Research Ideas and Outcomes 12: e214291
doi: 10.3897/rio.12.e214291

Grant Proposal

Biodiversity Genomics Europe plus (BGE+) Project - Abridged Grant Proposal

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Reviewable v 1

Received: 03 Sep 2026 | Published: 16 Sep 2026

Citation: Koureas D, Alonso E, Beja P, Böhne A, Bourlat SJ, Bužan E, Ekrem T, Heil KF, Melo-Ferreira J, Paupério J, Price BW, Addink W, Alioto TS, Aravanopoulos FA, Barnes I, Bayés M, Chadwick E, Chua P, Clark MD, De Panis D, Dunshea G, Fantoni K, Ferreira S, Gkagkavouzis K, Goble CA, Grabowski M, Gut M, Haggerty L, Hartop E, Iannucci A, Islam S, Juty N, Kaitetzidou E, Kamenova S, Karaiskou N, Kavakiotis I, Keskin E, Lewin HA, Marins LS, Martin FJ, Minoudi S, Monteiro R, Papakostas S, Pimenta J, Penev L, Porter TM, Soiland-Reyes S, Stange M, Thompson KA, Triantafyllidis A, Vinnere Pettersson O, Vos RA, Zakharov EV, Alonso JM, Casino A, Ciofi C, Daňková G, Hollingsworth PM, Lawniczak MKN, Mazzoni CJ, Waterhouse RM (2026) Biodiversity Genomics Europe plus (BGE+) Project – Abridged Grant Proposal. Research Ideas and Outcomes 12: e214291. https://doi.org/10.3897/rio.12.e214291

Abstract

The Biodiversity Genomics Europe plus (BGE+) Project builds on a pan-European collaboration to scale up the production and uptake of genomic evidence for taxonomy, monitoring, and policy. It widens participation, standardises methods, and prepares a distributed European system for biodiversity genomics that links molecules to ecosystems. The BGE+ consortium unites the International Barcode of Life in Europe (iBOL Europe, barcoding), the European Reference Genome Atlas (ERGA, reference genomes) and the Consortium of European Taxonomic Facilities (CETAF, taxonomic research and natural history collections) to align end-to-end workflows from field sampling to application. This publication is an abridged version of the successful grant proposal developed jointly by iBOL Europe, ERGA, and CETAF in response to the Horizon Europe call HORIZON-CL6-2025-01-BIODIV-03. BGE+ has four overarching objectives: (1) broaden participation and capacity; (2) make distributed genomic data production interoperable and FAIR (Findable, Accessible, Interoperable, and Reusable) by design; (3) translate evidence into practice through co-designed use-case roadmaps; and (4) define the service portfolio and assess the financial and technical feasibility of a

future European research infrastructure in biodiversity genomics. Through targeted cascade grants (Financial Support to Third Parties) and hands-on training, BGE+ enlarges community capacity while converging on shared protocols and standard practices, improving data interoperability and consolidating community efforts. Building on previous work, BGE+ carries forward the communities' long-term vision: turning fragmented efforts into a coherent, scalable system that delivers reliable genomic evidence for taxonomy and policy.

Keywords

iodiversity genomics, CETAF, DNA barcodes, ERGA, Horizon Europe, iBOL Europe, reference genomes, taxonomy

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Context

This paper is an abridged version of the original proposal developed to respond to the Horizon Europe call HORIZON-CL6-2025-01-BIODIV-03 (Strengthening taxonomic approaches for biodiversity, Area B), which was submitted in September 2025. It contains the overarching scientific case for the Biodiversity Genomics Europe plus (BGE+) Project, alongside a description of our major ambitions and activities. Differences between this paper and the full "Description of Work" include redactions, e.g. of financial and personal information alongside our risk analysis; addition of formatted citations that were not included in the original proposal; minor edits to improve readability; and the inclusion of high-resolution versions of the figures. The BGE+ Project started in May 2026, with a duration of 3.5 years, this abridged grant proposal is published to contextualise the publication of future outputs from the BGE+ Project and Consortium members.

1. Excellence

1.1 Objectives and ambition

1.1.1 Overarching goal

Biodiversity Genomics Europe plus (BGE+) will harness the power of genomic science and DNA-based reference resources to strengthen taxonomic approaches for biodiversity in Europe, enhancing understanding of species and genetic diversity, widening participation, building skills, developing protocols and solutions, enhancing policy uptake, and developing the foundations of a European biodiversity genomics system. The project capitalises on developments in genomics, previous work performed at European level, and large community participation, to catalyse transformative change in the characterisation, conservation, and sustainable use of biodiversity.

- **Objective 1**. Mobilise the distributed network of taxonomists and genomic researchers across Europe to scale up production and use of DNA barcode and genome sequence data to expand geographical coverage and participation, and deliver novel insights into species and genetic diversity.
- **Objective 2**. Address rate-limiting steps in generating, managing, and analysing Barcode and Whole Genome Sequence (WGS) data to remove technical barriers to data production and deployment.
- **Objective 3**. Increase the policy uptake, use, and impact of genomic data to support environmental management, environmental risk assessment, and sustainable use of biodiversity.
- **Objective 4**. Establish the foundations of a comprehensive biodiversity genomics system in Europe to ensure long-term sustainable service provision, harnessing the power of genomics for biodiversity characterisation, conservation, and use.

BGE+ will provide a step change towards a distributed, inclusive, and quality-enabled biodiversity genomics infrastructure and community in Europe, leveraging our leadership

of the established networks of the **International Barcode of Life Europe** (**iBOL-E** Link: https://iboleurope.org/) (Hollingsworth et al. 2026, Kaitetzidou et al. 2026), the **European Reference Genome Atlas** (**ERGA** Link: https://www.erga-biodiversity.eu/) (Mazzoni et al. 2023, Mc Cartney et al. 2024), and the **Consortium of European Taxonomic Facilities** (**CETAF** Link: https://cetaf.org/).

To deliver our objectives, we will:

- *Establish a cascade grants mechanism (WP2) and wider training programme (WP3) encompassing the **iBOL-E**, **ERGA**, and **CETAF** communities*, in order to mobilise the distributed network of taxonomists and genomic researchers across Europe to scale up production and use of DNA barcode and genome sequence data;
- *Undertake innovative Research and Development (R&D) activities to develop new laboratory protocols (WP4) and informatics solutions (WP5)* in order to address rate-limiting steps in generating, managing, and analysing barcode and WGS data;
- *Develop strategic partnerships, harmonised genomic-application road-maps, and a synthesis of relevant policy needs (WP6)* in order to increase the policy uptake, use, and impact of genomic data;
- *Strengthen and grow the **iBOL-E** (WP8) and **ERGA** (WP9) communities, and develop long-term biodiversity genomic infrastructure plans (WP7)* in order to establish the foundations of a comprehensive biodiversity genomics system in Europe.

The outputs of this project will provide immediate benefits in terms of skills, capacity, data, protocol development, and solutions to policy needs, and a long-term foundation for integrating biodiversity genomics into the European Research Infrastructure landscape.

1.1.2 Project premise and approach

The Project Premise

Despite more than 300 years of research in biosystematics, our understanding of life on Earth remains limited. Current estimates refer to 2.3 million extant species on the planet, recognised by taxonomists (Mora et al. 2011). Although this number has grown substantially over the years, it is impressively low in relation to the scale of biological diversity still to be described. Many published models project between 10 and 20 million species still unknown to science, with arthropods representing the largest group of undescribed species. At the same time, the need for evidence-based decisions in nature conservation has become a prerequisite for effective policymaking. Increasingly, European and international biodiversity goals, such as those emerging from the **Kunming-Montreal Global Biodiversity Framework (GBF)** (Convention on Biological Diversity 2022) or the **European Nature Restoration Regulation** (European Commission 2025), underscore the need for more and higher-quality evidence. These nature-related policies are only as good as the completeness and quality of the information they rely

upon. Given the gap in taxonomic knowledge and the aspirational policy and science goals ahead of us, it is clear that to **deliver on the promise of taxonomy to our societies, we must accelerate the production of biodiversity knowledge**. For such acceleration, it is crucial to mobilise, connect, and consolidate all available resources and expertise, and deliver a robust and sustainable research infrastructure, as a distributed system, that enables researchers to scale up their taxonomic knowledge.

The Project Approach

New technologies, including high-throughput genomics and the application of Artificial Intelligence (AI), open up avenues of opportunities for scaling up taxonomic and biodiversity knowledge production. Significant progress has been made in the field of biodiversity genomics, where the scientific and technological readiness has reached a very high level of maturity. Large international initiatives have formed around the two major strands of biodiversity genomics: **DNA barcoding** [iBOL Link: https://ibol.org/ - International Barcode of Life, (Ratnasingham and Hebert 2007, Hebert et al. 2016)] and **whole-genome sequencing** [EBP Link: https://www.earthbiogenome.org/ - Earth BioGenome Project, (Lewin et al. 2018, Blaxter et al. 2025)], aiming to connect and support distributed global efforts. In Europe, scientific networks have formed, including **iBOL-E** Link: https://iboleurope.org/ for DNA barcoding and **ERGA** Link: https://www.erga-biodiversity.eu/ for whole-genome sequencing, which connect European communities to global efforts. In alignment with iBOL and EBP goals, the **BGE+** approach is focused on the representative coverage of described eukaryotic biodiversity, excluding microbes where different methodologies are required.

In our journey to scale up biodiversity knowledge through the use of genomics, it is equally important to scale out and thereby benefit from the distributed efforts taking place through various-sized barcoding and whole-genome projects across the continent. These projects involve a large number of individual researchers and research labs, underscoring the importance of biodiversity genomics in the collective vision for a genomically enabled biodiversity knowledge space. Variation in approaches to sampling, wet-lab methods, and data curation practices and tools affects the comparability and interoperability of results, reducing the collective impact these distributed efforts could bring if they were better connected and consolidated. **These challenges hinder the European community of biodiversity scientists from connecting, aggregating, and ultimately accelerating knowledge production, which is required to understand, characterise, protect, and sustainably use Europe's natural capital**.

The BGE+ Project directly addresses the challenges described above, aiming at advancing the work already undertaken to establish a truly pan-European, genomically enabled knowledge production system. The project continues on the foundation established through the **European project BGE1 (2022-2026)** (Koureas et al. 2026).

1.1.3 BGE+ main Objectives

To achieve the project ambitions and deliver the expected topic outcomes of **HORIZON-CL6-2025-01-BIODIV-03 Area B**, **BGE+** has defined four key objectives, their relevance to the call in terms of expected outcomes and scope, and their Key Performance Indicators (KPIs) to measure and verify the results. These objectives, and their relations to the project Work Packages (WPs) are presented here:

Objective 1. Mobilise the distributed network of taxonomists and genomic researchers across Europe to scale up production and use of DNA barcode and genome sequence data to expand geographical coverage and participation, and deliver novel insights into species and genetic diversity.

What we will do

Use cascade grants (WP2) to widen participation and expand geographic and taxonomic coverage of reference barcode libraries and reference genomes, with clear standards for open data, interoperability, and local capacity building. Provide targeted training and knowledge-transfer (WP3) to equip researchers and end-users with laboratory and bioinformatics skills, translating methods and tools into practice across Europe.

How we address Topic expectations (Area B)

- Widen participation. **BGE+** widens participation and improves accessibility of genomic data by mobilising distributed teams and delivering structured training and knowledge transfer.
- Establish a comprehensive biodiversity genomics system in Europe. Through the cascade-funded projects, **BGE+** pilots the orchestration of a future, scaled-out, interconnected European system for genomically enabled taxonomic research.
- Develop strategies and roadmaps for capacity building and knowledge transfer. **BGE+** co-designs national/regional capacity plans with partners and embeds them in a shared roadmap and training curriculum.

KPIs: Number and diversity of new participating researchers, institutions, projects, regions, countries; Number of local follow-up initiatives, publications, and new collaborations. Increased generation and use of reference barcodes and genomes. Number of training events delivered and their geographic coverage; Number of participants reached; Diversity of training offered; Number of training materials shared/ used/translated.

Objective 2. Address rate-limiting steps in generating, managing, and analysing Barcode and Whole Genome Sequence (WGS) data to remove technical barriers to data production and deployment.

What we will do

Deliver step-change protocols and workflows for distributed wet-lab operations (WP4) and improve open, FAIR-by-design (Findable, Accessible, Interoperable, and Reusable)

bioinformatics tools, data standards and pipelines (WP5) that connect data, metadata and knowledge for routine, interoperable use and reuse. Build on and extend established infrastructures and data systems with enhanced standardisation to connect data, metadata, and knowledge, making them accessible for use and reuse in downstream applications.

How we address Topic expectations (Area B)

- Consolidate and enhance the uptake/use/impact of genomic data. **BGE+** works towards the definition of a commons (a set of agreed-upon tools and practices) that helps consolidate the landscape of distributed efforts and lowers the access barrier to genomic and other interconnected data for taxonomists and other biodiversity scientists.
- Remove rate-limiting steps to boost uptake and impact. **BGE+** streamlines lab steps (batchable protocols) and bioinformatics (containerised, reproducible pipelines), and trials AI-assisted modules where they add value.
- Ensure data are FAIR. Improve (meta)data standards, data curation practices and tools to enhance FAIR-by-design, whilst promoting the use of open data repositories (the European Nucleotide Archive, ENA; the Barcode of Life Data System, BOLD; the Global Biodiversity Information Facility, GBIF), ensuring community-produced datasets are described/annotated and deposited to the corresponding aggregators.

KPIs: Number of new reference barcodes and genomes produced through distributed community efforts; Diversity of ecosystems and new taxa covered; Amount of institutional investment, e.g. sequencing done locally. Increase in datasets and tools meeting FAIR principles; Decrease in time from data production to mobilisation; Increase in interoperability across platforms, e.g. machine-actionable metadata.

Objective 3. Increase the policy uptake, use, and impact of genomic data to support environmental management, environmental risk assessment, and sustainable use of biodiversity.

What we will do

Promote and showcase the integration of genomic tools into real-world biodiversity science and monitoring programmes; co-develop and test use cases that generate policy-relevant evidence on species, populations, and habitats; and strengthen interfaces with regulators and managers to support decision-making and reporting (WP6).

How we address Topic expectations (Area B)

- Cooperate with policy interfaces and observation initiatives (Knowledge Centre for Biodiversity - KCBD, BioAgora, citizen science, large-scale observations). **BGE+** aligns outputs and formats with these interfaces and establishes regular exchange to support uptake.

- Ensure representative coverage, including lesser-known taxa and climate-indicator groups. **BGE+**, through the cascade-funded projects, selects target sites and taxa that close coverage gaps and brokers to bring together the results of these projects in policy making and conservation practices.
- Generate decision-ready evidence on species status, intra-species diversity and ecosystem condition. **BGE+** co-develops policy-facing use cases with agencies and produces traceable indicators and briefs for management and risk assessment.

KPIs: Number of new tools/protocols in use; Improved resolution/accuracy; Adoption by environmental agencies; Number of new species/ecosystems monitored/assessed using genomics. Number of use cases with policy relevance; Number of policy briefs; Number of policies integrating genomics evidence/tools; Number of outcomes from engaging stakeholders.

Objective 4. Establish the foundations of a comprehensive biodiversity genomics system in Europe to ensure long-term sustainable service-provision, harnessing the power of genomics for biodiversity characterisation, conservation, and use.

What we will do

Define user needs and a service portfolio for a European distributed system; assess options for integration into one or more European Research Infrastructures (WP7). Strengthen and expand **iBOL-E** and **ERGA** as Europe's nodes for DNA barcoding and whole-genome sequencing, connecting communities, standards, and facilities, and ensuring bi-directional knowledge flow (WP8, WP9).

How we address Topic expectations (Area B)

- Establish a comprehensive biodiversity genomics system in Europe and connect to existing global and European biodiversity data infrastructures. **BGE+** surveys the needs of taxonomists and biodiversity scientists, and provides a roadmap for the future upgrade of existing ESFRI (European Strategy Forum on Research Infrastructures) Research Infrastructures. It does so by working directly with the infrastructures DiSSCo (The Distributed System of Scientific Collections) and ELIXIR (Europe's distributed research infrastructure for life science data), and engaging with others, such as LifeWatch and eLTER (European Long-Term Ecosystem Research).
- Establish a European network of taxonomy and genomics experts. Widens participation in **iBOL-E** and **ERGA** networks, improves governance, and the national nodes organisation. In collaboration with **CETAF** it strengthens the links between the genomics and taxonomic communities.
- Develop coordinated capacity-building strategies and roadmaps. Through **iBOL-E** , **ERGA**, and **CETAF**, it outlines development and engagement roadmaps, mapping long-term needs and promoting standard procedures and practices across the involved communities.

KPIs: Increased **iBOL-E** and **ERGA** membership, especially in underrepresented regions; Number of guidelines, best practices, and standards shared/used by the communities, and joint outputs with global networks. Deliver infrastructure design study; Pilot distributed service network; Number of facilities connected, standard procedures adopted, and stakeholders engaged.

1.1.4 Helping the community go beyond current limitationsInnovation supporting the consolidation and enhancement of genomics uptake

To prepare a future system capable of scaled-out biodiversity genomics knowledge production, **BGE+** invests in innovation efforts by: (a) **Understanding** which tools, services, and procedures enable system-level change; (b) **Surveying** current capacity and readiness across Europe; and (c) **Innovating** to close the highest-value gaps.

Understanding. BGE+ will define what **"good enough at scale" means for barcoding, metabarcoding, and reference-genome workflows**, and what interoperability, provenance, and comparability are required for routine, distributed use. Starting with knowledge requirements derived from national and international biodiversity policy frameworks, **BGE+** will identify the shared components necessary to support the critical path for delivery at scale in a cross-border (transnational) European system for scaled-up biodiversity genomics.

Surveying. BGE+ will use these technical baselines to **map existing services and tools, understand their robustness and sustainability, as well as their interoperability**. This mapping exercise will then highlight the areas that need to be strengthened so that these technical baselines can be served in the future.

Innovating. Where the mapping identifies gaps, **BGE+ will deliver targeted, reusable solutions**. These solutions will cover, among others, a) laboratory practices and protocols, b) data informatics pipelines and data curation and management tools and c) data infrastructure components.

Together, this sequence - **understanding requirements, surveying readiness, and innovating where it matters** - supports a purpose-driven approach to **BGE+**, scaling and consolidation efforts, aimed at the future operation of a European distributed system for biodiversity genomics as a research infrastructure.

