Ref. Ares(2025)5316444 - 02/07/2025

Data Management Plan

DATE: DAY, June 2025

VERSION 1.0

DELIVERABLE NUMBER: D6.2

General Information

Call identifier:	HORIZON--CL6-2024-BIODIV-01
GA Number:	101181589
Start date of project:	01/01/2025
Work Package:	WP6
Type:	Deliverable
Number:	D6.2
Version:	1
Due Date:	30/06/2025
Submission date:	30/06/2025
Responsible organisation:	UEDIN
Prepared by:	Clémence Fraslin
Contributing organisations;	UNIPD, INRAE, UB

Document type		
R	Document, report (excluding the periodic and final reports)	
DEM	Demonstrator, pilot, prototype, plan designs	
DEC	Websites, patents filing, press & media actions, videos, etc.	
DATA	Data sets, microdata, etc.	
DMP	Data management plan	X
ETHICS	Deliverables related to ethics issues	
SECURITY	Deliverables related to security issues	
OTHER	Software, technical diagram, algorithms, models, etc.	

Dissemination level		
PU	Public	X
SEN	Sensitive, limited under the conditions of the Grant Agreement	

Table of Contents

1. Project summary

The implementation of selective breeding programmes tailored to the unique characteristics of organic production holds immense promise to address the challenges faced by OA. EUAqua.Org aims to spearhead this effort by leveraging key technological advancements in phenotyping, genotyping, and genomic prediction. Through the integration of different disciplines and approaches, EUAqua.Org will provide essential tools for cost-effective, welfare-conscious and environmentally friendly Organic Aquaculture (OA). The implementation of these tools at the industry level will be ensured by a comprehensive scientific, public, and industrial communication and dissemination programme, with exploitation of the project objectives and key results to create impact, including a multi-module open-access online training course that will be co-developed with key stakeholders (breeding companies, fish farmers, feed producers). In parallel, a tailored set of intervention strategies will be designed to promote awareness and acceptance of OA products in European consumers, through a behavioural economics approach. The overarching mission of EUAqua.Org is to invigorate OA in Europe by adopting a problem-solving ethos and pioneering highly innovative solutions to fill key knowledge gaps and overcome the primary factors limiting the competitiveness of Atlantic salmon, European sea bass, gilthead sea bream, and rainbow trout organic production.

2. Data summary

The overall data management plan is to ensure the data generated in the course of the EUAqua.org project are i) high quality *i.e.,* linked to detailed methods and metadata, ii) stored on resilient servers, and iii) made publicly available in a timely and responsible manner.

The data generated in this project fall into 10 main categories:

1. **Whole Genome Sequence data** (source of genetic diversity) obtained by sequencing individuals will be generated (WP1) or re-used by downloading from NCBI in .fasta.gz, .fasta, .bam, .vcf formats depending on the origin.
2. **Genotype of animals** (source of genetic diversity) obtained by genotyping individuals with SNP array (WP1, WP2, WP3). Genotypes will be produced or re-used in .CEL format or post genotype calling in PLINK {.ped and .map or .bed .bim .fam} or in .vcf formats.
3. **Phenotype of animals** for traits of interest such as individual feed intake (WP2), resistance traits (WP1, WP3), will be produced or reused (stored and shared in .xlsx, .txt or other tabulated format, or in Plink {.ped or .fam} formats).
4. **Transcriptomic data** (bulk or single-cell/nuclei RNA sequencing) will be generated (WP3) or re-used (WP1), obtained and stored in .bam, .fasta and .gtf for raw data and in .txt or other tabulated formats for processed data.
5. **Proteomic data** will be produced (WP3), stored and shared in the open format mzML and .fasta the standard for mass spectrometry data.
6. **Epigenetic markers data** will be produced (WP1), stored and shared in .fastq and .txt format.
7. **Videos** (recording of individual and group phenotypes, WP1, WP2, WP3) will be generated in mp4 format, annotated (.coco and .pt formats) and analysed to extract phenotype information (.txt or other tabulated file).
8. **Survey/interview output (WP2, WP4)** will be produced, stored and shared in .txt and .docx, .jpeg format.
9. **Dataset of labels for organic products (WP4)** will be produced, stored and shared in .csv and .xlsx format.
10. **Pipelines for analysis of WGS imputation and functional annotation** will be generated (WP1 and WP3), stored and shared via appropriate platforms (GitHub, protocols.io and others) depending on the coding language used.

