Reconstructing the Holy Loch Ecosystem: The Holy Loch Food Web Project
A foundational framework for a long-term ecosystem census integrating barcoding, environmental DNA, classical taxonomy, and niche architecture.

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1. Abstract

The Holy Loch Food Web Project has the single aim of clarifying all of the definable taxa and their associated ecological niches in our entire ecosystem comprising sea loch, saltmarsh, temperate rainforest, vegetated shingle, carr woodland and freshwater swamp. Although a simple idea, in reality, there are huge numbers of hurdles to get there. This note founds the whole project which will comprise, probably, hundreds of checklists from fungal, plant and animal taxa, updated as results from ongoing DNA barcoding via UK BIOSCAN led by the Wellcome Sanger Centre, eDNA metabarcoding and updated taxonomic understanding continue to clarify my simple species inventory. The project has no obvious end point. At the time of writing on 30th December 2025, the total number of eukaryote species listed at the Holy Loch exceeds 3000, and that is before we embark on eDNA techniques for soil fungi and large, unexplored taxa such as Nematoda. I expect the number of species to increase significantly in future.

2. Introduction

Understanding how many taxa occupy a landscape is a central challenge in ecology. Biodiversity underpins ecosystem stability and services including carbon storage,

nutrient cycling, water purification, and pollination. Without a reliable inventory, conservation planning becomes speculative and vulnerable to bias. Globally, around two million species have been formally described, yet estimates suggest as many as 8.7 million may exist (Mora et al., 2011; Chapman, 2009). Cryptic species—organisms that appear identical but are genetically distinct—further widen this gap (Bickford et al., 2007). These challenges are acute in groups such as Diptera and fungi, where undescribed diversity is common.

The Holy Loch, a tidal sea loch in western Scotland, represents an instructive test-case due to its combination of temperate rainforest remnants, carr woodland, saltmarsh, post-industrial shoreline, and pelagic and benthic marine environments. Historical biological knowledge of the area has been fragmented, shaped by recorder expertise and taxonomic scope rather than ecological completeness. The establishment of a high-resolution, continuous species inventory is therefore a vital management necessity for the Holy Loch Nature Reserve (HLNR), providing the essential ecological baseline required to measure the impact of external threats, particularly climate-driven sea-level rise, and inform effective conservation strategies.

3. Project Rationale

A meaningful biodiversity census of the Holy Loch must accommodate multiple detection systems, taxonomic instability [where names change and Biological Index Numbers (BINs; Ratnasingham & Hebert, 2007) derived from DNA barcoding appear before species], and continuous data flux. For this reason, the project adopts a dynamic inventory philosophy: identifications are accurate to the moment of publication but expected to change.

3.1 Curiosity-Driven Science

Beyond the management necessities, the Holy Loch Food Web Project is fundamentally rooted in curiosity-driven science. It is driven by a personal interest in the sheer scale of the challenge and a desire to see what an exhaustive, integrated inventory reveals about the hidden complexities of a single location. This "bottom-up" exploration seeks to answer fundamental questions about ecosystem composition that only emerge when one commits to the long-term task of identifying every definable taxon.

3.2 Integration of Niche Architecture

Central to this project is the integration of niche architecture. By documenting trophic levels, larval requirements, and functional roles alongside taxonomic names, the project reconstructs the functional reality of the landscape. To ensure this reconstruction is scientifically rigorous, every record in the Holy Loch inventory incorporates three critical metrics:

Abundance:
Tracking the number of individuals per sample to identify dominant vs. rare species.

Trapping Dates & Phenology:
Recording specific capture dates and activity windows to understand seasonal interactions and climate synchrony.

Habitat Specificity:
Documenting the exact micro-habitat where the specimen was caught (e.g., saltmarsh, shingle ridge, or regenerated carr woodland).

3.3 Longitudinal Stability

Crucially, unlike research programmes constrained by short-term funding cycles, this project is structured to continue indefinitely. Its continuity is not dependent on grant renewal, allowing consistent methodology, stable data acquisition, and long-term ecological insight that funded snapshots often fail to capture. The integration of classical morphospecies identifications with DNA barcoding and environmental DNA (eDNA) metabarcoding (Barnes & Turner, 2016) demands continual cross-referencing as reference libraries expand and taxonomic concepts shift (Keck et al., 2023).

The rigidity of traditional paper publishing is fundamentally incompatible with this dynamic model. Conversely, electronic publication allows for modular, versioned data releases. To formalise this system, all project data is referenced through a continuously updated index file, serving as the single, authoritative point of reference for all current species concepts, BIN assignments, and data release versions. The

project's technical standards are anchored by two foundational deposits: the taxonomic confidence criteria (Table 1; Hammatt, 2025a) and the generic DNA-barcoding and assignment protocols (Hammatt, 2025b).

4. General methodology

For morphospecies identifications, I use printed guide books with or without diagnostic keys, web-based keys, apps such as ObsIdentify, experts via Facebook pages, sending vouchers in the post to known experts.

For DNA barcoding-derived identifications, I follow protocols for the UK BIOSCAN project led by the Wellcome Sanger Centre, in 2024 and 2025, at two locations. The generic protocol is archived on Zenodo (Hammatt, 2025b; doi: 10.5281/zenodo.18094544).

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Library Construction: https://www.protocols.io/view/high-throughput-dna-barcoding-library-construction-8epv5jzxdl1b/v1