Beyond technical and infrastructure barriers, comprehensive uptake of biodiversity genomics solutions in Europe is limited by challenges of translating genetic data into regulatory indicators, calibration with existing methods, inertia around change from traditional approaches, and slow regulatory acceptance of new methods. **These barriers will be explored within the BGE+ project**, and roadmaps will be produced for operationalising biodiversity genomic approaches to **meet the needs of policy and practice**.

Continuing efforts towards a sustainable future for Biodiversity Genomics

BGE+ builds on the success of the BGE1 Project (2022-2026) (Koureas et al. 2026), a direct response to the call by the European Commission to deliver European capacity in the field of biodiversity genomics and strengthen European presence in the global landscape. Specifically, BGE1 had three objectives a) Establish functioning biodiversity genomics networks at the European level to connect and grow community capacity to tackle the biodiversity crisis using genomic tools, b) Establish and implement large-scale biodiversity genomic data generation pipelines for Europe to accelerate the production and accessibility of genomic data for biodiversity characterisation, conservation, and biomonitoring and c) Apply genomic tools to enhance understanding of pan-European biodiversity and biodiversity declines to improve the efficacy of management interventions and biomonitoring programmes.

BGE1 work delivered scientific and systemic impact across the European taxonomic and biodiversity genomics communities. Systemic changes focused on increasing the rate of production of genomic data across communities and borders, and improving the efficacy of management interventions and biomonitoring programmes with sound genomic tools. Scientific impact focused on establishing positive feedback loops between scientific knowledge and policy needs. BGE1 presented proofs of concept demonstrating how cross-border collaboration can support entire value chains, including field sampling, sequencing, analysis, and application. The project specifically focused on establishing the necessary international collaborations, networks, and practices to enable such scaled-up operations. **BGE+ is taking a further step in this direction of systemic and scientific transformation**, examining the required mechanisms that will enable such cross-border collaboration and consolidation to be effective, sustainable, and impactful in the long term (Table 1).

Table 1.

Comparative analysis of how BGE1 and BGE+ complement each other in the key focal areas of work and how BGE+ paves the way for the future operation of a biodiversity genomics European system (Research Infrastructure)

Work Area	Goal of BGE1 (2022-2026)	Goal of BGE+ (2026-2030)	Research Infrastructure (European System) (2031 onwards)
Scaling out - Strengthening Participation & Skills	**Pilot** Pilot cross-border production by connecting a small number of project beneficiaries (proof-of-concept)	**Scale out (WP2)** Scale cross-border collaboration using the cascade grants mechanism and piloting how a future distributed model would work	**Routine distributed operations** Fully scaled up cross-border collaboration, sampling, sequencing and processing can be achieved across multiple laboratories and teams (fully distributed model)

Work Area	Goal of BGE1 (2022-2026)	Goal of BGE+ (2026-2030)	Research Infrastructure (European System) (2031 onwards)
	Training needs assessment Map training gaps for DNA barcoding and whole-genome technologies	**Targeted training (WP3)** Deliver targeted training connected to the use of standard tools, technologies, and connected to the needs of the broader community of cascade-funded projects	**Continuous training** Standardised training is provided at national level, and capacity-building activities offered by national nodes of the infrastructure
Innovation	**Solution prototyping & data foundations** Drive development of solutions to support in-project needs; Support fundamental European data infrastructure (e.g. European BOLD)	**Consolidate lab & informatics innovations (WP4, WP5)** Innovation linked to lab and informatics needs for the generation and curation of reference libraries (for barcodes and whole genomes)	**Sustain and expand the service portfolio** Continuous targeted innovation efforts to improve the service portfolio of the infrastructure to meet community needs
Translation to Policy and Practice	**Demonstrated value** Connected in-project-generated data with real-world applications through BGE1 case studies	**Evidence-to-policy pipelines (WP6)** Co-design and establish value chains from genomic data to application - produce guidance, indicators, and reporting workflows aligned with EU policies & GBF	**Deployed policy-aligned services** Operate decision-support and reporting services as part of the RI
Operations as a distributed system & Community Engagement	**Setting roadmap** Evaluate the options for the sustainable provision of services linked to the needs of the biodiversity genomics community	**Integration options analysis (WP7)** Evaluate which European infrastructure would be able to serve the needs of the community and plan steps for integration	**Deploy and operate** Develop and operate the services linked to the needs of the biodiversity genomics community as part of the service portfolio of an ESFRI Research Infrastructure
	Network set-up Support to develop network capabilities (e.g. structure, communications) for iBOL-E and ERGA	**Strengthen & professionalise (WP8, WP9)** Enlargement of networks, increase of organisational and technical maturity - improve connections between networks	**Consolidate** Networks fully supporting the research infrastructure operation at national and European level

1.2 Methodology

1.2.1 Overview of BGE+ methodology

The structure of the **BGE+** work programme builds on previous community efforts (namely the BGE1 project), advancing the work towards the delivery of a European distributed system for biodiversity genomics. The overview of the **BGE+** methodology is linked to the work areas (Table 1) as follows (Fig. 1).

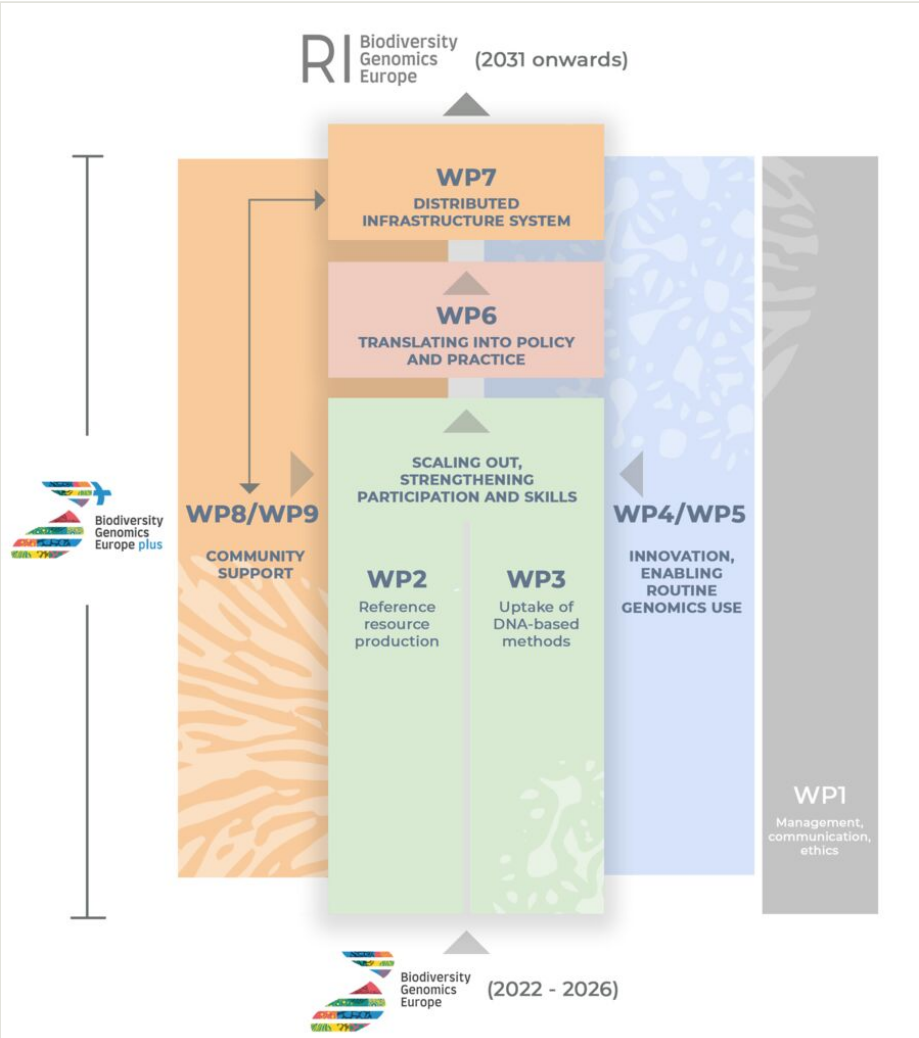


Figure 1.

BGE+ work programme and connections with previous work (BGE1 2022-2026) and hand-over/sustainability plans (Biodiversity genomics European system - Research Infrastructure).

Scaling-out - Strengthening Participation & Skills (WP2 & WP3) The project focuses on **widening participation (scaling out)**, emulating and assessing future continental-scale orchestration and collaboration models for a highly distributed system for biodiversity genomics knowledge production. **WP2** deploys cascade grants to mobilise researchers across Europe, aligning activities with local conservation, bioeconomy, and policy needs. The cascade grants will facilitate interoperable outputs contributing to the consolidation of the landscape. **WP3** converts methods and tools into practice through targeted training and knowledge transfer, onboarding cascade-funded teams and end-users, and feeding back capacity needs that guide the innovation WPs.

Innovation (WP4 & WP5) Linked to the content delivery branch is the innovation branch of **BGE+**. **WP4** and **WP5** focus on innovation activities that aim to raise the effectiveness and complementarity of distributed efforts by improving the interoperability of produced data, lowering the entry barrier to available technology and tools, and developing best practices and community standards. **WP4** and **WP5** serve the innovation branch, focusing on step-change laboratory protocols and improving open bioinformatics tools and services, respectively.

Translation to Policy & Practice (WP6) WP6 synthesises outputs from **WP2–WP5** into policy-aligned roadmaps and use cases for biodiversity monitoring and management, covering both barcodes/metabarcoding and whole-genome applications.

Operations as a distributed system & Community engagement (WP7, WP8, & WP9) **WP7** maps user needs, audits existing services. It develops an options analysis and service portfolio for long-term integration within the European Research Infrastructure landscape, drawing evidence and priorities from the preceding WPs. **WP8** (**iBOL-E**) and **WP9** (**ERGA**) maintain the project's interface with the broader communities. They co-develop standards and best practices, host knowledge hubs, and ensure a bi-directional flow between **BGE+** and European nodes of global initiatives. They also provide scientific support to cascade projects and channel community feedback to **WP3–WP5**, strengthening coherence across strands.

Coordination, ethics, and DEC (WP1) **WP1** provides scientific and administrative coordination, ethics oversight and the dissemination-exploitation-communication (DEC) framework, including the Knowledge Platform. Through the Scientific Steering Board (SSB), WP1 aligns cascade-grant governance and ensures that WP synergies remain tight and purposeful.

1.2.2 Detailed methodology

WP1 Project management, communication and ethics

WP1 coordinates the Project in both administrative (T1.1) and scientific aspects (T1.2). The WP further provides support to Project partners with communication, dissemination, and exploitation activities (T1.3). Guided by the strategic Dissemination, Exploitation, and Communication plan, T1.3 will refine, update, and expand the mechanisms put in place by BGE1 while adding new tools designed to serve the new endeavour. Such is the case of the Knowledge Platform, which will be expanded to accommodate the new project's outputs, the project's communication impact assessment report, and the **BGE+** final event that focused on application and science-policy connection. T1.4 oversees the alignment of project activities with ethical standards, particularly in relation to diversity and inclusion, personal data protection, the use of AI, and the handling of biological material and digital sequence information (DSI) in compliance with the Nagoya protocol and Access and Benefit Sharing (ABS) obligations. Relevant ethical standards will be identified with Project members at the beginning of the project through a survey. A Project Code of Conduct will be established to provide information about the ethical aspects and

guidance for high ethical integrity throughout the diverse Project activities. Follow-up surveys will be conducted to monitor partners' ethics-related practices, and the Code of Conduct will be updated as needed. A Project ombudsperson will be selected to provide just resolution of potential issues in an impartial, confidential, and independent manner. The WP will also take responsibility for the co-organisation of the Synergy Alignment Group (connecting to the project funded for Area A of the Topic) and the SSB (the **BGE+** governance body to support the definition and implementation of the cascade-funded projects framework).

WP2 Community support for knowledge production

WP2 plays a pivotal role in achieving the **BGE+** objective O1 by its work to scale up production and use of DNA barcode and genome sequence data. Its focus is community support for knowledge production (a) increasing geographical and species coverage in reference barcode libraries and improving the biodiversity monitoring toolkit for ecological assessments, (b) producing reference genomes for conservation and monitoring applications, and (c) providing novel insights into species and genomic diversity, detailed in section 1.2.3 below. WP2 will establish a comprehensive framework for the Cascade Grants mechanism, guiding calls for proposals, evaluation, and project selection aligned with **BGE+** objectives. Secondly, WP2 will act as a broker connecting cascade-funded project outputs with WPs and Tasks across the **BGE+** work programme, essentially amplifying the impact of individual cascade-funded projects. To achieve this, we will develop a robust framework that ensures open access, data harmonisation, local capacity building, and adherence to best practices (T2.1). This framework will be operationalised through the selection and evaluation of cascade-funded projects, which will be onboarded and monitored for their implementation, progress, and impact (T2.2). To ensure alignment across other WPs, we will establish the selection and evaluation criteria, as well as topic areas for the projects to be funded under T2.2, in conjunction with representatives of other WPs and the **BGE+** SSB. This will enable the publication of calls and the successful onboarding of selected projects. Our framework will facilitate the integration of new participants into the **BGE+** distributed infrastructure, expanding the **ERGA** and **iBOL-E** networks and enhancing data production and applications of reference genomes and barcodes for biodiversity research (T2.2). A detailed report (D2.2) will summarise the integration of new partners into the **BGE+** distributed infrastructure, highlighting their contributions to the project's goals. Furthermore, we will assess the added value of cascade projects, evaluating their individual and collective impacts and integrating them into **BGE+** outcomes in a policy brief (D2.3). This will enable us to understand the effectiveness of the cascade grants mechanism and make informed decisions for future project development. Through WP2, we aim to create a sustainable and inclusive community that supports knowledge production, driving the advancement of biodiversity research and conservation, enabled by the cascade funding. By establishing a robust framework for cascade grants, we will foster collaboration, innovation, and impact, ultimately contributing to the Project's overall objectives.

WP3 Training and knowledge transfer for scientists and end-users

WP3 plays a central role in ensuring that the project's strategic goals can be realised by building the human and institutional capacity necessary for biodiversity genomics in Europe. To address the uneven distribution of expertise across the continent, the work package will deliver targeted training and knowledge transfer and will directly support objective O1 (mobilise the distributed network of taxonomists and genomic researchers across Europe to scale up production and use of DNA barcode and genome sequence data). The activities will begin with a systematic mapping of the current training landscape, carried out through surveys and community engagement, to identify gaps in capacity and priority needs within the **iBOL-E** and **ERGA** networks (T3.1). Based on this evidence, WP3 will design a roadmap for structured capacity building, ensuring that resources and training efforts are deployed strategically across the European research community. Training events will incorporate and cover wet lab and dry lab topics on sample collection and processing, library construction and sequencing, genome assembly, curation and annotation, barcode production and curation (T3.2). The training courses will respond to the needs of the community, including the cascade-funded projects. The translation of new protocols and pipelines emerging from WP4 and WP5 into accessible training materials will directly contribute to O2, lowering technical barriers to the production and analysis of genomic data. Capacity building initiatives will be designed as field-based, class-based, laboratory-based, and online events. Training activities will be delivered at multiple levels, ranging from introductory courses that establish essential background knowledge to advanced and highly targeted modules that address specific methodological challenges and project needs. This tiered approach will ensure that cascade-funded projects and community partners can adopt best practices in both wet-lab and bioinformatics methods, while also creating opportunities for stakeholders from management and industry to acquire the skills needed to use genomic data in real-world applications. In this way, WP3 contributes directly to O3 by fostering the policy uptake and societal impact of biodiversity genomics. To ensure sustainability and a long-term legacy, WP3 will develop a Capacity Building Resource Platform, providing a central point of access to the training programme and its outputs via an established GDPR-compliant (General Data Protection Regulation) tool (T3.3). This will build on and expand the existing **ERGA** Knowledge Hub (EKH 2026) and create a new **iBOL-E** Knowledge Hub, both of which will serve as enduring community resources beyond the lifetime of the project. By embedding training materials and outputs into these open infrastructures, WP3 will help lay the foundations for a European biodiversity genomics system that can continue to grow and evolve in the future, thus contributing to O4 and ensuring that the skills and knowledge base underpinning the Project remain a permanent asset for European research and society.

WP4 Improving laboratory protocols and approaches

WP4 serves as the laboratory innovation engine of **BGE+**, directly addressing multiple Project goals through systematic cost reduction and standardisation. The primary focus of WP4 is objective O2, working to address rate-limiting steps in generating, managing, and analysing Barcode and Whole Genome Sequence (WGS) data. This includes catalysing

decentralised production of reference barcodes and genomes through multiple complementary approaches, including revolutionising specimen utilisation by facilitating easy to use protocols for fresh specimen barcoding (T4.1), optimising historical DNA protocols for museum collections (T4.2), breaking expensive cold chain dependencies through room-temperature preservation methods (T4.3), and enabling genome sovereignty through cost-effective reference genome production using portable sequencing platforms (T4.4). The work package also delivers a laboratory intercalibration framework (T4.5) for meta-barcoding-based biomonitoring studies. This laboratory-based standardisation enables reliable integration of innovative genomic tools into real-world biomonitoring programmes, providing the quality assurance necessary for evidence-based environmental reporting and management decisions, and supports the delivery of O3, to increase the policy uptake, use, and impact of genomic data. All protocols, workflows, and training materials will be designed as FAIR resources, openly shared through established platforms. This modular, community-supported approach ensures protocols remain current while facilitating widespread adoption and adaptation across the European research landscape and beyond. Through systematic benchmarking across taxonomic groups, preservation methods, and sequencing scales, WP4 will provide the methodological foundation early in the Project to ensure cascade-funded projects in WP2 benefit from validated methods. This comprehensive approach aims to support the transformation of biodiversity genomics from a high-cost, centralised activity into an accessible, distributed capability that can be deployed anywhere, anytime, by anyone. Thus, WP4 also contributes to O1 by removing the primary barriers (complexity and cost) that limit access to genomic technologies. WP4 democratises DNA barcoding (T4.1), museum specimen genomics (T4.2), and reference genome sequencing (T4.3, T4.4) by developing ultra-low-cost, fully documented and modular open access workflows that accommodate both resource-limited users and high-throughput laboratories. The work package contributes to O4, to establish the foundations of a comprehensive biodiversity genomics system in Europe through its commitment to open science and standardisation.