The data summary table below presents all the data that EUAqua.org is expected to produce or re-use associated with the work package (WP) and task (T).

Data summary table

WP No.	Task No.	Lead beneficiary	Task Title	Research asset name	Research asset ID*	Generated / Reused
WP1	**1.1.1**	UNIPD, UEDIN	Producing novel WGS for gilthead sea bream and rainbow trout	Datasets of WGS for gilthead sea bream and rainbow trout	D1.1.1	Generated
	1.1.2	UNIPD, UEDIN, INRAe	Creating reference genome sequence panels for the four species	Datasets of WGS for rainbow trout and Atlantic salmon, sea bass and seabream	D1.1.2	Reused
	1.1.3	UNIPD, UEDIN	Developing an optimized pipeline for WGS data imputation reference genome sequence panels for the four species	Pipeline for WGS imputation with new reference populations	S1	Reused (D1.1.2) And Generated (D1.1.1)
	1.2	UNIPD, UEDIN, INRAe	Optimising genomic prediction using functional prioritisation of genetic variants	Dataset of functional annotation for the four species	D1.2	Reused
	1.3	IRTA, UNIPD, VISIFIH	Developing methods to obtain optimal mating schemes in the European seabass	Dataset of video recordings for phenotyping behaviour for sea bass	D1.3.1	Generated
				Created annotation files from the video footage.	D1.3.2	Generated
				Retrain model files.	D1.3.3	Generated
	1.4	INRAe	(Epi)genetic markers for spontaneous masculinisation in all-female rainbow trout populations	Dataset of individual genotype (SNP markers) from female rainbow trout	D1.4.1	Generated
				Dataset of phenotype for spontaneous masculinisation in female rainbow trout	D1.4.2	Generated
				Dataset of individual epigenetic markers for spontaneous masculinisation in female rainbow trout	D1.4.3	Generated
WP2	**2.1**	USTIR, UB, VISIFISH, UEDIN	Estimation of genetic parameters for feed efficiency in Atlantic salmon	Dataset phenotype (stable isotopes analysis) for individual feed intake in A. Salmon	D2.1.1	Generated
				Dataset of individual genotype (SNP markers) in A. salmon	D2.1.2	Generated
				Dataset of video recordings of feed intake	D2.1.3	Generated
				Created annotation files from the video footage.	D2.1.4	Generated
				Retrain model files.	D2.1.5	Generated
	2.2	INRAe, UB, USTIR, UNIBIO	Life cycle assessment of organic feeds	Databases with life cycles inventories for feed ingredients	D2.2.1	Reused
			Newly developed organic diet	Dataset of phenotype (growth performance and filet quality) for fish fed a newly developed organic diet	D2.2.2	Generated

