, replacing income lost due to seasonal closures and rewarding active participation in the stocking programme (Rogissart et al., 2024). Together, mandatory data transparency and shared economic gains demonstrate that scientific management need not be a one-way street. Knowledge returns to those who generate it, and so do the proceeds.

Step 5 - Plan for long-term engagement and knowledge transfer.

The collaboration on Lake Leman continued after whitefish catches recovered. To determine spawning peaks of fé-ra and European perch, INRAE limnologists use droplet-digital PCR (ddPCR) on environmental DNA samples (Vautier et al., 2023). The genomic time-series complements the annual bulletins issued by the commission, which provide license holders with detailed catch statistics and fry-release numbers (Commission Franco-Suisse, 2023). The outreach program extends beyond the fishing industry. The “Écomusée de la Pêche” in Thonon-les-Bains exhibits archival photographs, historical catch curves, and simplified genetic graphics developed by INRAE–CARRTEL staff, preserving the conservation narrative for school groups and tourists alike. In ensuring that data, interpretation, and public storytelling are shared with the community, the programme demonstrates that both ecological and cultural benefits can be realized through long-term, transgenerational engagement.

3. References

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