WP5 Improving bioinformatic tools and services

The primary focus of WP5 is to tackle critical informatic challenges to address rate-limiting steps in generating, managing, and analysing Barcode and Whole Genome Sequence (WGS) data (O2). Thus WP5's focus on informatics complements WP4's focus on laboratory methods. The specific goals of WP5 are to enhance bioinformatic tools, data management systems, and integrate research infrastructures to support broader engagement in biodiversity genomics across Europe. This WP will build on previous efforts under BGE1 (Heil et al. 2026) and other European projects, and will develop innovative work in three major areas: (i) Scaling up reference library production for genome and barcode generation and curation. A comprehensive framework for benchmarking genome workflows will be developed (T5.1), and assembly and annotation pipelines will be improved to democratise community access (T5.2). Current bioinformatic barriers in reference barcode generation and curation pipelines will be addressed to facilitate wider use and standardisation (T5.3). (ii) Improving biodiversity

genomics infrastructure and FAIR data management systems. The WP will build on emerging standards, e.g., RO-Crates (Soiland-Reyes et al. 2022), and align with international best practices to improve the capture of provenance and source information, and develop metadata curation systems that increase interoperability between genomics and other biodiversity infrastructures (T5.4). Reference library data access via dedicated data portals and scholarly publications will be streamlined in line with FAIR-by-design principles (T5.5). (iii) Developing frameworks for downstream analysis for biodiversity monitoring. The focus will be on the analysis of intra-specific genomic data and the standardisation of genetic composition metrics (T5.6), as well as on prototyping a scalable system for metabarcoding data analysis to ensure data comparability across European biodiversity monitoring surveys (T5.7). The work of this WP will contribute to **BGE+** objectives O1, O3, and O4 by supporting the cascade-funded projects (WP2), resulting in the production of guidelines and best practices to be shared with the communities (WP8, WP9). These guidelines will be converted into training materials for capacity building in WP3. Data produced in WP4 will be integrated into the developed bioinformatic pipelines, while the biodiversity application framework tasks (iii) will support the roadmaps for genomics uptake in biodiversity monitoring (WP6). The technical developments and enhancements of RI services in the biodiversity landscape will help address gaps identified in WP7. Overall, the results of WP5 will support the **iBOL-E** and **ERGA** communities (WP8 and WP9) in data production, analysis, management, and publication in a distributed system for biodiversity genomics.

WP6 Biodiversity genomics knowledge exploitation - Science and Policy cases

The focus of WP6 is to increase the policy uptake, use, and impact of genomic data (O3). It will promote the use of cutting-edge genomic tools in biodiversity assessment and monitoring, in support of European biodiversity policy frameworks (O3), connected to existing initiatives and infrastructures. It aims to advance the application of genomics, from barcodes to whole genomes, to address the European Union's critical biodiversity objectives, including species and ecosystem assessments, as well as restoration efforts. Identifying and using high-impact application use cases, WP6 will contribute to establishing biodiversity genomics as a fundamental pillar for evidence-based decision-making across Europe. The activities of WP6 will be strategically integrated into the European landscape of biodiversity initiatives, stakeholders and policies, aligning goals, avoiding redundancy of actions and enhancing complementarity. To achieve this, WP6 activities will establish such a foundation through a comprehensive effort to identify, prioritise, and connect with key European biodiversity policies, directives, projects, initiatives, and stakeholders who can most benefit from genomic applications (T6.1), aligning with the EU Biodiversity Strategy for 2030 (European Commission 2020) and the Nature Restoration Regulation (European Commission 2025). This will result in a report on the strategic integration of genomic applications in biodiversity policies, programmes, and stakeholder networks (D6.1). WP6 will build two complementary roadmaps, based on use cases, that aim to detail the paths for the practical integration of genomic methodologies. The first roadmap (T6.2) focuses on the adoption of DNA barcoding and metabarcoding for widespread biodiversity monitoring, addressing major current gaps in

coordinated organisational structures, harmonised workflows, and interoperable infrastructure required for coherent implementation across countries. It will benefit from key innovations developed in WP4 and WP5 to define essential components for cross-border application. Alignment with stakeholder needs will be achieved through consultation, utilising interviews and targeted workshops. Simultaneously, a second roadmap (T6.3) will be developed for the strategic application of whole-genome-based data, specifically addressing intra-species genetic diversity. It leverages gold-standard use cases with extensive genomic data across different taxonomic groups and will benefit from harmonised bioinformatics pipelines (implemented in WP5) to establish cost-efficient workflows for generating and analysing WGS data to derive meaningful Essential Biodiversity Variables (EBVs) (Pereira et al. 2013), providing clear guidelines for scientists, biodiversity managers, and policy makers from sampling to policy uptake. These roadmaps will integrate relevant results from cascade-funded projects (WP2) that expand the reach of use cases, and align with the strategic development of a pan-European system for biodiversity genomics (WP7). It will result in two complementary guidance documents, each one focused on a specific dimension of the genomic methods to be employed (D6.2 and D6.3). The conclusions of stakeholder mapping and the two complementary roadmaps will feed the final phase, which consolidates the strategic role of genomics by proposing a governance-oriented framework (T6.4). Through consultation with stakeholders, the task will refine implementation scenarios, resulting in a strategic synthesis report (D6.4) with actionable recommendations for institutional coordination and the sustained integration of genomic tools into European biodiversity monitoring and policy. Stakeholder consultations in T6.1 and roadmap development (T6.2, T6.3) deliberately bring together genomics researchers, taxonomists, environmental managers, and policy advisors. These consultations produce technical requirements that guide innovation priorities in WP4-5 and identify training needs for WP3, creating a bidirectional flow between data generation and application.

WP7 Towards a European distributed system for Biodiversity Genomics

WP7 will undertake options appraisals to drive decisions regarding the development and operation of a pan-European research infrastructure on biodiversity genomics. It addresses the current gap between research needs and the infrastructure services required to operate at scale, and directly addresses **BGE+** Objective O4 to establish the foundations of a comprehensive biodiversity genomics system in Europe.

1. Users, needs, and current landscape (T7.1, T7.2). WP7 will define priority user groups (research, monitoring, and policy actors), map existing infrastructures and services, assess their maturity and accessibility, and identify gaps in relation to real-world use cases. Through this work, the WP will deliver a User Needs Assessment (D7.1) and a Service Scope & Gap Analysis (D7.2). Both reports will be used in the subsequent steps in the evaluation of the options for a future RI on biodiversity genomics.
2. Scientific and technical case (T7.3). Following the work on user needs, WP7 will develop a proposal on a suitable service portfolio - covering data generation and access, analytical tools, training, application support, and interoperability/policy

requirements - through participatory workshops and interviews. As part of this work, the WP will deliver a Technical Service Portfolio (D7.3) report. The Report will help in understanding which of the existing RIs in the ESFRI landscape could potentially provide any of the services identified.

3. Following the mapping of infrastructure and users, WP7 will evaluate, through a series of thematic workshops (T7.4), the potential integration of the proposed biodiversity genomics service portfolio into one or more existing European RIs. Building on the mapping, WP7 will co-design solutions with existing RIs via thematic workshops, assess feasibility and upgrade routes (ESFRI-aligned), and deliver Actionable Recommendations for Integration (D7.4). **BGE+** has already engaged with several RIs in the landscape to ensure willingness for engagement in the process, including DiSSCo, ELIXIR, and others (Arvanitidis et al. 2025). The approach of the WP includes a close collaboration with WP4 & WP5 (laboratory and bioinformatics developments) to ensure the service catalogue is grounded on current community practices; WP6 (policy roadmaps) so that proposed services meet regulatory and reporting needs; and WP2, WP8 and WP9 to align with cascade-funded activities and the **iBOL-E** and **ERGA** communities for broad, equitable uptake. By delivering a user-grounded service catalogue (D7.1–D7.2), a co-designed technical portfolio (D7.3), and integration recommendations (D7.4), WP7 provides the evidence base for decision making and will enable one or more ESFRI RIs to engage in delivering a distributed European biodiversity genomics system.

WP8 Network enlargement and support to iBOL-E

WP8 focuses on supporting, strengthening, and expanding the work of the DNA barcoding community in Europe via **iBOL-E** (Hollingsworth et al. 2026, Kaitetzidou et al. 2026), the European node of the International Barcode of Life (iBOL) (Ratnasingham and Hebert 2007). This work directly addresses O4, working to establish the foundations of a comprehensive biodiversity genomics system in Europe. WP8 will provide the secretariat support for **iBOL-E**, and coordinate and manage the activities of the network (T8.1). Through supporting, developing and/or establishing national or regional DNA Barcoding Nodes of iBOL (T8.2), WP8 will also develop model approaches for the set-up and roll-out of distributed low/medium throughput sequencing laboratories in Europe, to democratise access to data generation, and capitalise on the availability of low-cost portable DNA sequencing machines (T8.3). WP8 also serves to connect the DNA barcoding community to taxonomic experts linking sequence data and morphology, to enhance the quality of DNA barcode reference libraries as a resource for species identification, species discovery, and biomonitoring (T8.4). Collectively, these activities all contribute to the development of the European biodiversity genomics landscape (Kaitetzidou et al. 2026). WP8 has synergies across the **BGE+** project, acting as the nexus between the consortium and the wider DNA barcoding community. The continually updated understanding and in-depth knowledge of the DNA barcoding landscape in Europe, as provided by WP8, will inform the appraisal of biodiversity genomics infrastructure options in WP7, further supporting the delivery of O4. Likewise, WP8 has been designed to

closely align in structure and intent with WP9 (Network enlargement and support to **ERGA**), promoting synergies through joint efforts that support the delivery of a pan-European biodiversity genomics system. Beyond O4, WP8 supports O1, O2, and O3 by connecting **iBOL-E** community support to cascade-funded projects (WP2). Likewise, identified community needs will be fed through to WP3 (training), WP4 (laboratory protocols), and WP5 (data and informatics). In turn, the outputs of these other WPs will be made available to the iBOL community, creating a positive feedback loop.

WP9 Network enlargement and support to ERGA

WP9 is dedicated to consolidating and extending the **ERGA** network (Mazzoni et al. 2023) driving the production and exploitation of reference genomes for eukaryotic biodiversity, representing the European bioregion's participation in global efforts of the Earth BioGenome Project (EBP) (Lewin et al. 2018, Blaxter et al. 2025). Thus, WP9 (genomes), is designed to be complementary to WP8 (barcodes), to support delivery of objective O4: establish the foundations of a comprehensive biodiversity genomics system in Europe. WP9 goals are centred on a community support framework that: Widens participation and increases the accessibility and use of genomics data for biodiversity management through scientific direction and support for the **ERGA** community to scale distributed production (T9.1 & T9.2); Empowers researchers to generate high-quality reference genome resources efficiently through community-based support systems with an open forum to build methods consensus, share expertise, and implement genomics-based biodiversity assessments (T9.2 & T9.3); Grows and aligns the network of genome production hubs and application/use actions through coordination efforts to cultivate synergies and harmonise translational actions supporting country and researcher needs with respect to biodiversity monitoring and reporting (T9.3 & T9.4); Strengthens taxonomic expertise in applying genomics technologies for biodiversity identification and monitoring, including genetic diversity within and between populations (T9.4). WP9 thus consolidates the coordination role of **ERGA** as the European node of the EBP, as well as contributing to broadening the impact of **BGE+** objectives O1, O2, and O3. This community support framework also forms a bridge between the tasks and activities of **BGE+** and the **ERGA** network. This involves guiding members in designing projects that leverage expertise to secure financial support for increased biogenome production and exploitation, as well as providing and directing technical support services to cascade-funded projects (WP2) through Community and **BGE+** resources. Monitoring training and capacity building needs will inform the work of WP3, and relevant outputs of WP3 will be disseminated by WP9. Similarly, WP9 will disseminate the outputs from WP4 supporting field and laboratory work, and from WP5 providing data and informatics solutions, as well as feeding back needs to WP4 and WP5. For WP6, leveraging community expertise and experiences will inform stakeholder engagement tasks, particularly in relation to policy and decision-making, as well as the harmonisation and standardisation of whole-genome data and analyses to support biodiversity assessments, especially for intra-species diversity. WP9's support of the forum and network of expertise for reference genomes provides the means for identifying existing biodiversity genomics services and understanding user needs to support the work of WP7. Finally, as part of the mission to

build and maintain a strategic partnership with **iBOL-E**, joint actions with WP8 will promote synergies and alignments of efforts, as well as support a unified approach to delivering a distributed system for biodiversity genomics in Europe.

1.2.3 Financial Support to Third Parties (Cascade Grants) - Enlarging and consolidating the biodiversity genomics community

Scope

Financial Support to Third Parties - FSTP (cascade grants) is a core **BGE+** instrument for connecting currently dispersed efforts in biodiversity genomics and piloting the operating model of a distributed, pan-European knowledge-production system. A multitude of teams across Europe already generate Barcode and WGS data. When aligned on common methods, standards, and data services, these efforts can deliver cumulative impact, address priority knowledge gaps, and create economies of scale. **BGE+** will also strengthen capacity in genomic taxonomy in data-limited areas, such as Central and Eastern Europe, the Mediterranean, and outermost regions, linking genomic evidence production to species discovery, local conservation, and biodiversity management needs. **Cascade-funded projects are to specifically support the following areas**:

Addressing gaps in biological knowledge

- **Filling priority gaps** in reference libraries (barcodes and genomes) across taxa, biogeographic regions and ecosystems, explicitly targeting so far under-represented regions and groups. Groups, such as alien or endangered species and species of economic importance, including pollinators, will be specifically targeted, as well as species groups of policy relevance for biomonitoring. Additionally, taxonomic groups underrepresented in current national or international barcode and genome reference databases will be prioritised. The results will contribute to filling specific regional and national biological knowledge gaps.
- **Translating data to policy-ready baselines** that can be directly mobilised into monitoring and management roadmaps. Projects could also contribute to the development of regional or national baselines, providing the required background knowledge for future monitoring of shifts in population sizes and richness.

Addressing gaps in innovation and best practices - additionally to the reference libraries production efforts, cascade-funded projects may also:

- Contribute to improving the public offering of tools and resources at the national or European level.
- Contribute to the development of best practices and Standard Operating Procedures, as well as the dissemination of such products through **iBOL-E**, **ERGA** , and **CETAF** networks.
- Improve metadata quality and taxonomic efforts (provenance, sampling, vouchers, legal compliance), which increases reuse and reliability for downstream analyses.

For cascade-funded projects managing samples and data in a transnational manner a pre-award ABS/DSI compliance requirement will be included in the proposal templates. As an underlying premise, **BGE+** will ensure, through a list of criteria for awarding and evaluating the cascade grants, that each project will:

- Make use of standard, shared services and tools that ensure the comparability of knowledge outputs and interoperability of all produced data;
- Curate, annotate, and deposit all data produced to agreed-upon open public data repositories (e.g. ENA, BOLD, GBIF, DiSSCo, etc.);
- Receive practical support for training personnel and onboarding them to the European communities of **iBOL-E**, **ERGA**, and **CETAF**;
- Connect their work and results to **BGE+** work programme;
- Use citizen science activities for co-creation efforts, engaging local communities when possible and applicable.

Cascade-funded projects connected to the rest of the BGE+ work programme

BGE+ connects the cascade-funded projects to the objectives of the project by design (Fig. 2). Facilitated by the work in WP2, WP3 to WP9 are consulted in the process of the definition of the requirements, expected outcomes and conditions for the Topics to be funded under the FSTP scheme (T2.1). Furthermore, the participants in these WPs also provide support and guidance as needed to the grant recipients (T2.2). Finally, the outputs of the cascade-funded projects are connected to the WPs (T2.3) while simultaneously being integrated into the **ERGA**, **iBOL-E**, and **CETAF** networks, as well as the distributed infrastructure and policy applications. This framework ensures that the FSTP scheme is used not only to widen and consolidate participation but also to provide distributed capacity in the innovation and exploitation agenda of **BGE+**.

Building on BGE1 and network experience

In BGE1, subcontracting was used to engage external teams. These teams took on parts of the BGE1 content-delivery pipeline - field sampling, taxonomic identification, sample processing, and sequencing. In **BGE+**, as we scale out the content delivery, this previous experience will be used to set clear requirements, deliverables, and performance standards for the cascade-funded projects.

1.2.4 Connecting BGE+ to relevant initiatives and projects

Aligning efforts to increase taxonomic capacity (Connecting to the project in area A of the Topic)

In addition to **BGE+** serving as the primary carrier for the advancement and development of **iBOL-E** and **ERGA**, it aims to contribute directly to **CETAF**'s taxonomy agenda. As such, **BGE+** will work closely with the project selected for funding in Area A of the same Topic (HORIZON-CL6-2025-01-BIODIV-03). Specifically, together with the selected project, **BGE+** will form a Synergy Alignment Committee. The role of this committee will be to work towards the harmonisation of morphological and genomic data streams,

strengthening interoperability and adoption of genomics-informed approaches in taxonomic work. Forming and operating the committee will be under shared responsibility between **BGE+** and the project selected in Area A. Preliminary agreements are already in place regarding this approach with consortia addressing Area A of the Topic. Alignment activities have already started between the projects BGE1 and TETTRiS and shall continue as the projects mature. **CETAF** (leading partner in TETTRiS) is also a core partner in BGE1 and **BGE+**, which streamlines communication and allows for planning of joint activities.

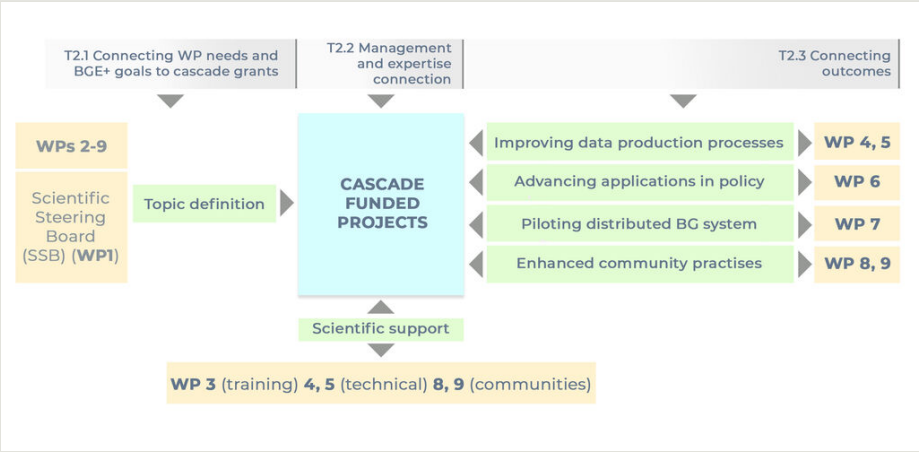


Figure 2.