WP3	**3.1**	UNIPD, UEDIN, IRTA, VISIFISH	Next generation transmission experiment in sea bass with *Vibrio aguilarum*	Dataset of disease from seabass and bacterial strains	D3.1.1	Generated
				Dataset of video recordings of feed intake.	D3.1.2.1	Generated
				Created annotation files from the video footage.	D3.1.2.2	Generated
				Retrain model files.	D3.1.2.3	Generated
				Dataset of individual genotype (SNP markers) from sea bass	D3.1.3.1	Generated
				Simulated genomic and phenotypic disease data from sea bass (infectivity, resistance and tolerance)	D3.1.3.2	Generated
	3.2	CII, UEDIN, VISIFIH	Non-invasive tools for early disease diagnosis of *Yersinia ruckeri* in rainbow trout	Datasets of transcriptomic data in healthy and moribund rainbow trout	D3.2.1	Generated
				Datasets of proteomic data in healthy and moribund rainbow trout	D3.2.2	Generated
				Video recordings of behaviour-based welfare	D.3.2.3	Generated
	3.3	UNIPD	Intermediate phenotypes for VNN resistance	Datasets of transcriptomic data in healthy and moribund sea bass	D3.3.3	Reused
	3.4	UNIPD, UEDIN	Use of functional variants for accurate prediction of sea lice resistance in Atlantic salmon	Dataset of individual genotype (SNP markers) and phenotypes from A salmon imputed in WP1	D3.4.1	Reused
			Use of functional variants for accurate prediction of viral nervous necrosis virus resistance in gilthead seabream	Dataset of individual genotype (SNP markers) and phenotypes from seabream imputed in WP1	D3.4.2	Reused
WP4	**4.1**	UNIBO, UNIPD, WRG, CROMARIS	Understanding labelling and information on aquaculture products	Dataset of information around labels, awareness campaign typologies, target group	Do4.1	Generated
	4.2		Testing aquaculture labels and awareness interventions via choice experiments in virtual reality settings	Dataset of Interviews and consumer experience	Do4.2	Generated
	4.3		Developing guidelines for effective labels and awareness interventions	Dataset of guidelines for organic label of aquaculture products	Do4.3	Generated

*D: dataset/database, S: software/app/pipeline, Do: documents/datasets for internal use

The EUAqua.org project will generate and re-use data that were produced in previous projects and made publicly available, are available upon request to the authors or produced by partner companies.

The type (format) of data that will be generated or re-used, the expected size of the generated data and the data provenance of re-used data are presented in the table below

Data type and availability summary table

Research asset ID	Research asset format	Research asset size	Research asset name	Data provenance (Reused or Generated)	Made available on repositories
D1.1.1	.fasta.gz, .fasta, .bam, .vcf	TBs	Datasets of WGS for gilthead sea bream and rainbow trout	Generated	ENA
D1.1.2	.fasta.gz, .fasta, .bam, .vcf	TBs	Datasets of WGS for rainbow trout and Atlantic salmon, sea bass and seabream	Reused: NCBI, ENA, Ensembl.org, AQUAImpact (Rainbow Trout), AQUA-FAANG (sea bass)	
S1	R, python, .sh, or other language	MBs	Pipeline for WGS imputation with new reference populations	Reused (D1.1.2) GitHub, protocols.io and Generated (D1.1.1)	GitHub, protocol.io
D1.2	.txt, .csv, .bed	MBs	Dataset of functional annotation for the four species	Reused: AQUA-FAANG, Ensembl.org	
D1.3.1	AVi, mp4, other	TBs	Dataset of video recordings for phenotyping behaviour for sea bass	Generated	IRTA-data repository, local at Visifish
D1.3.2	.coco	GBs	Annotation files from the video footage (D1.3.1)	Generated	Local at Visifish, Digitalocean
D1.3.3	.pt	MBs	Retrain model files (from D1.3.1/1.3.2)	Generated	Digitalocean
D1.4.1	.CEL .vcf .ped &.map	GBs	Dataset of individual genotype (SNP markers) from female rainbow trout	Generated	Data INRAE
D1.4.2	.txt .xlsx	MBs	Dataset of phenotype for spontaneous masculinisation in female rainbow trout	Generated	National data repository (datagouv.fr)
D1.4.3	.fastq, .txt	TBs	Dataset of individual epigenetic markers for spontaneous masculinisation in female rainbow trout	Generated	ENA
D2.1.1	.txt, .xlsx	MBs	Dataset phenotype (stable isotopes analysis) for individual feed intake in A. salmon	Generated	Figshare and DDUB
D2.1.2	AVi, mp4, other	TBs	Dataset of video recordings of individual feed intake	Generated	Local at visifish, Digitalocean
D2.1.3	.coco	GBs	Annotation files from the video footage (D2.1.2)	Generated	Local at visifish, Digitalocean
D2.1.4	.pt	MBs	Retrain model files (from D2.1.2/2.1.3)	Generated	Digitalocean
D2.1.5	.CEL .vcf .ped &.map	GBs	Dataset of individual genotype (SNP markers) in A. salmon	Generated	Figshare, ENA
D2.2	.txt, .docx	MBs	Databases with life cycles inventories for feed ingredients	Generated	Figshare