Role of the Financial Support to Third Parties (cascade-funded projects) scheme in **BGE+**. The diagram is showing inputs for the definition of the cascade grant calls, the support provided during implementation, and the connection of the outputs to **BGE+** WPs. WP2 Tasks provide brokerage, facilitation, administration, and monitoring functions in the process.

Biodiversity Meets Data (BMD) Project (HORIZON-CL6-2024-BIODIV-01: Digital for Nature)

The BMD project Link: https://www.bmd-project.eu/ represents a significant investment in consolidating and organising available biodiversity data at a level of granularity that would enable detailed spatio-temporal biodiversity analyses. BMD will “create a centralised digital platform, referred to as a Single Access Point (SAP), for managers of natural resources and policymakers to support biodiversity conservation across Europe”. **BGE+** and BMD will work together in a) using the BMD SAP for developing and offering analytical pipelines, where those rely on the availability and combination of spatio-temporal biodiversity data, and b) curate and serve all produced data from **BGE+** to the BMD data infrastructure (directly or through mediating aggregators, such as GBIF or BOLD). Furthermore, **BGE+** and BMD will work together to identify additional services and resources that could rely on the BMD infrastructure to serve the genomics community. **BGE+** and BMD share a significant number of partners (including the coordinator - Naturalis), ensuring that such efforts will be prioritised from both projects.

Connecting to ESFRI Research Infrastructures

BGE+ is looking into a sustainable long-term future of service provision through the lens of our European Research Infrastructures. During BGE1, the community clearly supported this vision. As the first step, the community surveyed the landscape of RIs, their position, and the possibility of them offering added-value services that address the needs of biodiversity genomics for taxonomy and conservation purposes. In this context, RIs that have been previously identified as candidates for taking on the biodiversity genomics user needs are now direct partners in **BGE+**, including DiSSCo and ELIXIR. A dedicated WP (7) is tasked with assessing the technical, financial, and organisational feasibility of a major upgrade of one or more of those RIs so that they will be able to develop the necessary (to be defined also during the project) services and offer them as part of the portfolio to the European community of biodiversity scientists. In addition to DiSSCo and ELIXIR, WP7 will consider service portfolios of other Environmental RIs, including LifeWatch and eLTER (Arvanitidis et al. 2025).

Collaboration with other Projects under other relevant Topics

The **BGE+** consortium is especially interested in connecting with the projects selected for funding under the Topics (i) HORIZON-CL6-2025-01-BIODIV-02: Strengthening the capacity of citizen science in biodiversity observation and (ii) HORIZON-CL6-2025-01-BIODIV-04 on large-scale biodiversity observations. Specifically, for (i) significant investments in engaging local communities in biodiversity genomic surveys have been made in the BGE1 project. **BGE+** is committed to continuing to engage these local communities, as co-creation efforts are necessary for acceleration and impact delivery. As it is now expected that a dedicated project on citizen science will be funded, **BGE+** is exploring the potential to leverage its previous investments (BGE1) through collaboration with the new project under 01-BIODIV-02. Regarding (ii), **BGE+** expects that projects selected for funding in this Topic will propose the integration of (meta)barcoding methods for delivering high-throughput local biodiversity observation solutions. As such, it is expected that the need for engaging with local actors and supporting them in sample collection, management and processing, as well as lowering barriers to high-throughput sequencing or low-cost sequencing methods, would be a prerequisite to scaling up any future continental-scale in situ observation systems. In this context, **BGE+** will connect with the projects under this Topic and establish a dialogue to understand the needs for capacity and access to resources and tools. These needs will be taken into account in establishing the requirements and designing the future European system (research infrastructure) for biodiversity genomics, as planned in **BGE+**.

1.2.5 Integrating efforts: Connecting the taxonomic, barcoding, and reference genome communities

As the European nodes of the iBOL and EBP global initiatives advancing the comprehensive application of genomic science to biodiversity research, **iBOL-E** and **ERGA** represent the two communities of practice operating in the European bioregion. As Europe's network of biological and geological collections, **CETAF** brings together natural

history museums, botanical gardens, and biodiversity research centres holding a wealth of biological collections, including animals, plants, fungi, and genetic resources. Aligning efforts through leadership and participation of these communities in the BGE1 Project has laid the foundation for closer collaborations through integrative taxonomy approaches and the development of a joint vision to transform how Europe organises, coordinates, and delivers genomics data for biodiversity research, monitoring, and policy applications. The commitment to work towards common goals, leveraging genomic science, was formalised in 2024 with the signing of the Memorandum of Understanding between **iBOL-E** and **ERGA**, establishing the basis for the development of a shared scientific and societal mission. The communities recognise the importance of facilitating the completion of reliable barcode and genome reference libraries for European taxa, which form the foundation upon which genomics-enabled biodiversity science and impact are delivered. Their complementarity forms a natural partnership contributing to breadth - broad-scale biodiversity assessments using DNA barcoding and metabarcoding for species discovery, monitoring, and ecosystem diagnostics - and depth - whole genome data supporting evolutionary research, conservation, and precision genetic composition monitoring - across a variety of applications. Building on the experience and achievements to date, **BGE+** serves to advance the work of the communities towards the long-term goals of establishing an integrated European biodiversity genomics landscape. The identification of shared challenges and opportunities present clear areas of convergence: they require well-curated, legally compliant, and taxonomically verified samples; harmonised standards for field metadata, laboratory protocols, informatics workflows, and data deposition; they depend on skilled researchers across taxonomy, genomics, bioinformatics, and data science; demonstrating the utility and importance of integrating genomics and taxonomy into biodiversity monitoring and assessments is also a common goal. By delivering best practices in genomics **BGE+** will equally serve to the overarching goal of building a robust integrative taxonomic system, aligning efforts and ensuring cross-fertilisation among **ERGA**, **iBOL-E**, and **CETAF** networks. A core feature of **BGE+** is the co-development of standardised, interoperable components that promote reusability, consistency, and integration across the biodiversity genomics value chain: from Standard Operating Procedures (SOPs) for sample collection and data generation steps to shared metadata frameworks compliant with international standards, as well as from common best practices and technical implementations for data processing, submission, and analysis to centralised knowledge hubs, documentation platforms, and training materials to serve the communities and foster widespread adoption. By aligning distributed efforts under a common framework, **BGE+** ensures that local activities contribute to regional and global goals, while respecting national priorities and expertise, creating a federated yet coordinated system that captures the strength of distributed European biodiversity genomics infrastructures.

1.2.6 Gender dimension

The Project Consortium commits to promoting gender equality in research and innovation throughout all phases of the Project's implementation in alignment with Horizon Europe's inclusivity objectives. With the support of the Advisory Board and T1.4 Ethics, we will

oversee our performance and strategy for addressing gender and wider inclusivity and diversity. In training, communication, and community and stakeholder engagement activities, we will emphasise our aim to reach underrepresented groups, including women, local communities, and early-career researchers. Through this approach, we strive to improve gender representation and equity across European research with a focus on the biodiversity genomics and taxonomy communities. In scientific content, the only meaningful gender dimension of biodiversity genomics data is that we will seek to sample the heterogametic sex for reference data generation, containing both sex chromosomes where they exist and are relevant.

1.2.7 Open Science Practices

BGE+ is committed to implementing open science practices that align with Horizon Europe requirements and community best practices in biodiversity genomics. Our approach follows the principle of "open science, open data, open source" while acknowledging necessary provisions for quality assurance and publication processes. The project will deliver a Data Management Plan (DMP) that will refine the specific practices within the project. Still, the points of departure for data, metadata, source code and other computational deliverables, and provenance records are outlined below. All sequencing data generated will be deposited in established FAIR data repositories according to data type specifications. Genomic data and raw sequencing reads will be submitted to the European Nucleotide Archive (ENA) (O'Cathail et al. 2024), while DNA barcoding sequences will be deposited in the Barcode Of Life Data Systems (BOLD) (Ratnasingham and Hebert 2007). Occurrence records derived from metabarcoding analyses will be made available through the Global Biodiversity Information Facility (GBIF), ensuring broad accessibility for the research community. Additional project data, including analytical outputs and processed datasets, will be deposited in generic FAIR repositories such as Zenodo, preferably using the Creative Commons Public Domain (CC0) or Attribution (CC-BY) open licences. Data and metadata will conform to established community standards, including FASTA format for barcode and genome sequences, FASTQ for raw reads, GFF3 (Generic Feature Format Version 3) for genome annotations, BCDM (Barcode Core Data Model) for enriched barcode datasets, and DarwinCore for metabarcoding occurrences. Tabular data generated within the project (e.g. various types of analytics during data processing or downstream statistical analysis) will be packaged as FAIR digital objects using RO-Crate (Soiland-Reyes et al. 2022) with applicable data profiles and frictionless data standards to ensure interoperability. All computational deliverables will be developed as open source software using OSI-compliant (Open Source Initiative) licences, meeting Horizon Europe requirements for software accessibility. Source code will be made available through appropriate repositories based on the deliverable type. For example, Python packages will be published via PyPI, executable tools and wrappers through BioConda, workflow implementations via WorkFlowHub (Gustafsson et al. 2025) for Snakemake pipelines, and Galaxy-deployed tools through the Galaxy ToolShed (The Galaxy Community et al. 2026). Physical protocols for laboratory and field procedures will be documented and deposited in suitable repositories such as WorkFlowHub, ensuring methodological

transparency and reproducibility across the research community. The project will maintain provenance records for computational analyses using standards-compliant formats, for instance, RO-Crates with workflow run profiles. These records will be deposited and linked to associated data in FAIR repositories, enabling reproducibility of research outputs. This approach ensures that analytical processes can be independently understood, verified, and built upon by other researchers. While maintaining our commitment to open science principles, the project acknowledges the need for short-term embargoes in specific circumstances. These may be applied to ensure data quality validation or to accommodate publication timelines for research outputs currently under review. Such embargoes will be minimal in duration and clearly justified, with all data ultimately made publicly available in accordance with FAIR principles. In cases where the datasets cannot be publicly shared, the reasons will be mentioned in their metadata description (e.g., ethical rules of personal data, intellectual property, commercial, privacy-related, security-related).

2. Impact

BGE+ will harness the power of genomic science and DNA-based reference resources to strengthen taxonomic approaches for biodiversity in Europe, enhancing understanding of species and genetic diversity, widening participation, building skills, developing protocols and solutions, enhancing policy uptake, and developing the foundations of a European biodiversity genomics system. **BGE+** will provide a step change towards a distributed, inclusive, and quality-enabled biodiversity genomics infrastructure and community in Europe. **BGE+** is carefully threading its value chain, starting from the Objectives (O1-O4) → that drive the structure of project WPs (WP1-WP9) → leading to specific Outputs (Deliverables) → and directly derived Outcomes → that have Impact contributing to **BGE+** Objectives (O1-O4). The outputs of this project will have immediate impacts in terms of skills, capacity, data, protocol development, and solutions to policy needs, as well as a long-term foundation for integrating biodiversity genomics into the European Research Infrastructure landscape.

Our impact arises directly from our four Objectives:

- **Objective 1**. Mobilise the distributed network of taxonomists and genomic researchers across Europe to scale up production and use of DNA barcode and genome sequence data to expand geographical coverage and participation, and deliver novel insights into species and genetic diversity. (2.1.1)
- **Objective 2**. Address rate-limiting steps in generating, managing, and analysing barcode and whole genome sequence (WGS) data to remove technical barriers to data production and deployment. (2.1.2)
- **Objective 3**. Increase the policy uptake, use, and impact of genomic data to support environmental management, environmental risk assessment, and sustainable use of biodiversity. (2.1.3)
- **Objective 4**. Establish the foundations of a comprehensive biodiversity genomics system in Europe to ensure long-term sustainable service-provision, harnessing

the power of genomics for biodiversity characterisation, conservation and use. (2.1.1)

2.1 Project's pathways towards impact

2.1.1 Scientific Outcomes and Impact of BGE+

Our immediate scientific impacts centre on widening participation in the production and use of DNA barcode and genome sequence data; generating reference resources to underpin biomonitoring; providing novel insights into species and genetic diversity; building skills and capacity; and strengthening and growing the **iBOL-E** and **ERGA** communities. These immediate impacts are summarised in Table 2. The longer-term impact of **BGE+** is linked to its efforts to establish the foundations of a comprehensive biodiversity genomics system in Europe. The pathways to long-term impact are summarised in Table 3.

Table 2.

BGE+ Scientific impact pathways operationalising a European biodiversity genomics distributed system.

Output	Outcome	Impact
Production of DNA barcode and genome reference resources via Cascade funding (WP2)	Novel insights into (a) patterns of species diversity and taxonomy, including the discovery of cryptic species, and (b) patterns of genomic diversity, including the composition and structure of genomes across a phylogenetically broad set of species	The understanding of the diversity of species and genomes in Europe is enhanced via fundamental biodiversity insights and baselines for future research
Production of metabarcoding and resequencing datasets via Cascade funding (WP2)	Novel insights into the distribution of species and genetic diversity in relation to environmental gradients and pressures	Biological understanding of drivers of change and the efficacy of management interventions at species and genetic levels is enhanced, which in turn informs policy decisions and management strategies
Cascade funds effectively distributed to research teams across Europe (WP2)	Widened participation from underrepresented regions in the production and use of DNA barcode and genome sequence data	The ability to characterise and monitor biodiversity across Europe is increased, particularly in biodiversity hotspots in southern and eastern Europe
BGE+ Capacity Building Resource Platform and European Biodiversity Genomics Education Programme (WP3)	The academic and stakeholder communities have increased access to training resources and training courses in the field of biodiversity genomics	Increased bioliteracy in biodiversity genomics enhances the production of genomic data, and its use in policy setting and decision making
Resources and infrastructure for iBOL-E and ERGA networks and nodes (WP8,9)	DNA barcoding and genome sequencing communities in Europe have increased access to resources, community events, and connections to related initiatives	Increased support for the generation and use of biodiversity genomic data by strengthening and growing the iBOL-E and ERGA communities

Output	Outcome	Impact
Community forum and workshops for distributed DNA barcode sequencing (WP8)	Expertise shared across institutions and countries in the use of low-cost, distributed sequencing methods	Laboratories across a wide range of resource settings will have increased access to low-cost sequencing platforms, resulting in increased data production
Refined DNA barcode gap-list and reference library curation workshops (WP8)	Involvement from the taxonomic community in the expert curation of (a) a DNA barcoding gap-list, and (b) the DNA barcoding records in existing databases	The barcoding community has clear guidance on prioritisation of species; researchers and stakeholders involved in biomonitoring have access to better quality reference resources for species characterisation and monitoring
ERGA BioGenome Hub Network services (WP9)	Strengthening technical expertise in field and laboratory work for biogenome generation	Increased quality and production of reference genomes in Europe to underpin scientific discovery in genomic science and stakeholder applications
ERGA BioGenome Applications Network services (WP9)	Translational tools and resources to facilitate meeting stakeholder needs in how best to use whole genome sequence data for conservation, agriculture, forestry, aquaculture, and the broader bioeconomy	Increased awareness in research community of stakeholder needs, and their subsequent uptake of genome sequence methods in setting and implementing biodiversity policy

Table 3.

BGE+ Scientific impact pathways establishing foundations of a biodiversity genomics system in Europe.

Output	Outcome	Impact
Analysis of resources and tools needed as services to support consolidated transnational genomic data production and evaluation of current service offerings (WP7)	European Research Infrastructures have a catalogue of the (additional) services (functional specifications) needed in support of scaled out biodiversity genomics efforts.	RIs can evaluate their ability to deliver services as part of their European service portfolios and propose plans for action regarding service development and operation.
Study of the financial feasibility and organisational requirements for the provision of services supporting the future European system of distributed data production (WP7)	Calculation of costs linked to the future provision of services and the development of the required knowledge resources, as well as needs in governance and management.	
Engagement with ESFRI RIs to evaluate interest and ability to serve the community (WP7)	Clarity on which specific RI(s) would commit to delivering required portfolio services and supporting the wider community.	
Deployment of a wide participation model for distributed genomic knowledge production (WP2)	Participants (cascade grant receivers) engage with standardised processes and the use of shared resources, analysis tools and data deposition systems	Genomic assay outputs are more comparable, and data are more interoperable, leading to better knowledge aggregation. Cross-border collaboration is easier.
Training workshops and development of material for enhancing local capacity in the use of genomic tools (WP3)	Increase in the number of research groups that know how to engage with standardised genomic methods and tools for integrative taxonomy.	

2.1.2 Technological Outcomes and Impact of BGE+

BGE+ will deliver transformative technological innovations in laboratory protocols and bioinformatic solutions that fundamentally democratise access to biodiversity genomics across Europe. Building on BGE1's proof-of-concept achievements, the project advances from demonstration to implementation of scalable, cost-effective technologies that enable distributed genomic data production. Through systematic benchmarking across preservation methods, sequencing scales, bioinformatic tools and taxonomic groups, **BGE+** provides the methodological foundation for Europe's distributed biodiversity genomics infrastructure. The technological outcomes transform biodiversity genomics from an exclusive, high-cost activity concentrated in well-resourced centres to an inclusive, accessible capability deployable by any motivated researcher or institution. This democratisation is essential for achieving the scale of biodiversity monitoring required by European policy frameworks, positioning Europe as a global leader in the deployment of distributed, equitable genomic technology. Table 4 summarises the main technological outputs, outcomes and impacts.

2.1.3 Societal and Policy Outcomes and Impact of BGE+

BGE+ builds on the achievements of the BGE1 project to deliver clear societal and policy outcomes through enhancing the uptake of genomic evidence into biodiversity research, monitoring, and decision-making across Europe. The project progresses from demonstration to implementation, contributing to the policy-aligned inclusion of DNA-based data as a routine part of conservation planning, ecological restoration, and sustainable management of natural resources. **BGE+** will provide harmonised protocols, interoperable data infrastructures, and validated applications that directly support European and global biodiversity strategies (Table 5). The development of policy-relevant use cases, aligned with the EU's landscape of biodiversity projects and initiatives, will guide how genomic evidence, from barcodes to whole genomes, can enhance biodiversity assessments, restoration monitoring, and informed management decisions. These progresses are crucial to halt the societal impacts of the current biodiversity crisis.

2.2 Measures to maximise impact - Dissemination, exploitation and communication

BGE+ advances the mission and methodology of BGE1 towards our ultimate goal of establishing a distributed European system for biodiversity genomics. As such, **BGE+** builds on the experience and developments of BGE1 also in Dissemination, Exploitation, and Communication (DEC). **BGE+** will refine, update, and expand the mechanisms put in place by BGE1 while adding new tools designed to serve the new endeavour.

Table 4.

BGE+ Technological innovation outcomes and impacts removing barriers to production and deployment.

Output	Outcome	Impact
Protocols: Modular, scalable protocols compiled, validated, and published openly for major taxonomic groups to suit diverse workflows and needs for high throughput barcoding, museomics for historical specimens, room-temperature genomic preservation, reference genome production and metabarcoding (WP4)	Democratized access to genomic data generation through open and validated protocols, reducing per-sample costs across barcoding, museomics, reference genome production, and resequencing for whole-genome data, enabling the processing of more specimens through standardised workflows. Room-temperature preservation eliminates cold-chain requirements, enabling sample collection without specialised infrastructure.	Elimination of cost and infrastructure barriers enabling expansion in genomic data generation capacity across European institutions. Standardised protocols reduce training requirements and enable laboratories with minimal equipment to produce reference-quality data.
Pipelines: Reproducible pipelines for reference barcode generation and curation, containerised genome annotation, intra-specific population genomics analysis, and metabarcoding validation and intercalibration (WP5)	Widespread adoption of standardised, reproducible pipelines, eliminating computational bottlenecks and reducing infrastructure requirements for genomic data processing. Enhanced research efficiency and data quality consistency achieved through uptake of validated workflows deployed via open platforms. Strengthened analytical capacity implemented through containerised, scalable approaches accessible across local HPC, cloud platforms, and public infrastructure	Elimination of computational and analytical rate-limiting steps through containerised, scalable workflows that reduce infrastructure barriers and democratize access to advanced genomic analysis regardless of institutional computational capacity.
Infrastructure and Standards: Comprehensive benchmarking system for genome workflow performance analysis, enhanced interoperability frameworks integrating sequence repositories (BOLD, ENA) with biodiversity infrastructures, and FAIR publication workflows incorporating RO-Crate metadata standards for scholarly publishing of genomic data (WP5)	Standardised quality assessment and performance metrics are adopted across the ERGA community, enabling objective evaluation of genome workflows and driving continuous improvement in analytical approaches. Enhanced data discoverability and integration are achieved through streamlined exchange mechanisms between major repositories and improved metadata standards. Accelerated scientific publishing and data reuse facilitated by FAIR-by-design workflows that capture rich provenance metadata and ensure long-term accessibility of biodiversity genomics datasets.	Elimination of data management and interoperability bottlenecks through standardised benchmarking systems and automated metadata workflows, removing technical barriers to data sharing, reuse, and collaborative analysis.

2.2.1 Plan for the dissemination and exploitation, including communication activities

BGE+'s most important mechanism to maximise long-term impact for the Project's results is the strategic Dissemination, Exploitation, and Communication (DEC) plan. This plan will guide all activities aimed at increasing the visibility and uptake of the Project's outcomes across key stakeholder groups, including policymakers at European and national levels, the communities of **ERGA**, Cascade-funded projects connected to the rest of the **BGE+** work programme, and **CETAF**, the broader scientific community,

industry, and the general public. A first version of the DEC plan will be submitted by Month 6 (D1.3), to be then updated further down the project's calendar (D1.4, in M34), after tangible results from the project's WPs allow for a renewed, reliable analysis of the project's Key Exploitable Results (KERs) and the best pathways for exploitation. The DEC plan will ensure consistency in the actions, KPIs and alignment with **BGE+** goals and the needs/drivers of its stakeholders. All consortium members will contribute to DEC activities by mobilising their communication channels and contributing to collecting the results from the WPs so that the WP1 team can effectively utilise them.

Table 5.

BGE+ pathways to societal and policy impacts.

Output	Outcome	Impact
Overview of European biodiversity-related policies, programmes, initiatives, and stakeholder networks at the European level; identification of opportunities for integration and collaboration (WP6)	Enable non-redundant pan-European efforts for biodiversity applications and monitoring, positioning biodiversity genomics within European policies, initiatives and networks. Promote engagement with the EU Biodiversity Observation Coordination Centre (EBOCC), the Knowledge Centre for Biodiversity and BioAgora, and projects such as the COST action GENOA and Biodiversa+ GINAMO.	Enhance the efficiency of conservation planning, ecological restoration, and sustainable management of natural resources through the integration and mainstreaming of cutting-edge DNA-based tools and knowledge.
Use case-based roadmap for methodological, infrastructural and organisational needs, method implementation, data integration and interoperational requirements for the transnational use of (meta)barcoding methods (WP6)	Enable the transnational application of DNA (meta)barcoding methods to support biodiversity management and monitoring, and use by biodiversity policy, regulatory and monitoring bodies.	Reinforce Europe's leadership in global biodiversity applications, by providing tools to halt the societal impacts of the biodiversity crisis, establishing genomics as a cornerstone of biodiversity monitoring and restoration in Europe, Support the EU Biodiversity Strategy for 2030, the Nature Restoration Law, the European Climate Law, and the European Green Deal, where ecosystem health is recognised as central to climate mitigation and adaptation. Contribute to the Kunming–Montréal Global Biodiversity Framework, especially Targets 2–4, which call for ecosystem restoration, safeguarding of species, and monitoring of genetic diversity. Impact Sustainable Development Goals, notably SDG 15 (Life on Land), SDG 14 (Life Below Water), and SDG 13 (Climate Action), while advancing SDG 17 (Partnerships for the Goals) through its commitments to open knowledge, and inclusive international collaboration.
Use case-based roadmap for harmonised and standardised estimation of genetic composition Essential Biodiversity Variables from whole genome data: technical requirements, methodological needs, policy recommendations, and identification of areas for further development (WP6)	Enable the inclusion of whole-genome evidence of intra-specific diversity in biodiversity assessments, monitoring, and management, thereby supporting the policy uptake of genome-based methods.	

Output	Outcome	Impact
Strategic guidelines for operational recommendations and coordination pathways for the transnational integration of genomic barcode and genome-based tools, into EU biodiversity monitoring (WP6)	Guide the policy uptake and use of genomic evidence, from (meta)barcoding to whole genome data, to support and improve environmental management, environmental risk assessment, and sustainable use of biodiversity.	

2.2.2 Communications

In BGE1, our communication strengthened awareness about the relevance of biodiversity genomics for biodiversity assessment and sustainable use in Europe. **BGE+**'s approach will be more hands-on. In line with the project's general goals, communications will support mobilising practitioners across countries, bridging technical gaps, increasing awareness among policymakers, and supporting service provision. **BGE+** will also have the added task of communicating about the process and impact of its cascade grants scheme. The different approach will be reflected in the types of messages that **BGE+** will address to its target audiences, as well as in the intensity of its communications. A range of mechanisms and tools will be developed to target a broad stakeholder community, and ambitious KPIs have been established (see Table 6 below). All communication actions will run throughout the full lifecycle of **BGE+** and, at the end of the project, a Communication impact assessment will be conducted (D1.8).

Table 6.

BGE+ Communication Key Performance Indicators (KPIs).

KPI	Channel	Description	Target (M42)
C1	Website	24/7 digital portal of all BGE+ information (expanding current biodiversitygenomics.eu)	≥ 15,000 visitors ≥ 2 website updates
C2	Digital content	Posts and news items on BGE+ site	≥ 20 items posted
C3	BGE+ featured on 3rd-party sites	Posts and news items about or mentioning BGE+ on 3rd party sites and platforms	≥ 10 mentions of BGE+ in other sites
C4	Social media	Post in Bluesky, YouTube and LinkedIn	≥ 650 Bluesky followers ≥ 500 YouTube subscribers ≥ 2,250 LinkedIn followers
C5	Newsletters	Periodical digital publication showcasing recent developments of BGE+	≥ 10 newsletters sent ≥ 600 newsletter subscribers
C6	Press releases	Communication to be distributed to selected mainstream and specialised media	2 press releases
C7	Media appearances	Interviews, features, news items in mainstream and specialised media	≥ 45 appearances (all partners combined)
C8	Specialised information material	BGE+ brochure, project flyer, poster, sticker, roll-up banner	≥ 500 units distributed 2 posters, 2 banners

KPI	Channel	Description	Target (M42)
C9	Videos	Corporate video, interviews, workshops, recordings and educational items	1 corporate, 1 event ≥ 10 interviews/ educational
C10	Outreach activities at events	General BGE+ presentation in conferences, workshops, exhibitions, and other events	Showcased in ≥ 50 events (all partners included)

2.2.3 Dissemination

BGE+ goals, such as removing technical barriers to genomic data production and deployment, and setting up the basis for biodiversity genomics services at the European level, speak of a project with a significant technical component. This requires a decisive effort to provide open access to results, materials, and data, so that the project can foster collaboration and promote the uptake of results. For this purpose, **BGE+** will continue developing and expanding BGE1's Knowledge Platform (MS1.7, M40) as the central hub for disseminating the project's resources. Embedded in **BGE+**'s website, the Knowledge Platform will function as a comprehensive and systematically organised repository of the project's outputs, classified by topic, format, and scientific strand. It will provide continuous open access to the whole body of knowledge generated, while ensuring sustainability for **BGE+**'s outputs beyond the lifecycle of the Project. Beyond the renovated Knowledge Platform, T1.3 will continue to support dissemination activities throughout the **BGE+** consortium with pre- and post-activity actions (e.g., promotion, recordings, compilation of materials for further distribution, and accessible summaries). A preliminary summary of those activities is provided in Table 7.

Table 7.
BGE+ Dissemination Key Performance Indicators (KPIs).

KPI	Mechanism	Description	Target (M42)
D1	Knowledge Platform	Digital repository of all outputs from the BGE+ project, hosted on the project's website	≥ 2 new sections added ≥ 100 new items added
D2	Publications	Open-access, peer-reviewed publications in specialised journals	≥ 5 publications (beyond Cascade-funded projects)
D3	BGE+ Workshops and training sessions	Primary channel for the dissemination of project developments, while strengthening the ties between BGE+ and its stakeholders	≥ 20 sessions
D4	Scientific presentations in 3rd-party events	BGE+ partners' participation in events (e.g., conferences, webinars), including scientific talks/ posters, and education/training actions	≥ 16 actions
D5	Capacity building	Accessible summaries of specific BGE+ developments (e.g. tutorials, factsheets, use cases, and online materials)	To be specified in the DEC Plan (D.1.3)

2.2.4 Exploitation

The DEC plan will provide details of how **BGE+** plans to maximise the chance of its outputs being taken up by its main stakeholders while ensuring their sustainability beyond the project's lifecycle. All data, data standards, best practices, knowledge, pipelines, protocols, and policy recommendations will be openly accessible, providing a level of granularity that is central to **BGE+**'s long-term ambition of scaling biodiversity genomics practice across European countries. For the same purpose, particular relevance will be granted to the exploitation of developments of methodologies, processes, and pipelines that support standardised approaches to characterisation and monitoring of biodiversity. In line with what is described above, **BGE+** will implement a two-step mechanism. The first version of the DEC plan (D1.3, M6) will include a survey addressed to Work Package and Task Leaders. The survey aims to identify the main Key Exploitable Results (KERs), key stakeholders, and how they map to the KERs. The description and mapping of the KERs will subsequently be reviewed and expanded in MS1.5 (M30) to incorporate new insights based on the actual results of **BGE+** after two years (e.g. key partners in continuing/maintaining the work beyond the project; potential uses of KERs in future work). The new description will then be inserted into the updated DEC plan to be delivered in M34 (D1.4). Beyond the description and analysis of KERs, WP1 will provide support to the project's efforts in Exploitation of its results (see Table 8 below), in particular to the work done in WP6 (knowledge exploitation) and WP7 (service portfolio), and will strengthen collaboration with WP8 and 9 to pass on the project's outputs to **BGE+** communities (**iBOL-E**, **ERGA** and **CETAF**) through specific actions at community level. A final **BGE+** event (D1.6), focused on the application and exploitation of outputs, will mark the culmination of the Project's exploitation efforts. A central piece to this endeavour is the organisation of a major in-person international conference near the end of the project (D1.6), focusing on the application and exploitation of the research outputs and seeking further opportunities for joint funding.

2.2.5 Intellectual Property

The terms of its Intellectual Property Rights (IPRs), including ownership rules, joint ownership arrangements, access rights, protection possibility and decision-making mechanism, will be specified in the Consortium Agreement at the start of the Project in alignment with HE requirements. Background IP will remain the property of the owners. At the same time, foreground IP will belong to the partners who actively participated in its creation, with joint ownership agreements in place where relevant. As needed, a distinct ownership agreement will be formulated and signed by co-owners to specify their rights and responsibilities. Beneficiaries will be required to take measures to implement the principles set out in the Code of Practice annexed to the Commission Recommendation on the management of intellectual property in knowledge transfer activities. The IPRs management strategy will be included in the **BGE+** Data Management Plan (D1.2, M6) together with guidelines on (meta)data handling and Project output licensing in alignment with HE requirements on open access. Detailed provisions on IPRs will be further described in the **BGE+** consortium agreement.

Table 8.
BGE+ Exploitation Key Performance Indicators (KPIs).

KPI	Pathway	Description	Target (M42)
E1	End-of-project event	Final BGE+ event, focused on application and exploitation of outputs	≥ 100 participants
E2	Policy briefs	Policy recommendations targeting EU, national and regional authorities	≥ 2 briefs
E3	Technical briefs	Science-focused recommendations targeting EU, national and regional authorities	≥ 8 briefs
E4	Direct engagement with communities	Engagement with the iBOL Europe, ERGA and CETAF via their own community meetings	≥ 6 actions (to be specified in the DEC Plan (D.1.3)
E5	Direct engagement with stakeholders	Engagement with several actors, such as European/national institutions, genomics platforms and networks (e.g. the EU Biodiversity Observation Coordination Centre, EBOCC), end-user communities (e.g. uptake training sessions) and science-policy initiatives (e.g. BioAgora)	≥ 5 initiatives (to be specified in the DEC Plan (D.1.3)

2.3 Summary

The Project dissemination, exploitation, and communication measures associated with the expected results and aligned with the specific needs are summarised in Table 9, expected impacts from Project outcomes are summarised in Table 10.

Table 9.
Summary of dissemination, exploitation, and communication measures.

SPECIFIC NEEDS	EXPECTED RESULTS	D & E & C MEASURES
To widen participation and strengthen capacity for genomically enabled taxonomy and integrative taxonomy, especially focusing in selected European regions	European Biodiversity Genomics Education programme delivered, Capacity Building Resource Platform openly accessible and promoted in iBOL-E, ERGA and CETAF communities	DEC actions will follow the strategic **Dissemination**, **Exploitation, and Communication (DEC) Plan** (D1.3, updated in D1.4). **Communication**: T1.3 will support mobilisation across countries, bridging technical gaps, increasing awareness, and supporting service provision and the project's cascade grants scheme. Mechanisms: website, newsletters, socials, videos, outreach activities, media, and printed materials. **Dissemination**: BGE+ will expand BGE1's Knowledge Platform (MS1.7) as the central hub for open sharing of the project's outputs. It will also support dissemination activities across WPs: publications, workshops and capacity building actions, presentations. **Exploitation**: The 1st DEC plan (D1.3) includes a KERs-focused survey for WPs and Task Leaders, which will subsequently be reviewed and expanded in MS1.5 to incorporate new insights into the updated DEC plan (D1.4). Other mechanisms: BGE+ final event, Horizon Europe's Results Platform.

SPECIFIC NEEDS	EXPECTED RESULTS	D & E & C MEASURES
To scale and consolidate distributed production of barcodes and reference genomes, making use of existing distributed efforts	Comprehensive cascade grants scheme deployed supporting distributed, harmonised data & knowledge production	
To embed genomic tools into taxonomy to support policy, biodiversity monitoring, assessment and management	Strategic roadmaps for implementing genomics in biodiversity assessments co-developed with stakeholders and actionable recommendations provided through synthesis report	
To address gaps in FAIR-by-design systems for data management and informatics	Standardised data and metadata processing practices, interoperability frameworks, FAIR publishing workflows implemented	
To investigate feasibility and describe the path towards a European biodiversity genomics system as a distributed Research Infrastructure	Service portfolio, scientific and technical description, and feasibility assessment for biodiversity genomics research infrastructure.	
To deliver a common agreed-upon corpus of community standards, best practices and toolkits	Optimised protocols, pipelines, digital infrastructure and standards enabling harmonised data production and use openly accessible	

Table 10.

Summary of expected impacts from Project outcomes.

TARGET GROUPS	OUTCOMES	IMPACTS
European biodiversity genomics and taxonomic communities, biodiversity research community, citizen scientists, including organisations within the iBOL Europe, ERGA, and CETAF networks, as well as the overlapping communities of the nascent European eDNA society, the Coalition for Conservation Genetics, and GEO BON.	Genomic and taxonomic communities in Europe enlarged and supported to produce high-quality interoperable data	Competence within the European community to deliver impactful knowledge and support biodiversity policy is strengthened
iBOL-E, ERGA, and CETAF communities with focus on even distribution and strengthening existing capacity	European biodiversity genomics landscape scaled-out and novel biodiversity knowledge produced	European biodiversity genomics landscape scaled-out and novel biodiversity knowledge produced
Biodiversity policy makers and practitioners, biodiversity conservation and ecological organisation (including environmental protection agencies, nature conservation agencies, and government policy teams with responsibility for environmental / rural management, and compliance with national legislation, regional laws, the European Habitat Directive 92/43/EEC and the EU Biodiversity Strategy for 2030, and reporting on the Global Biodiversity Framework)	Upscaling of biodiversity genomics implementation and impact for harmonised biodiversity assessments, monitoring and sustainable management	European biodiversity genomics and taxonomic expertise facilitates effective environmental management, environmental risk assessment and sustainable use of natural resources
European biodiversity research community, scientific community at large	Increased uptake of FAIR-by-design (meta)data management and informatics practises	Improved efficacy, reduced redundancy and strengthened collaborations in biodiversity knowledge implementation
Users and providers of biodiversity genomics data and services, existing European Research Infrastructures, including Biodiversa+, DiSSCo, ELIXIR, EBOCC and eLTER	Actionable pathway for implementing European biodiversity genomics system as a distributed Research Infrastructure established	Distributed European system for biodiversity genomics transforms the power and scale of genomics studies to understand and sustainably use biodiversity
European biodiversity genomics and taxonomic communities, biodiversity research community (as outlined above)	Biodiversity genomics knowledge is produced in harmonised manner enabling standard quality, easily comparable, FAIR data	Democratised access to genomics innovation and tooling for orchestrated biodiversity characterisation and monitoring

3. Implementation

3.1 Work plan and resources

Work package WP1 – Project management, communication and ethics

Objectives: WP1 will oversee scientific coordination as well as overall administrative and financial management of the Project (including governance, monitoring, quality assurance, risk management and reporting), and facilitate the legal framework for cascade grants. The WP will support the consortium's communication, dissemination and exploitation activities. Together with the external advisory board, the WP will assess ethical considerations relevant to **BGE+** and will support the consortium's compliance with ethical standards.