Funded by the European Union

D2.3	.txt, .xlsx	MBs	Dataset of phenotype (growth performance and filet quality) for fish fed a newly developed organic diet	Generated	Data INRAE, AMS Acta and DDUB
D3.1.1	.txt .xlsx	Mbs	Dataset of disease from seabass and bacterial strains	Generated	Figshare
D3.1.2.1	AVi, mp4, other	TBs	Dataset of video recordings for disease behaviour in sea bass	Generated	Digitalocean
D3.1.2.2	.coco	GBs	Annotation files from the video footage (D3.1.2.1)	Generated	Digitalocean
D3.1.2.3	.pt	MBs	Retrain model files (from D3.1.2.1/3.1.2.2)	Generated	Digitalocean
D3.1.3.1	.CEL .vcf .ped &.map	GBs	Dataset of individual genotype (SNP markers) from sea bass	Generated	Figshare, ENA
D3.1.3.2	.csv, .txt, .xlsx	GBs	Simulated genomic and phenotypic disease data from sea bass (infectivity, resistance and tolerance)	Generated	GitHub
D3.2.1	.fastq .bam .gtf	GBs	Datasets of transcriptomic data in healthy and moribund rainbow trout	Generated	ENA
D3.2.2	mzML, .fasta	GBs	Datasets of proteomic data in healthy and moribund rainbow trout	Generated	ENA
D.3.2.3	.mp4	TBs	Video recordings of behaviour-based welfare	Generated	Local at CIIMAR available upon request
D.3.3.3	.fastq .bam .gtf	GBs	Datasets of transcriptomic data in healthy and moribund sea bass	Reused: AQUA-FAANG	
D3.4.1	.vcf .ped &.map	GBs	Dataset of individual genotype (SNP markers) and phenotypes from A salmon imputed in WP1	Reused: GenoLice (BBSRC funded)	
D3.4.2	.vcf .ped &.map	GBs	Dataset of individual genotype (SNP markers) and phenotypes from seabream imputed in WP1	Reused: PerformFish (EU funded)	
Do4.1	.docx, .xlslx	MBs	Dataset of information around labels, awareness campaign typologies, target group	Generated	UNIBO repository, EC Portal
Do4.2	.csv, .xlsx	MBs	Dataset of Interviews and consumer experience	Generated	UNIBIO repository
Do4.3	.docx, .jpeg	MBs	Dataset of guidelines for organic label of aquaculture products	Generated	UNIBIO repository, EC Portal

*D: dataset/database, S: software/app/pipeline, Do: documents/datasets for internal use

Functional annotation of genomes (eQTL, ATAC-seq, miRNA sequence data) have been produced by the AQUA-FAANG project and are available on the Functional Annotation of Animal Genomes (FAANG) dataset web page and/or on Ensembl.org along with metadata sheets.

(https://www.aqua-faang.eu/datasets.html ; https://projects.ensembl.org/aqua-faang/ ; https://data.faang.org/projects/AQUA-FAANG)

Funded by the European Union

The data generated in this EUAqua.org project might be useful for:

- **Scientific community**
- **University community**: teachers/lecturers/students

3. FAIR data

3.1 Making data Findable, including provision for metadata

Data sets will be clearly identified with unique and appropriate digital object identifiers (DOIs) in recognized public repositories to ensure maximum access and exposure to the data. The main repositories used for the 10 types of data generated in this project are described in the Data type and availability summary table above.