Description:

Task 1.1 Project Management: Financial and administrative management, internal communication, liaison with the EC and stakeholders, day-to-day management, documentation, resource planning, monitoring and reporting. Support with a legal framework for cascade grants.

Task 1.2 Scientific Coordination: Overall scientific coordination of the Project, quality assurance and risk management. The Project Director leads this Task in collaboration with WP leaders to ensure implementation and realisation of Project objectives. The task will establish the Scientific Steering Board as a governance body to support the definition and implementation of the cascade-funded projects framework, the project's Advisory Board of external experts, and the Synergy Alignment Group (connecting to the project funded for Area A of the Topic).

Task 1.3 Communication, Dissemination, and Exploitation: This task will develop an integrated Communication, Dissemination, and Exploitation strategy for the project. Communication activities will utilise a broad suite of tools to ensure effective visibility and provision of information on the project's developments. Dissemination efforts will use a fully renovated Knowledge Platform as the primary vehicle for collecting and sharing the project's technical findings with practitioners and other key stakeholders. Exploitation and engagement efforts will utilise targeted outreach strategies to promote the uptake of the Project's key exploitable results and identify key policy engagement opportunities. In connection with the latter, a final exploitation event will be organised to bridge biodiversity genomics with environmental and policy-related stakeholders.

Task 1.4 Ethics: Assessment of ethical aspects of the Project activities (including diversity and inclusion, handling biological material and DSI, use of AI) in collaboration with the Advisory Board. Monitoring and consortium support for aligning with relevant ethical requirements.

Work package WP2 – Community support for knowledge production

Objectives: WP2 will establish a comprehensive framework for the Cascade Grants mechanism, select projects, and monitor their implementation, progress, and impact. This framework will guide the call for proposals, evaluation, and selection of projects aligned with **BGE+** objectives, requiring open access, data harmonisation, local capacity building, and adherence to best practices. **BGE+** will provide projects with budgets for sequencing, sampling, reference taxonomic and genetic voucher management, consortium coordination, communication, stakeholder engagement, citizen science, and travel.

Description:

Task 2.1 Topic definition and framework establishment: In interaction with all other WPs, T2.1 will establish the framework under which the cascade grants mechanism will operate for calls to be launched under T2.2. The framework defines topic areas and objectives and specifies eligibility criteria, target groups, scope, timeframes, evaluation and selection procedures, and monitoring mechanisms. Final topic selection will be done in interaction with the **BGE+** SSB. T2.1 will define performance oversight mechanisms, ensuring compliance with the standards established in **BGE+**, ethical, legal and FAIR principles as well as the relevant guidelines provided by **ERGA** and **iBOL-E**. The task will establish risk mitigation measures.

Task 2.2 Augmenting and applying reference libraries: extending the **BGE+** network through cascade grants: T2.2 shall strengthen and extend the **BGE+** distributed infrastructure in interaction with WP7, 8, 9 through attributing cascade grants. T2.2 will implement the framework developed under T2.1, ensuring clarity, transparency, and compliance with the applicable funding rules and principles. T2.2 will launch the calls, evaluate the applications and report the progress and results back to the oversight mechanism established under T2.1, feeding into a critical feedback loop to inform decisions on the next call round. Scientific support to cascade-funded projects will be provided by BGE + project partners within WPs 3 (training support), 4 (laboratory support), 5 (bioinformatic/data support) and the **BGE+** networks **iBOL-E**/WP8 (T8.2), **ERGA**/WP9 (T9.2), and **CETAF** (taxonomic support). T2.2 will serve as a lightweight help desk to dispatch such support requests. T2.2 and the **BGE+** SSB, together with the members of the **BGE+** Executive Board, will form a group responsible for monitoring the progress of the scientific contribution of each cascade project. Subtask 2.2.1: Advance genomic data production hubs: This subtask will support hubs that produce critical reference resources, specifically high-quality reference genomes and reference barcodes, which underpin the broad application of DNA-based methods in biodiversity science and conservation. The subtask will help substantiate new hubs and scale up existing ones, preparing them to connect their data and scientific outputs to the project through training (WP3), protocol support (WP4), and bioinformatic tools (WP5). All projects are expected to integrate into the **iBOL-E** (WP8) and **ERGA** (WP9) networks under WP8 and WP9 guidance. The approved projects shall complement in project expertise and contribute to strengthening the **BGE+** network. Subtask 2.2.2: Support the

use of genomic data for monitoring: This subtask will assist projects that aim to address the nature conservation emergency, support ecological restoration, demonstrate sustainable use of biodiversity, and contribute to one health (e.g., climate change indicator, management of alien species). **BGE+** will provide financial support to projects at an advanced stage of data production (i.e., reference genomes/barcode libraries accessible for applied use cases) to help them transition to a more elaborate data analysis phase and/or to advance and integrate additional implementation aspects. To ensure the feasibility of such an expected upgrade, applicants for funding will be required to integrate strong components of stakeholder engagement and/or policy link established by WP6. Subsets of the call shall be dedicated to directly addressing the targets and goals of the EU Nature Restoration Law and the Global Biodiversity Framework to fulfil reporting requirements (e.g., genetic diversity indicators, species diversity indicators).

Task 2.3 Dissemination and exploitation of cascade-funded projects, compilation of results: T2.3 will ensure the connection and alignment with **BGE+** goals and that the expected outcomes to be achieved by the different projects funded under the cascade grants mechanism fulfill their objectives. This task supports the communication, dissemination, and exploitation of the cascade project's findings. T2.3 amplifies knowledge exchange with stakeholders by translating the results into non-technical summaries to maximise policy traction. The outputs of the cascade projects will be connected to the other **BGE+** WPs. Result dissemination to the wider communities of **iBOL-E** (WP8) and **ERGA** (WP9) will be executed via the project-wide communication strategy established in WP1.

Work package WP3 – Training and knowledge transfer for scientists and end-users

Objectives: WP3 aims to build capacity and enhance skills in biodiversity genomics across Europe through targeted training and knowledge transfer initiatives for researchers and stakeholders. WP3 will identify capacity building gaps in the European barcoding and reference genome communities, develop a road map for capacity building within the region, and provide theoretical and practical training through a distributed network of European partners, leveraging the connections to the barcoding and reference genomes communities in WP8 & 9. We will translate output from method development activities in WPs 4 & 5 into training materials and collaborate closely with cascade-funded projects (WP2) to ensure access to relevant educational resources. The ultimate goal is to offer an Europe-wide multi-layered training strategy for scientists and end-users that can be promoted by the **iBOL-E** and **ERGA** networks beyond the lifetime of **BGE+**.

Description:

Task 3.1 Identify training needs for cascade-funded projects and in the ERGA and iBOL-E communities: T3.1 will utilise the knowledge obtained in BGE1 and existing networks, along with tailored surveys distributed by WP8 and WP9 to map the current training landscape for biodiversity genomics in Europe. The results will be used to

develop strategies and a roadmap for systematic capacity building and knowledge transfer in biodiversity genomics. Based on experience from the BGE1, **iBOL-E**, and **ERGA** communities, the training required to accommodate the content for cascade-funded projects in WP2 will be identified, developed, and implemented in a distributed and timely manner.

Task 3.2 Develop and deliver capacity building activities and training materials: T3.2 will engage partners of the **ERGA** and **iBOL-E** communities to develop and deliver courses and on-site training to meet the needs identified in T3.1. While some training is currently given within the respective communities, novel contributions will be developed and provided by **BGE+** partners. This includes outputs from WPs 4 & 5 transformed into training materials as new protocols and pipelines are developed. Theoretical and practical courses as well as seminars and workshops relevant to the research community and stakeholders, will be delivered throughout the project period. Introductory training to serve the needs of cascade-funded projects (WP2) will be offered upon their start to ensure smooth onboarding, proficiency of essential tools, and a thorough understanding of requirements. The course and training portfolio will include advanced courses and follow-up training in years 2-3 to ensure that the production and delivery of data follows best practices in the field. A selection of application-focused capacity-building activities will be targeted at end-users, including private industry, Non-governmental organisations (NGOs), and governance bodies. Training events will incorporate and cover predefined wet lab and dry lab topics to establish background knowledge on sample collection and processing, library construction and sequencing, barcode production and genome assembly, curation and annotation. The availability of human resources and technical facilities at host institutions will be crucial for the success of these activities. At the same time, we will be mindful of cultural sensitivities and the geographical imbalance in existing knowledge gaps. The courses will be aligned with planned activities in the successful project for Part A of HORIZON-CL6-2025-01- BIODIV-04, and incorporated in the European Biodiversity Genomics Education Program. Special attention will be given to incorporating FAIR data principles and practices into relevant training modules to support data stewardship, interoperability, and long-term usability in collaboration with the **ERGA** and **iBOL-E** communities (WP8 & 9).

Task 3.3 Develop an online BGE+ Capacity Building Resource Platform: The Capacity Building Resource Platform on the **BGE+** website will facilitate an overview of the Training Program and course descriptions, and link to an improved **ERGA** Knowledge Hub (EKH 2026) and the novel **iBOL-E** Knowledge Hub. Two separate hubs are deliberately chosen, as the **ERGA** and **iBOL-E** communities will maintain them after the end of **BGE+**. They will thus be pillars of the European biodiversity genomics research infrastructure (WP7). The hubs will enable the registration of participants in compliance with the GDPR and will hold and openly share digital training materials developed in **BGE+** for reuse beyond the project period.

Work package WP4 – Improving laboratory protocols and approaches

Objectives: WP4 will innovate in the lab to enable widening participation in genomics across Europe and globally by developing standardised approaches for preserving, extracting, and sequencing diverse biological materials while significantly reducing per-sample costs to drive adoption. We will implement ultra-low-cost, modular barcoding workflows integrated with high-throughput specimen imaging (T4.1), revolutionize the utilization of museum specimens through optimised historical DNA protocols (T4.2), establish preservation methods that eliminate cold chain requirements (T4.3), enable distributed low-cost reference genome production (T4.4) and develop laboratory intercalibration protocols that ensures that biodiversity data produced via metabarcoding are comparable across distributed monitoring networks (T4.5).

Description:

Task 4.1 OPENBAR: Open Barcoding for All Researchers: Third-generation sequencing technologies have enabled ultra-low-cost, high-throughput DNA barcoding using portable platforms like Oxford Nanopore Technologies (ONT) MinION. However, technical and financial barriers still limit widespread adoption of decentralised workflows. This task will consolidate, benchmark, and expand proven protocols to democratise DNA barcoding across taxa, regions, and research scales through standardised yet flexible solutions. We will develop a comprehensive, modular resource covering end-to-end workflows from DNA extraction to sequencing and bioinformatics (with WP5). Key deliverables include: a standardised low-cost plate-based imaging system for specimen photography, a universal plate-based tagging system for streamlined 1-step, 2-step and 2-in-1 step PCR (Polymerase Chain Reaction) protocols, and cost benchmarking at multiple scales. In consultation with industrial collaborators (e.g. IDT and NEB), we will develop cost-effective freeze-dried plates (e.g. iBOL ONTOLOGY) as universal standards for multiplexed PCR across markers and taxa, with both commercial and DIY alternatives. All workflows and materials will be made available via open-access platforms (with WP8) as a living resource for the iBOL community. Comprehensive training materials co-developed and delivered via WP3 will empower researchers to adopt and adapt workflows tailored to their specific taxa, resources, and project scale.

Task 4.2 Innovating museomics for all taxa and all preservations: Bridging between reference genomes and diagnostic genes, this task will accelerate the use of museum specimens for both iBOL and EBP communities by optimising extraction and library building protocols across a range of taxa and sample types. By leveraging approaches from the **BGE+** and ancient DNA communities, we will employ our network to identify approaches for high-throughput historical DNA processing. Our work will identify, review, and implement methods to generate sequence data from museum collections at scale, significantly reducing costs while improving sequencing complexity and coverage. We will begin with a comprehensive desktop analysis of DNA quality in historic materials, a survey of the availability of lab facilities in the **BGE+** community, and a review of state-of-the-art lab methods. This will be followed by laboratory implementation of promising methods across predefined samples, where we will develop robust, validated protocols

across the major phyla and museum preservation types. This initiative will maximise data utility for downstream analysis while minimising costs, ultimately democratizing access to museomics.

Task 4.3 Breaking the cold chain and future proofing specimens across the tree of life: Currently, cold chain-supported field collection and shipping are required for reference genome quality material; however, this is expensive, vulnerable and often inaccessible in the field. Task 4.3 aims to develop approaches that do not require a cold chain for collection and transportation. Room temperature preservation approaches (e.g. ethanol) work well for barcoding and short read WGS, but have not been systematically evaluated or implemented for high molecular weight DNA and nuclei preservation. This methodological gap is addressable through rigorous and systematic assessment of preservation approaches to protect specimens for maximal future use, especially as specimen collection is expensive and repeated recollection is ethically unsound. The protocols developed and released through this task will enable anyone to collect samples and specimens anywhere and preserve them at room temperature, resulting in a significant step forward in field sampling for genomics. This task will systematically identify and benchmark 10 different DIY and commercial preservation approaches across representatives from 10 major taxon groups (e.g., plants, fungi, marine invertebrates, molluscs, arthropods) to establish guidelines and associated protocols for the most appropriate, maximally future-proofed preservation methods for high molecular weight (HMW) DNA and nuclear preservation. The costs of different approaches will be considered, and the focus of the work will prioritise low-cost preservation solutions. This work will be completed in the first third of the project to enable cascade-funded projects to benefit from the resulting protocols.

Task 4.4 Genome sovereignty through cost-effective reference genomes: Current approaches to reference genomes are expensive and developed for well-provisioned core sequencing facilities. T4.4 closes the affordability gap in reference-genome production by developing and validating low-cost, e.g. ONT-MinION–based workflows that can run in minimally equipped labs, preserving genome sovereignty in widening countries. We will optimise end-to-end lab protocols to deliver reliable, reference-quality draft assemblies meeting predefined contiguity/completeness thresholds at a fraction of current costs. A pilot on selected taxa representing a range of genome sizes and complexities will quantify performance (contiguity, completeness, accuracy) and true cost per-sample, define practical limits for existing pipelines, and produce ready-to-adopt SOPs for distributed hubs. Outputs are designed to maximise adoption, including a concise protocol collection with associated recommendations, step-by step methods, quality control (QC) checkpoints, troubleshooting, costings, and training materials aligned with WP3. T4.4 provides a reproducible and scalable blueprint for in-house reference genomes, facilitating equitable participation in biodiversity genomics.

Task 4.5 Laboratory Intercalibration Framework for DNA Metabarcoding: Variation between samples, labs and protocols prevents accurate comparisons of metabarcoding data across time and space. Task 4.5 will develop and validate a harmonised intercalibration protocol that corrects for laboratory biases and ensures biodiversity data

are comparable across monitoring networks. Formal power analyses will guide experimental design to determine optimal sample sizes and replication for DNA extraction, PCR and library preparation, and comprises three elements: (1) independent laboratories will analyse arthropod mock communities with individually barcoded specimens spanning realistic gradients of richness and abundance using standardised workflows to estimate biases and derive calibration coefficients; (2) the same laboratories will process real Malaise trap samples from the previous BGE1 project to validate intercalibration by assessing convergence of richness and presence–absence patterns after applying calibration coefficients; and (3) synthetic spike-in controls at defined concentrations will be added to lysates and processed with mock and field samples to monitor workflow performance and establish minimum sequencing depth for detecting low-abundance targets. Detailed metadata on reagents, equipment, protocols, operators and deviations will be captured and made FAIR using RO-Crate. These data will be used to calibrate models that calculate per-laboratory and per-taxon detection probabilities, richness bias factors, and confidence intervals. We will compare pre- and post-calibration metrics, such as the inter-laboratory coefficient of variation for richness and the Jaccard index for presence–absence, to quantify the effectiveness of the correction. The resulting calibration tables and model outputs will be provided to T5.7 for integration into the bioinformatic framework. Finally, we will compile SOPs for workflows, metadata capture, and QC metrics for spike-ins and mock samples into a general intercalibration protocol to guide future distributed metabarcoding monitoring efforts.

Work package WP5 – Improving bioinformatic tools and services

Objectives: WP5 aims to tackle identified challenges in reference library production, data management and biodiversity genomics analysis and applications through innovative developments in bioinformatic tools and services. It will enhance the quality, availability and accessibility of informatics tools used in the analysis of genomic data for applied conservation and sustainable use of European biodiversity; establish common data formats, metadata standards, and improve APIs to enable seamless integration across the network; improve and integrate services provided by sequence, biodiversity infrastructures and publishers to ensure long-term sustainability, and to facilitate access and re-use of biodiversity genomics data.

Description:

Task 5.1 Benchmarking system for genome workflows: This task will implement a comprehensive framework for benchmarking genome workflows, particularly those producing genome assemblies. Building upon the datasets and genomes produced in the BGE1 project, this task will establish a systematic evaluation system for **ERGA** community workflows, providing critical performance metrics on computational cost and output quality across diverse taxonomic groups and data types. Core activities will include standardisation of quality and performance metrics, development of the benchmarking framework, implementation via an online platform such as OpenEBench

(https://openebench.bsc.es/) and integration with **ERGA** Sequencing and Assembly Committee activities.