They are: the European Nucleotide Archive (ENA; for transcriptomic, proteomic, whole genome sequence, genotype datasets), Figshare (individual genotypes and matched phenotypes), Digitalocean (video recording, annotated files and retained models), and local institute or government based storage such as Data INRAE , data.gouv.fr, IRTA-data repository, DDUB and CORA.

All data sets will be accompanied by metadata that is compliant with community approved standards, including but not limited to the 15 Dublin Core Metadata Element Set to ensure maximum usability by others.

The descriptive metadata will include relevant information such as: unique DOI, title, abstract, keyword, authors and affiliations, project acronym (EUAqua.org), project GA number (101181589), Call identifier (HORIZON--CL6-2024-BIODIV-01), research asset type, research asset ID and publication date (in ISO 8601 format, YYYY-MM-DD). If relevant, a ReadMe sheet describing the transformations made on raw data (e.g SNP calling, QC, formatting) will be included in the metadata.

The use of title and keywords will optimize the possibility of discovery of the data generated in the EUAqua.org project and the potential re-use of the datasets.

Additionally, detailed bioinformatic pipelines and experimental protocols accompanying the datasets will be shared via GitHub and protocols.io to enable proper scrutiny, evaluation and interoperability.

3.2 Making data Accessible

Data will be made publicly available in a timely manner prior to publication according to the **FAIR** (Findable, Accessible, Interoperable, Reproducible) data principles and managed in compliance with the EU Charter and Code for Researchers (DOIs) and include relevant documentation describing the methods used.

3.2.1 Repository:

As mentioned above, the data and appropriate metadata will be shared through trusted repositories such as ENA and Figshare, as well as university, institutions and government-based repositories. Those repositories allow to use DOI for each dataset.

All methods to generate and analyze the data will be provided via GitHub and protocols.io.

Data sharing with collaborators during the project will be done using the available resources from each partner university/research institute such as:
UEDIN local data repository (DataSync) and UniPD Local data repositories (Research Data UniPD, PHAIDRA) that are secured file hosting services.

3.2.2 Data:

Research data and outputs arising from the project will be made as open as possible unless restriction applies for industry data, in a timely manner.

Some data will not be made publicly available for various reasons: proprietary data from company (i.e., individual genotype files D2.1.5, D3.1.3.1), data not usable as is (i.e., Dataset of video recordings (D1.3.1, D3.1.2.1, D3.2.3), annotation files from video footage (D1.3.2, D3.1.2.2), simulated genomic and phenotypic data (D3.1.3.2), personal data about human participants involved in consumers' perception analysis (Do4.2)).

All results will be disseminated to the scientific community via **open access peer-reviewed publications**, as well as **presentations at national and international conferences** and **industry-facing meetings**.

To ensure adherence to the requirement of the **FAIR** data principle, the raw data, metadata and analysis will be made available on open access repositories, identified with a DOI and publications will include information on how to access the supporting data.

Proprietary data: The data providers (collaborators) will be acknowledged and we will follow the terms and conditions under which the data will be accessed as well as published, unless restriction applies regarding ownership of the proprietary data from industrial partners. No personal or sensitive data will be generated in the project. Company data (collaborators) may be made available upon reasonable request to identified company member.

Ownership of the data generated from the research funded by this project resides with the researchers or their institutions.

The Data Management Board (DMB) will be responsible for monitoring potential exploitable research output and, as a consequence, identifying and handling IPR underlying promising innovations in the field of aquaculture. In case of datasets with significant commercial value or product development potential an embargo period may be applied. For this reason, the

DMB works in close collaboration with the Technology Transfer Offices of the involved beneficiaries in IP measures. This will be done in a timely manner.