Task 5.2 Empowering community annotation of non-vertebrates: Ensembl will develop and validate a containerised version of the Ensembl eukaryotic genome annotation pipeline. This will be built using Nextflow and will scale across both data-rich and data-sparse assemblies using state-of-the-art tools for gene prediction and functional assignment. Following initial benchmarking on selected BGE1 assemblies, the pipeline will be rigorously tested by partners from the Sanger and UU using local high-performance computing (HPC) or cloud platforms. The resulting annotations will be ready for integration into Ensembl, allowing access through the Ensembl genome browser. The work will also generate clear technical guidelines and best practices for the iBOL and EBP communities, lowering barriers to high-quality, reproducible eukaryotic genome annotation throughout Europe.

Task 5.3 Scaling up reference barcode generation and curation: This task tackles bioinformatics challenges in barcode generation, from data creation to dataset curation. Key issues include the complexity of tool installation, the lack of standardisation for third-generation sequencing technologies (ONT, Pacific Biosciences - PacBio), and poor integration between analysis pipelines and repositories such as BOLD. We will refine frameworks for scaling barcode generation from specimens and genome skimming, develop streamlined amplicon pipelines, and create benchmark datasets for museomics. We will improve tool accessibility, establish quality control frameworks across platforms, and ensure automated reference library curation with BOLD Europe integration. All tools will be standardised and deployed through platforms like Galaxy toolshed (The Galaxy Community et al. 2026), enabling distributed assembly via local computers, HPC, or public infrastructure like usegalaxy.eu. This democratizes access and reduces technical barriers for researchers.

Task 5.4 Scaling up interoperability between sequence repositories and biodiversity infrastructures: Building up from previous European projects, e.g. BiCIKL (Penev et al. 2022), BGE1 (Koureas et al. 2026), this task will enhance data integration and interoperability within the biodiversity genomics data ecosystem (including sequence and other RIs such as taxonomic, specimen, etc). Emerging FAIR standards and international best practices will be aligned and consolidated in the databases, considering the European Open Science Cloud (EOSC) Interoperability Framework and FAIR Digital Object (FDO) implementations like RO-Crate and FAIR Signposting. Core activities will include streamlined sequence data exchange mechanisms between BOLD and ENA, increased integration efforts with taxonomic resources (e.g. Catalogue of Life), integration of digital specimen persistent identifiers to improve capture of provenance and source information in sequence metadata, using the BGE1 datasets as use cases, streamlined mechanisms for feedback of contextual data curations through available resources, and enhancements of processes for serving data to the community via the dedicated data portals, feeding into T5.5.

Task 5.5 Streamlining publication with FAIR access to biodiversity genomics data: Existing reference data portals (e.g. **ERGA** Data Portal, BOLD Europe) that serve the biodiversity barcode and genome communities will incorporate emerging metadata standards (e.g. RO Crate, Bioschemas, Data Catalogue Vocabulary Application Profile - DCAT-AP) to improve data filtering, search, bioinformatics analytics, and overall usability by the community. Task 5.5 will also streamline the scholarly publication of genome reports and barcode data, including conversions of metadata into manuscripts via the ARPHA Writing Tool. In line with FAIR-by-design principles, workflows and datasets will be documented and published using RO-Crate to capture rich metadata and ensure the provenance, citability, and reusability of data outputs and cumulative knowledge building across related projects and initiatives. The RO-Crate metadata editor Crate-O will be customised and embedded in the ARPHA article submission system, including a human-readable rendering of the metadata. This task will also explore ingestion of the **BGE+** RO-Crate to and from metabarcoding pipelines (T5.7, T4.5) and the **ERGA** and BOLD Europe data portals, from which a generalised Publication RO-Crate profile will be developed in collaboration with EOSC and the EuroScienceGateway publisher forum, to support linking articles to biodiversity repositories and detailed data provenance.

Task 5.6 Harmonised framework for the analysis of intra-specific genomic data: To increase cost-efficiency, reproducibility, and comparability of metrics derived from WGS data, this task will develop a harmonised framework that simplifies analytical outputs, supports genomic-health assessments, and promotes WGS uptake in monitoring programmes. Development will focus on modular, user-friendly pipeline(s) that integrate metadata interpretation and quality control to standardise analytical steps for intra-specific genomic data at the (multi)population level. Outputs will include genome-wide single nucleotide polymorphism (SNP) sets and objective metrics such as Runs of Homozygosity, supporting standardised tools for estimating genetic diversity indicators aligned with stakeholder and policy needs (linked to WP6). Pipelines, developed in line with the project's FAIR data framework, will be flexible in tool choice and generate standardised outputs and reporting, using common Workflow Management Systems (e.g. SnakeMake). Input data will include datasets from BGE1. The task will address heterogeneity in WGS data, ensuring comparable metrics despite variation in sequencing depth, sample quality, etc. Results will feed into WP6 (task 6.3) for evaluation across broader taxonomic use-cases.

Task 5.7 Pilot framework for future-proofing metabarcoding-based monitoring: Following from BGE1 and T4.5, this task will address systematic biases during processing of metabarcoding data, such as taxonomic inflation, technical artefacts and cross-platform normalisation, while working on promoting FAIR publication of Amplicon Sequence Variant (ASV) tables and associated taxonomic annotations, following current eDNA standards initiatives, e.g. eDNAquaPlan (Kavakiotis et al. 2026), FAIRe (Takahashi et al. 2025). The publication of ASV tables and taxonomic annotations is not yet fully standardised, despite ongoing initiatives and efforts. The new ENA submission system for ASV tables supports decoupled taxonomic annotation, allowing taxonomic reannotation. An updated RO-Crate profile will be developed to allow all analytical steps to be

documented, audited, and reused across projects and beyond. This will facilitate reprocessing of archived ASV tables by re-application of taxonomic annotation pipelines, with updated reference libraries, and feeding these new taxonomic interpretations back to the sequence repositories. This pilot scalable system will contribute to ensuring long-term interoperability of European metabarcoding surveys and maximise the value of distributed biodiversity monitoring investments.

Work package WP6 – Biodiversity genomics knowledge exploitation - science and policy cases

Objectives: WP6 aims to integrate harmonised and standardised frameworks to advance the uptake, use and impact of genomic approaches, from DNA barcoding and metabarcoding to high-resolution reference-based genomes, in European biodiversity policy and monitoring. This work will connect with European biodiversity policies, programmes, stakeholders and initiatives to strengthen the role of biodiversity genomics as a cornerstone of evidence-based decision making in Europe.

Description:

Task 6.1 Strategic Engagement for Genomics Integration in European Biodiversity Landscape and Policy: T6.1 will connect, through dedicated workshops/meetings, with priority European policies, directives, programmes and stakeholders, to position the biodiversity genomics community in the European landscape for biodiversity application and monitoring and strengthen the capacity of the biodiversity genomics community to engage with and support policy and decision-making in Europe. Building on available maps from Horizon Europe BGE1 and EuropaBON, it will foster cooperation with key entities, as the EC Knowledge Centre for Biodiversity (KCBD), BioAgora, the pilot on the EU Biodiversity Observation Coordination Center (EBOCC), the European Alien Species Information Network (EASIN), and projects like the COST action GENOA and Biodiversa+ GINAMO, and bridge gaps, identifying other European initiatives, organisations, agencies, and infrastructures involved in the science policy interface. The strategic stakeholder connections will support alignment with the EU Biodiversity Strategy for 2030, the Nature Restoration Law, and feed T6.2 and 6.3, and the strategic synthesis in T6.4.

Task 6.2 Roadmap for the Transnational Integration of DNA Barcoding and Metabarcoding in Biodiversity Monitoring: T6.2 will produce a roadmap for the transnational integration of DNA barcoding and metabarcoding into biodiversity monitoring across Europe, addressing the lack of coordinated organisational structures, harmonised workflows, and interoperable infrastructure for effective transnational use. The roadmap will contribute to harmonised reporting and assessment at national and EU levels, defining the components for the consistent application of metabarcoding, including harmonised field sampling, laboratory processing, bioinformatic analysis, intercalibration, standards for data management, storage, and reporting, as well as strategies to future-proof monitoring systems. It will incorporate innovations from WP4 and WP5, as well as relevant inputs from BGE1 and cascade-funded projects (WP2), to

ground the roadmap in wider practical applications. It will be informed by consultations with entities identified in T6.1, conducted through interviews and workshops, and aligned with the infrastructure model (WP7) and the **iBOL-E** community (WP8).

Task 6.3 Roadmap for Whole Genome-based Biodiversity Genetic Diversity Indicators: T6.3 will produce a policy-aligned roadmap for harmonising and standardising assessments of intra-specific genetic diversity using WGS data, to increase the uptake and impact of genomics in European biodiversity monitoring, conservation, management, and sustainable exploitation. It will focus on deriving harmonised genetic composition Essential Biodiversity Variables (EBVs) that inform biodiversity indicators, centred on gold-standard use-cases across taxonomic groups, using existing WGS datasets (from BGE1, partner initiatives, and publicly available sources). It will apply bioinformatic pipelines from T5.6 for reliable EBV estimation, integrate results from cascade-funded projects (WP2) to broaden taxonomy, and link to the **ERGA** Data Analysis Committee and the **ERGA** EBV working group (WP9). Aligned with the infrastructure model (WP7), the roadmap will link to entities identified in T6.1 and establish guidelines for cost-efficient workflows for estimating the genetic composition (as an EBV) from WGS, encompassing sampling, data production, analysis, and policy recommendations, aligned with EU biodiversity strategies, directives, and frameworks.

Task 6.4 Synthesis and Strategic Positioning of Genomic Tools in Support of European Biodiversity Policy and Monitoring: T6.4 will produce a strategic synthesis report with actionable recommendations for institutional coordination, long-term implementation, and transnational integration of genomic tools into EU biodiversity monitoring and policy. It will build on the stakeholder mapping (T6.1) and roadmaps (T6.2, 6.3) to develop a framework for the adoption of genome-based monitoring systems, ensuring alignment with EBOCC for harmonised monitoring, and the KCBD for science-policy support. It will consider the European Environment Agency's role in biodiversity reporting and data infrastructure, as well as the European Committee for Standardisation's compatibility with standardisation processes, aligning with the infrastructure model (WP7) and the genomic communities (WP8, 9). Activities towards the synthesis will integrate results from the WP, expert interviews, thematic workshops and consultation meetings with stakeholders, supporting a policy brief for uptake by relevant EU and national bodies.

Work package WP7 – Towards a European distributed system for Biodiversity Genomics

Objectives: WP7 will describe key components of the biodiversity genomics infrastructure. It will define the vision, mission, and scientific and technical case, including a structured service portfolio aligned with European research priorities and user needs. This work will provide a comprehensive understanding of the possibilities and implications of a significant upgrade of existing European Research Infrastructures.

Description:

Task 7.1 Defining user needs for service portfolio development: T7.1 will undertake a systematic mapping exercise of the user community for biodiversity genomics in Europe (**ERGA** and **iBOL-E**), with a strong emphasis on engaging stakeholders involved in both basic and applied research. These groups act as critical bridges between data generation and its translation into practical outcomes for sectors such as environmental management (including decision-making bodies), conservation, agriculture, fisheries, forestry, public health, and other industries. A mixed-methods approach—including workshops, surveys, and interviews with researchers —will be used to identify and characterise key user groups. Dialogue with this broad user base will help identify both their specific needs and requirements, as well as their unique contributions to the biodiversity genomics landscape.

Task 7.2 Positioning genomics technical infrastructure services within the European research ecosystem by identifying existing and missing services and resources: The work will begin by assessing the status of existing services and resources that support biodiversity genomics across the current landscape of relevant European research infrastructures (ESFRI's core facilities amongst others). The mapping will identify reusable infrastructure assets and highlight opportunities for further technical development, suggesting a path from sampling to whole-genome annotation, barcoding, and beyond. The identified infrastructures will serve as foundational components for integration into genomics hubs and national nodes, supported by training and technical development to address specific technical needs and interoperability requirements. We will map current services against the user and community needs identified in T7.1, highlighting existing and emerging gaps in infrastructure with consideration of future technological developments. A workflow/pipeline as well as a catalogue of existing and missing services, will be developed to provide a comprehensive understanding of gaps in the current technical and data landscape on national and regional levels.

Task 7.3 Developing the scientific and technical description for the biodiversity genomics infrastructure: Building on T7.1 and 7.2, this task will develop the scientific and technical case for a European biodiversity genomics infrastructure, defining a flexible service portfolio aligned with user needs, community capabilities, and interoperability requirements. The portfolio will encompass genomic data services, analytical platforms, training, application support, and policy aspects, including data sharing and compliance. At the same time, a technical conceptual structure will be developed to detail how components such as databases, computational platforms, labs, and knowledge hubs interact, scale, and integrate with EOSC. A co-creation approach will be employed throughout, using structured consultation and engagement processes (e.g. design-thinking workshops, interviews, and iterative feedback loops) involving key actors from **ERGA**, **iBOL-E**, and **BGE+** governance bodies, as well as representatives of genomics and data analysis RIs.

Task 7.4 Integrating Biodiversity Genomics into Existing European Research Infrastructures: Building on previous tasks, this work will explore how to upgrade

existing Research Infrastructures (RIs) to support genomics integration. A series of structured workshops with interested RIs will assess feasibility across scientific, technical, organisational, and financial dimensions: (i) Explore scientific opportunities from genomics integration, (ii) Identify technical and operational requirements, (iii) Address financial, governance, and sustainability issues, (iv) Highlight barriers and enablers. Each workshop will focus on a key theme and engage stakeholders, including RI operators, domain experts, and policy advisors.

Work package WP8 – Network enlargement and support to iBOL-E

Objectives: The mission for **iBOL-E** is to produce, curate and provide access to a complete DNA barcode reference library of European eukaryotic biodiversity, catalysing species discovery and enabling comprehensive, harmonised species identification and biomonitoring, and supporting the global iBOL programme. To deliver this mission, WP8 focuses on community engagement and capacity building for DNA barcoding at Europe-wide (T8.1) and national (T8.2) scales, driving the development of a network of distributed DNA barcoding facilities (T8.3) and coordinating dynamic community-driven DNA-barcode reference library curation (T8.4).

Description:

Task 8.1 Network coordination: fostering community cohesion and collaboration across Europe: This task focuses on developing the iBOL community in Europe and will host and run the **iBOL-E** hub-secretariat. Activities include: coordinating working groups on key strategic issues (e.g., training, data standards, capacity building); evolving **iBOL-E** 's governance arrangements to meet community and stakeholders' needs, building and maintaining strategic partnerships, including delivering joint initiatives with the reference genome community in Europe (**ERGA**). The task will also include organising an international DNA barcoding community event, running community meetings, and maintaining and developing the **iBOL-E** web presence, including establishing and coordinating community support forums developed within the WP. T8.1 will also work to communicate the outputs of **BGE+** cascade-funded projects to the wider **iBOL-E** community and interested stakeholders to maximise impact.

Task 8.2 National and regional nodes: Developing capacity and supporting delivery: This task focuses on building national/regional capacity for DNA-based species identification and biomonitoring with a particular emphasis on supporting new/nascent barcoding nodes in regions where DNA barcoding reference libraries are at an early stage of development. This includes developing and sharing a registry of expertise and best practice, and producing and sharing practical resources such as strategy documents, cases for support, MoUs, and policy brief templates. To support translation to impact, T8.2 will also convene regular practitioner events that connect research communities to agencies responsible for DNA-based biomonitoring. Finally, T8.2 will provide a 'help-desk' service to signpost available community resources to national/ regional initiatives and barcoding projects (including cascade-funded projects in WP2).

This will encompass guidance on community standards and approaches for integrating project activities into the wider work programmes of iBOL and **CETAF**.

Task 8.3 Sequencing capacity: Supporting and growing a distributed network of DNA-barcode sequencing facilities: T8.3 will capitalise on the potential for roll-out of lab-in-the-box low-cost integrated solutions for DNA barcoding based around the portable DNA sequencers, e.g. Oxford Nanopore Technologies. The task will bring together a distributed network of experts/research teams/institutions to share experiences and create accessible, end-to-end, documented solutions for DNA barcoding and the production of reference libraries via a low-cost laboratory setup. The primary activities of the task will be (a) establishing a community forum, hosted on the **iBOL-E** webpage for sharing technical expertise, (b) workshops for collective problem solving and ideas exchange, and (c) the production of a user guide for operationalising low-cost distributed DNA barcoding, synthesising the expertise of task partners and the wider community.

Task 8.4 Reference libraries: Harnessing community efforts for gap-list development and reference library curation: T8.4 will capitalise on the recent development of the **iBOL-E** gap list and BGE1 Reference Library Pipeline and Curation Tool and their planned future developments in T5.3, providing open, community-driven resources that visualise the status of reference libraries across taxonomic groups and support library curation. The task will focus on connecting professional taxonomists, amateur expert citizen scientists, and data experts (a) to refine the gap-list by correcting nomenclatural inconsistencies, and also promoting awareness of essential priority gaps, and (b) to harness distributed efforts for DNA barcode reference library curation. Activities will entail targeted curation campaigns, consisting of multi-week periods of sustained curation efforts, and a combination of online and in-person workshops, supported by a community forum to build and maintain momentum.

Work package WP9 – Network enlargement and support to ERGA

Objectives: WP9 is dedicated to consolidating and extending the network of researchers and projects producing and exploiting reference genomes for eukaryotic biodiversity in Europe: the European Reference Genome Atlas (**ERGA**) Community (Mazzoni et al. 2023) that represents the participation of the European bioregion in the global efforts of the Earth BioGenome Project (EBP) (Blaxter et al. 2025). Tasks are designed to widen participation and increase accessibility and use of genomics data for biodiversity and ecosystem management, empower researchers to achieve high-quality datasets, and strengthen expertise in genomics technologies for species identification and biomonitoring. WP9 forms a bridge between the tasks and activities of the **BGE+** project and the **ERGA** Community.

Description:

Task 9.1 ERGA Network Development and Coordination: T9.1 delivers support for the reference genomes research community via the **ERGA** Secretariat and Committees. It enhances access to and usability of services that foster high-quality, community-driven

biogenome production and exploitation. Community Meetings, Support, & Management: This coordinates **ERGA** Council, Plenary, and Committee Meetings with Affiliates, Associates, and 38 Member Countries, strengthening governance, engagement, and knowledge sharing. Knowledge Hub & Communications: This manages the **ERGA** website and interactive forum for member engagement and communication, overseeing the Knowledge Hub (EKH 2026), curating new materials, and coordinating events to foster knowledge exchange, collaboration, and participation. Global & Regional BioGenome Coordination & Partnerships: This coordinates **ERGA**'s partnership with the EBP to align global efforts. It builds partnerships with ENA, GBIF, and GGBN, and enhances collaborations with **iBOL-E** and **CETAF** to foster cooperation and integrate genome data into broader biodiversity efforts.

Task 9.2: ERGA biogenome node and project development: T9.2 delivers widened participation in biogenome production and exploitation through supporting **ERGA** Members to develop nodes and projects and managing the **ERGA** Community genomes quality control system. Node/Project Development & Support: This supports members in designing projects leveraging **ERGA** expertise to secure financial support for increased biogenome production and exploitation. It also provides and directs technical support services to cascade funded projects (WP2) through Community and **BGE+** resources that promote high-quality outcomes. Genomes Quality Control (QC) System: This manages **ERGA**'s genome quality control system to ensure FAIR datasets, maintaining a buddy review system and QC reporting and managing bioinformatics workflows in collaboration with WP5 and **ERGA** Committees.

Task 9.3: ERGA BioGenome Hub Network: T9.3 develops the network of hubs for strengthening technical expertise in field and molecular laboratory work required for biogenome generation, creating a platform in Europe of facilities that drive distributed biogenome production efforts. Network Coordination & Organisation: This strengthens the network of **ERGA**-**BGE+** BioGenome Hubs, defining specifications, showcasing expertise, and facilitating technical exchanges with online seminars for problem solving and collaboration, complemented by an online workspace on the **ERGA** website. Management of Outputs: Enhancing operational capacity involves managing a registry of services, expertise, costs, and turnaround times, as well as overseeing the sharing of SOPs and Best Practices, and supporting capacity building by incorporating technical expertise into **ERGA** Knowledge Hub materials.

Task 9.4: ERGA BioGenome Applications Network: T9.4 develops the research network to strengthen technical expertise in genome-wide data analysis, creating the platform in Europe that drives the widespread uptake and use of high-quality genomics data in biodiversity assessments. Network Coordination & Organisation: This develops the network within **ERGA**, building on work of BGE1 and defining best practices for monitoring intra-species biodiversity, fostering collaboration and exchange via webinars enhanced by an interactive workspace in the **ERGA** website. Management of Outputs: This manages **ERGA**'s SOPs and Best Practices, bioinformatics workflows and training materials, ensuring high-quality data generation and analysis for using whole-genome

data. It also engages with conservation practitioners, agriculture, forestry, aquaculture, and the broader bioeconomy.

Project Milestones and Deliverables

The Project milestones and deliverables are listed with their due dates (in months with respect to Project duration) in Table 11 and Table 12, respectively.

Table 11.
Project milestones.

Milestone	Due Date (month)
MS1.1 Project kick-off meeting	3
MS1.2 Ethical assessment and guidelines	9
MS1.3 All hands meeting 1	15
MS1.4 Ethics monitoring mid-term report	24
MS1.5 All hands meeting 2	26
MS1.6 KER description	28
MS1.7 Revised Knowledge Platform	36
MS2.1 Defined call topics & evaluation process	10
MS2.2 Calls launched, selected projects onboarded	24
MS2.3 Exploitation plan for the cascade funded projects	28
MS3.1 Deployment of iBOL-E Knowledge Hub, update of ERGA Knowledge Hub, and Resource Platform launched on BGE+ website	6
MS3.2 Offer training activities to cascade projects	10
MS3.3 Capacity building for biodiversity genomics in Europe - overview and gap analysis	12
MS3.4 Capacity building action plan for BGE +	18
MS3.5 75% of courses and training activities incorporated in the European Biodiversity Genomics Education Program	24
MS4.1 Existing protocols for museomics (extraction, library prep) collated on community portal, gap analysis & prioritisation completed	5
MS4.2 All preservation approaches identified, procured, and all test taxa across major taxon groups procured	6
MS4.3 Integration of the complete high- WP4, WP5 throughput barcoding workflow, including imaging, amplification and sequencing	12
MS4.4 Complete pilot benchmarking on 3 species (insect, plant, vertebrate) & compare assembly metrics against existing references	18
MS4.5 Completion of intercalibration experiments and submission of raw data for central processing	21
MS5.1 Robust tooling for reference barcode generation and QC available	9
MS5.2 Benchmarking Framework Deployed, portal with functional submission system available	12

Milestone	Due Date (month)
MS5.3 A first version of the intra-specific genome analysis pipeline is available within the project	12
MS5.4 Workflow Evaluations Completed, results generated for selected genome assembly workflows and available via portal	18
MS5.5 Consolidated mechanisms for data linking and interoperability in ENA and BOLD	18
MS5.6 Pilot implementation of RO-Crate system for data and metadata associated with journal articles	24
MS5.7 Containerised pipeline deployed for partner testing	27
MS5.8 Initial pipeline testing completed with a report from partners on issues and suggested improvements	30
MS5.9 Pipelines for addressing bioinformatics biases in metabarcoding analysis and taxonomic annotation published	34
MS6.1 Stakeholder engagement and roadmap structure for (meta)barcoding applications validated	21
MS6.2 Genomic data requirements, methods and use case datasets	24
MS6.3 Preliminary outline of the strategic synthesis through stakeholder consultations	36
MS7.1 Preliminary outcomes overview for user mapping initiatives	12
MS7.2 First version of a catalogue of existing services - supporting biodiversity genomics across the current landscape of European RIs and beyond	14
MS7.3 Definition of mission and vision of biodiversity genomics infrastructure	24
MS7.4 Series of workshops with RIs, guided by ESFRI upgrade criteria	30
MS8.1 Inventory of relevant resources to support development of national capacity in DNA barcoding	12
MS8.2 Workshop bringing together expertise in low-cost distributed DNA barcode sequencing	12
MS8.3 Protocol for community engagement with GAP list and reference library curation established	14
MS8.4 Delivery of International DNA barcoding community event	36
MS9.1 Establishment and initial operational activities of ERGA BioGenome Hub Network	8
MS9.2 Establishment and initial operational activities of ERGA BioGenome Applications Network	8
MS9.3 Outcomes of node/project consortia proposals and roadmaps	12
MS9.4 ERGA Development and Coordination framework operational	14
MS9.5 ERGA BioGenome Hub Network operations expanded and extended	25
MS9.6 ERGA BioGenome Applications Network operations expanded and extended	25
MS9.7 Overview of ongoing and planned initiatives for widening ERGA participation and integration	26
MS9.8 ERGA Development Coordination framework updated and extended	28

Table 12.
Project deliverables.

Deliverable No	Deliverable Name	Type	Due Date (month)
D1.1	Project Handbook	R — Document, report	2
D1.2	Data management plan	R — Document, report	6
D1.3	Communication, dissemination and exploitation plan	R — Document, report	6
D1.4	Report on cumulative expenditure 1	R — Document, report	8
D1.5	Data management plan update 1	R — Document, report	18
D1.6	Report on cumulative expenditure 2	R — Document, report	20
D1.7	Update of the Communication, dissemination and exploitation plan	R — Document, report	34
D1.8	Data management plan update 2	R — Document, report	36
D1.9	Policy brief	R — Document, report	38
D1.10	Final event	R — Document, report	39
D1.11	Ethics monitoring report	R — Document, report	41
D1.12	Communication impact assessment	R — Document, report	42
D2.1	The Cascade Grants General Framework	R — Document, report	15
D2.2	Extension of the BGE+ network - data production	R — Document, report	32
D2.3	Added value of cascade projects	R — Document, report	42
D3.1	A roadmap for capacity building in biodiversity genomics in Europe	R — Document, report	18
D3.2	BGE+ Capacity Building Resource Platform WP3	R — Document, report	40
D3.3	European Biodiversity Genomics Education Program	R — Document, report	42
D4.1	Barcoding protocols	R — Document, report	18
D4.2	Museomic protocols	R — Document, report	23
D4.3	Preservation protocols	R — Document, report	24
D4.4	Intercalibration Protocol Package	R — Document, report	30
D4.5	Reference genome protocols	R — Document, report	36
D5.1	Frameworks for reference barcode generation and curation	R — Document, report	18
D5.2	ERGA Workflow Performance Analysis	R — Document, report	24
D5.3	Integrated system of sequence and biodiversity infrastructures	R — Document, report	24
D5.4	Intra-specific genome analysis pipeline	R — Document, report	24
D5.5	Containerised Annotation pipeline	R — Document, report	35
D5.6	Tools and workflows for scholarly publishing of barcoding and reference genome biodiversity data	R — Document, report	36

Deliverable No	Deliverable Name	Type	Due Date (month)
D5.7	Validation and calibration of DNA metabarcoding analysis framework	R — Document, report	40
D6.1	Strategic Integration of ERGA and iBOL-E into Biodiversity Policies, Programmes and Stakeholder Networks	R — Document, report	13
D6.2	Roadmap for the Integration of DNA Barcoding and Metabarcoding in Transnational Biodiversity Monitoring	R — Document, report	36
D6.3	Roadmap for Whole Genome-based Genetic Diversity Indicators for European Biodiversity Monitoring	R — Document, report	36
D6.4	Strategic Synthesis for the Integration of Genomic Tools for Biodiversity Monitoring	R — Document, report	42
D7.1	User needs assessment	R — Document, report	18
D7.2	Service scope report	R — Document, report	20
D7.3	Scientific and technical case for biodiversity genomics infrastructure (service portfolio)	R — Document, report	36
D7.4	Feasibility report of major upgrade of existing RIs	R — Document, report	42
D8.1	Registry of DNA barcoding resources and expertise	DEC —Websites, patent filings, videos, etc	40
D8.2	Reference library and gap list curation	R — Document, report	40
D8.3	DNA barcode community forums established	R — Document, report	42
D8.4	User guide for low-cost distributed DNA barcoding	R — Document, report	42
D9.1	ERGA BioGenome Hub Network services	R — Document, report	13
D9.2	ERGA BioGenome Applications Network activities	R — Document, report	13
D9.3	Consolidated ERGA BioGenome Hub Network	R — Document, report	41
D9.4	Consolidated ERGA BioGenome Applications Network	R — Document, report	41
D9.5	ERGA Development and Coordination framework	R — Document, report	42
D9.6	Widened ERGA Participation and Integration	R — Document, report	42

3.2 Capacity of participants and consortium as a whole

BGE+ brings together Europe's two principal biodiversity genomics communities - **iBOL-E** for DNA barcoding and **ERGA** for reference genomes - complemented by **CETAF** to anchor taxonomy and policy engagement. **iBOL-E** is represented by its coordination group (RBGE, Sanger, Naturalis) and the secretariat hosted by Naturalis; **ERGA** by members of its Executive Board (UU, UP, IZW) and the secretariat at SIB. **CETAF** is represented through its secretariat team. These networks connect **BGE+** to >250 European institutions and to the global nodes (iBOL via UGuelph, EBP via ASU). The consortium comprises 22 partners across 17 countries, spanning biodiversity science, genomics, informatics, research infrastructures and policy application, and is committed to open and equitable science.

Naturalis — Experience/expertise: Coordination of large interdisciplinary EU and national programmes; RI development (DiSSCo); national-scale monitoring and digital infrastructure (ARISE, eDentity); host of European BOLD; strong stakeholder brokerage and data-interoperability practice. **BGE+** contributions: Lead WP1 (management, DEC, ethics); support WP2 cascade framework; contribute to WP3 capacity building; WP4&5 innovation delivery; WP7 RI planning and WP8 community engagement.

LIB — Experience/expertise: Managing competitive funding schemes; metabarcoding wet/dry-lab capability; long experience with taxonomic data infrastructures and metadata; interoperability solutions for sequence repositories and infrastructure. **BGE+** contributions: Lead WP2 (cascade grants); contribute to WP4–WP5 technical pipelines; channel user requirements to WP7; support **ERGA** applications in WP9.

CETAF — Experience/expertise: European network of natural science collections; ABS/ Nagoya and ethics guidance; routes to national authorities; community standards and policy interfaces; TETTRIs project lead - taxonomy innovation, cascade grants scheme. **BGE+** contributions: Lead ethics monitoring (WP1); support WP2–WP3; co-lead stakeholder engagement and policy translation in WP6.

NTNU — Experience/expertise: Long-running training programmes (ForBio); advisory role to national nature management; proven hands-on curricula translating methods to routine practice; NorBOL coordinator. **BGE+** contributions: Lead WP3 (training); co-lead open barcoding framework in WP4; contribute to WP6–WP8.

UNIFI — Experience/expertise: Scaling genome/barcode production in small–medium labs (BGE1); WGS metrics; active in **ERGA**/**iBOL-E**; experience with TETTRIs/DiSSCo alignment to RI practices. **BGE+** contributions: WP3 capacity building; WP4 optimisation of metabarcoding/genome pipelines; WP5 metrics harmonisation; WP7 RI integration; WP9 network engagement.

NHMUK — Experience/expertise: Museomics; multi-national programmes lead (DiSSCo-UK, UKBOL); high-throughput digitisation; strengths in taxonomy and HMW DNA extraction. **BGE+** contributions: Lead WP4 (wet-lab innovation); deliver WP3 training; develop user-centred tools in WP5; support **iBOL-E** practice adoption.

Sanger — Experience/expertise: Large-scale genome production (DToL, BIOSCAN UK; >3,000 assemblies); robust QC and assembly validation. **BGE+** contributions: Innovate sampling to eliminate cold-chain needs (WP4); contribute to WP3 training; benchmark genome/annotation workflows in WP5; community engagement WP9.

EMBL-EBI/ELIXIR — Experience/expertise: Operation of ENA/Ensembl; data standards and long-term archiving; ELIXIR Platforms/Communities; policy engagement and equitable access. **BGE+** contributions: Lead WP5 (informatics innovation); WP3 training; lead service-portfolio planning in WP7; sustain **BGE+** data flows.

IZW — Experience/expertise: Wildlife conservation genomics; BeGenDiv; field-to-lab workflows; delivery in low-infrastructure contexts; Europe–Latin America links. **BGE+**

contributions: Grow communities (WP3, WP9); advance genomes/analytics (WP4–WP5); contribute to policy pilots (WP6) and RI design (WP7).

CIBIO — Experience/expertise: Evidence-to-policy translation; DNA-based monitoring; ancient DNA and HPC; track record in Teaming, EuropaBON and agency partnerships. **BGE+** contributions: Lead WP6 (policy-relevant applications); lead metabarcoding intercalibration (WP4); lead **ERGA** applications network (WP9); contribute to WP3 training and WP5 informatics.

UP — Experience/expertise: EOSC/EEA/EUA policy work; international genomics projects; governance schemes; practitioner and citizen-science engagement. **BGE+** contributions: Lead WP7 (towards a sustainable distributed system); support WP2 cascade grants design and WP6 operationalisation in policy context.

RBGE — Experience/expertise: Plant/lichen barcoding; HMW DNA extraction at scale; IUCN groups; national strategies and reporting. **BGE+** contributions: Lead WP8 (**iBOL-E** enlargement/support); deliver WP3 training; contribute WP4 lab skills, WP6 translation and WP7 RI strategy.

SIB — Experience/expertise: Bioinformatics for life sciences; **ERGA** secretariat; online knowledge hubs; population-genomics data publishing. **BGE+** contributions: Lead WP9 (**ERGA** enlargement/support); operate WP3 hubs/registration systems; co-manage WP2 cases; align WP5 innovations with **ERGA**; support WP6–WP7.

UGuelph — Experience/expertise: iBOL global secretariat and BOLD; >15M curated specimens; high-throughput barcoding; global capacity building. **BGE+** contributions: Support WP3–WP4 training and protocol adoption; advance BOLD alignment with ABS; strengthen **iBOL-E** via WP8.

ASU/EBP — Experience/expertise: EBP secretariat coordinating ~60 projects; cross-project standards and ethics frameworks; global governance. **BGE+** contributions: Strengthen alignment with global genomics through WP9; share best practices and governance models.

UU — Experience/expertise: SciLifeLab host; state-of-the-art genomics, bioinformatics services and training; robust data management; broad user support. **BGE+** contributions: Deliver WP3 training; contribute to WP4–WP5 innovation; support WP7 RI options and WP9 network development.

CNAG — Experience/expertise: Large-scale long-read WGS; accredited short-read sequencing (ISO 17025) with ISO 9001/27001; LIMS and secure data stewardship. **BGE+** contributions: Genome protocols and pipelines development (WP4–WP5); support WP3 training and WP7 services and resources assessment.

PENSOFT — Experience/expertise: Open-access publishing; informatics platforms; communications for >30 EU projects; data-paper workflows; BgBOL co-founder, wet-lab

expertise. **BGE+** contributions: Map training needs (T3.1); streamline FAIR access (T5.5); support knowledge exploitation (WP6); **iBOL-E** communications (WP8).

AU — Experience/expertise: End-to-end genomics hub; TurkBOL founder; extensive WHO/FAO/iBOL/COST/ERC workshops; reproducible pipelines; national/international project delivery. **BGE+** contributions: Lead cost-effective reference-genome enablement (T4.4); contribute WP3–WP4 training/democratisation; build networks via WP8–WP9.

UNIMAN — Experience/expertise: RO-Crate; FAIR provenance; workflow packaging across HPC/cloud; community training. **BGE+** contributions: WP5 workflow/provenance solutions; WP3–WP4 training, knowledge sharing and innovation; strengthen interoperability and open access practices.

UniLodz — Experience/expertise: (Meta)barcoding, integrative taxonomy and biomonitoring; PoLBOL coordination; citizen-science mobilisation. **BGE+** contributions: Advance barcoding democratisation and national capacity (WP3, WP8); contribute to WP4 wet-lab innovation and WP6 biomonitoring applications.

AUTh — Experience/expertise: Bioinformatics, GAP analysis and large-scale sampling; GrBOL leadership; stakeholder engagement. **BGE+** contributions: Build capacity (WP3, WP8); deliver innovation and application in both barcodes and genomes (WP4, WP6); support WP7 RI establishment.

Acknowledgements

The authors, comprising the **BGE+** Consortium's Executive Board and contributors to the original drafting and finalisation of the writing of the proposal presented in this publication, acknowledge the valuable input, feedback, and constructive discussions from all other contributors. Biodiversity Genomics Europe plus (grant agreement ID: 101289347, doi.org/10.3030/101289347) is funded by Horizon Europe under the Food, Bioeconomy, Natural Resources, Agriculture and Environment call, HORIZON-CL6-2025-01-BIODIV-03.

Grant title

Biodiversity Genomics Europe plus

Conflicts of interest

The authors have declared that no competing interests exist.

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