3.2.3 Metadata:

Metadata conforms to Dublin Core standards will be used to describe and link all datasets, they will be written in formal accessible language, and saved in commonly used format

All data sets will be accompanied by metadata that is compliant with community approved standards, including but not limited to the 15 Dublin Core Metadata Element Set to ensure maximum usability by others.

The descriptive metadata will include relevant information such as: unique DOI, title, abstract, keyword, authors and affiliations, project acronym (EUAqua.org), project GA number (101181589), Call identifier (HORIZON--CL6-2024-BIODIV-01), research asset type, research asset ID and publication date (in ISO 8601 format, YYYY-MM-DD).

If relevant, a ReadMe sheet describing the transformations made on raw data (software used for first step analysis as mapping, blast, SNP calling, QC, formatting) will be included in the metadata.

All data will be re-usable under the Creative Commons Open-Access CC-BY Licence, and available indefinitely as ENA, government or institute funded database and Figshare are unlikely to stop their services any time soon.

3.3 Making data Interoperable

Data will be collected and managed in compliance with the requirements of the Joint Funders Code of Practice for Research. Standard Operating Procedures, Data Management policy, local Policy documents and Best Practice will be used to gather data and ensure that the design, execution and outputs of experiments are accurately captured and documented.

This will be coordinated closely with the UEDIN dedicated Quality Management department and UNIPD International Research Office.

EUAqua.org will adopt universal, cross-platform, with open standards and open-source format that can be recapitulated in:

Text: Microsoft World XLM (.docs); OpenDocument Text (.fodt. .odt); Microsoft Powerpoint XLM (.pptx); OpenDocument Presentation (.fodp, .odp); Plain Text (.txt, .asc)

Tabular: Microsoft Excel XLM (.xlsx); OpenDocument Spreadsheet (.fods, .ods); Comma-separated valutes (.csv); Tab-separated values (.tsv, .tab)

Image/graphics: JEG2000 (.jpxml, .jp3d, .jpf, .jpm, .jpx, .jp2) coco

Video: MPEG-4 (.m4v, .m4r, .m4b, .m4p, .m4a, .mp4); AVi

Genetic/genomic format: .fasta, .bam, .vcf

See Table 2 Data type and availability summary table for details.

The specific vocabulary used will be detailed in documentations available in the EUAqua.org website and in the metadata following FAIRsharing.org recommendations: FAIRsharing | Home

All datasets will be accompanied by metadata complying with the Dublin Core Metadata Element set. Additionally, all the functional annotation data used in WP1 and WP3 will be accompanied by the Ensembl and Functional Annotation of Animal Genomes (FAANG) metadata sheets available in https://data.faang.org/validation/samples, which contains 39 biological sample-specific fields that capture all necessary information.

The specific vocabulary used is further detailed in https://dcc-documentation.readthedocs.io/en/latest/sample/biosamples_template/

3.4 Increasing data re-use

As mentioned above, the descriptive metadata will include relevant information such as: unique DOI, title, abstract, keyword, authors and affiliations, project acronym (EUAqua.org), project GA number (101181589), Call identifier (HORIZON--CL6-2024-BIODIV-01), research asset type, research asset ID and publication date (in ISO 8601 format, YYYY-MM-DD).

If relevant, a ReadMe sheet describing the transformations made on raw data (software used for first step analysis such as mapping, blast, SNP calling, QC, formatting) will be included in the metadata.

All data will be re-usable under the Creative Commons Open-Access CC-BY Licence, and available indefinitely as ENA and Figshare are unlikely to stop their services any time soon.

The data is not expected to lead to patentable intellectual property, but if it did, it would be dealt in line with the institutional recommendation.

4. Other research outputs

EUAqua.org comprises 25 deliverables across all WPs, including documents, reports, data, and other outputs, all of which are publicly accessible. Key deliverables and milestones will contribute to the aquaculture research community. Scripts used to manipulate, transform and analyze the data will be made publicly available on **GitHub** repositories and cited in the relevant publications, ensuring reproducibility of the science. Protocols will be made available on **protocol.io.**

5. Allocation of resources

The overall costs for data management during the project life cycle are expected to be limited to Personnel Costs of the Data Management Board. This cost will be covered by the EUAqua.org project.

Open access and long-term data preservation are secured at no-cost due to the use of appropriate publicly available repositories.

Data will be stored on a centralized, backed-up file storage system managed by institutional IT departments. Access is monitored and controlled via a secure log in system following the best practices in terms of identity management.

6. Data security

Data storage: All the data generated by the project will be stored on resilient networked University storages.

All repositories (see Table 2 Data type and availability summary table) have standard security protocol (login, user access tokens) are stored encrypted. Raw data (stored in institutional repositories) are locked and access is restricted to internal users.

7. Ethics

WP1, WP2 and WP3 will involve the use of animal models (i.e., rainbow trout, Atlantic salmon, sea bass and seabream). The partners involved will submit all the protocols and documents to their relevant Animal Welfare Board in compliance with the EU Regulation 63/2010 and national regulations. No experiments on animals will be conducted until the receiving of ethics approval.

WP4 will engage human participants for the analysis of consumers' perception using a Virtual Reality Settings to develop immersive and controlled virtual environments, such as virtual supermarkets, virtual restaurants, or virtual canteens. The choice experiments will involve selected groups of at least 150 consumers in at least three EU countries representative of 3 EU regions.

All the experimental procedures involving human participants will be reviewed by the Ethics Committee of the University of Bologna. No experiments on human participants will be conducted until the receiving of ethics approval.

Participants will be provided with an informed consent form. Only person that will sign the consent form will be involved in the study. Privacy sheet and consent for collection and processing of personal data will be also collected. No special categories of personal data will be collected.

Here is a summary of research activities raising ethical concerns and how to manage them.

HUMANS

Partner	Staff involved	WP, Task	Approval
UNIBO	Matteo Vittuari Matteo Masotti	T4.2	Pending: expected date July 2026

Declaration: All the experimental procedures involving human participants will be reviewed by the Ethics Committe of the University of Bologna. Protocol and documents will be submitted to the relevant ethic committee in June 2026 and the reply is expected by one month.
The analysis of consumers' perception will be conducted using a Virtual Reality Settings to develop immersive and controlled virtual environments, such as virtual supermarkets, virtual restaurants, or virtual canteens. The choice experiments will involve selected groups of at least 150 consumers in at least three EU countries representative of 3 EU regions.
Participants will be provided with an informed consent form. Only person that will sign the consent form will be involved in the study. Privacy sheet and consent for collection and processing of personal data will be also collected. No special categories of personal data will be collected.
No experiments on human participants will be conducted until the receiving of ethics approval

ANIMALS

Partner	Staff involved	WP, Task	Approval
INRAE	Delphine Lallias	WP1, Task 1.4	Available

Declaration: The protocols about animal experiments were evaluated and approved by the ethical committee CEFEA No 74 and authorized by the French Ministry of Higher Education and Research (APAFIS #51268-2024092715237651 v6). The letter authorising the project was dated the 8th of January 2025.

Partner	Staff involved	WP, Task	Approval
USTIR	Monica Betancor	WP2, Task 2.1	Pending: expected date end of April 2025

Declaration: All experimental procedures will be conducted in compliance with the Animals Scientific Procedures Act 1986 (Home Office Code of Practice. HMSO: London January 1997) under appropriate project and personal licences. Dr Betancor is a personal license holder and also holds project license PP2447791.
In addition, all experimentation must be approved by the Animal Welfare and Ethical Review Board (AWERB). It has been planned to submit the protocol to AWERB at the end of February 2025. The approval release takes approximately 1-2 months.
No experiments on animals will be conducted until the receiving of ethics approval.

Partner	Staff involved	WP, Task	Approval
UNIBO	Luca Parma	WP2, Task 2.2	Pending: expected date end of May 2025

Declaration: All experimental procedures will be reviewed and approved by the Ethical-Scientific Committee for Animal Experimentation of the University of Bologna.
UNIBO plans to submit the protocol in February 2025 and expect to receive authorization within approximately 2/3 months.
No experiments on animals will be conducted until the receiving of ethics approval.

Partner	Staff involved	WP, Task	Approval
IRTA	Dolors Furones	WP3, Task 3.1	Pending: expected date July-October 2025

Declaration: To get ethics approval for conducting experiments on animal model IRTA has 2-step process: internal IRTA committees make a first evaluation and when approved the documentation is submitted to the relevant Government office for final evaluation.
In details the 2-step process will involve 2 different committees:

- Committees for animal experimentation: The Ethical Committee of IRTA (first step)

- The Ethical Committee of the Generalitat of Catalunya, Direcció General de Polítiques Ambientals i Medi Natural (Catalan regional governament) (second step)

The PI in charge for task 3.1 is in the process of filling in the documentation which will submitted for evaluation during March 2025. From experience the evaluation process takes about 6 months and we expect a reply during the period July – October 2025.
Legislation applied: Directive 2010/63/EU and the Spanish regulations (law 1078 32/2007 and Royal Decree 1201/2015)
No experiments on animals will be conducted until the receiving of ethics approval.

Partner	Staff involved	WP, Task	Approval
CIIMAR	Sergio Boo	WP3, Task 3.2	Pending: expected date July 2025

Declaration: CIIMAR, has dedicated animal facilities certified by "Direção Geral de Alimentação e Veterinária (DGAV)" issued under Article 21°, of Decrete-Law Nº 113/2013 of 7th August.
All experimentation performed at these facilities are subjected to an ethical review process by each Ethical Committee along with the institution Animal Welfare Body (ORBEA) in compliance with the European Directive 2010/63/EU and its transposition to the Portuguese law. A "Laboratory Animal Sciences" (LAS) Education and/or a DGAV certification is mandatory for researchers to perform animal experimentation if involving vertebrate and cephalopod species.
No experiments on animals will be conducted until the receiving of ethics approval.

ENVIRONMENT, HEALTH AND SAFETY

Partner	Staff involved	WP, Task	Approval
IRTA	Dolors Furones	WP3, Task 3.1	Pending: expected date July-October 2025

Declaration: All the experimental procedures about the use of GMO *Vibrio anguillarum* will be reviewed by the relevant authorities, following a 2-step procedures: internal IRTA committees make a first evaluation (IRTA Biosafety Committee; first step) and when approved the documentation is submitted to the relevant Government office for final evaluation (The National Biosafety Commission, Comisión Nacional de Bioseguridad – CNB, Ministerio para la Transición Ecológica y el Reto Demográfico, Madrid; second step)
No experiments involving the use of GM bacteria will be conducted until the receiving of ethics approval

References

Relevant institutional, departmental or study policies on data sharing and data security

Policy	URL or reference
Data Management Policy & Procedures	http://www.ed.ac.uk/information-services/about/policies-and-regulations/research-data-policy https://www.unipd.it/sites/unipd.it/files/2018/policy%20dati%20ricerca.pdf https://www.unipd.it/sites/unipd.it/files/2023/CodiceIntegrita%CC%80Ricerca_ITA.pdf
Data Security Policy	https://www.ed.ac.uk/information-services/about/policies-and-regulations/security-policies

Data Sharing Policy	https://www.ed.ac.uk/data-protection/data-protection-policy
Institutional Information Policy (UEDIN) *Local Policies not available online but can be made available on request	**RI-POL-003** Internal data management policy, **RI-SOP-001** Internal SOP on Issue and use of Scientific Notebooks **RI-POL-008** Internal policy on manipulation of Images in Scientific Research **EB-POL-004** Internal policy on training

HISTORY OF CHANGES		
Version	**Publication date**	**Change**
1.0	30/06/2025	First version

Funded by the European Union