



Candwr Solar Farm

Pre Application Consultation

Environmental Statement

Appendix 6.6 Clavarioids, Hygrocybe, Entoloma, Geoglossum and Dermoloma (CHEGD) Fungi Survey Report

2 July 2026



Candwr Solar Farm

Appendix 6.6: CHEGD Fungi Survey Report



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1 INTRODUCTION

1.1 Background

- 1.1.1 Avian Ecology Limited (AEL) was commissioned by Pegasus Planning Group to undertake CHEGD¹ fungi surveys in relation to a proposed solar development (the 'Proposed Development') located within land north of Ponthir, Monmouthshire (hereafter referred to as the 'Site').
- 1.1.2 The purpose of this report is to present the methodology and results of the CHEGD fungi surveys undertaken to establish the baseline conditions with regards to CHEGD fungi at the Site.
- 1.1.3 The objectives of this report are to:
- identify the CHEGD fungi on the Site, or within 2 km of the Site; and,
 - establish the spatial distribution of CHEGD fungi.

1.2 Site description

- 1.2.1 The Site is dominated by cattle and sheep grazed pasture within a rolling pastoral farmland landscape. Pockets of broadleaved woodland are connected via hawthorn dominated hedgerows. Within the wider surrounding landscape, habitats include further agricultural fields and pockets of woodland. The Afon Lwyd flows between the pockets of land located within the Site, before flowing into the River Usk.

2 METHODOLOGY

2.1 Zone of Influence

- 2.1.1 The current guidance on ecological impact assessments (EclA) (CIEEM, 2024)² recommends that all ecological features that occur within a 'zone of influence' (Zol) for a proposed development are investigated. The Zol encompasses:
- Areas directly within the land take for the Proposed Development and access.
 - Areas which will be temporarily affected during construction.
 - Areas likely to be impacted by hydrological disruption.

¹ CHEGD is an initialism that represents five groups of fungi associated with unimproved and semi-improved grasslands. These groups are: **Clavarioids** (spindles, club and coral fungi), **Hygrocybe** (waxcaps), **Entoloma** (pinkgills), **Geoglossoids** (earthtongues and relatives) and **Dermoloma** (crazed caps and relatives).

² Chartered Institute of Ecology and Environmental Management. 2024. Guidelines for ecological impact assessment in the UK and Ireland. Terrestrial, freshwater, coastal and marine, version 1.3. Available online: <https://cieem.net/wp-content/uploads/2018/08/EclA-Guidelines-v1.3-Sept-2024.pdf>.

- Areas where there is a risk of pollution or physical disturbance during construction and/or operation.

2.1.2 The ZOI is variable depending on the ecological receptors affected. The size of study areas is determined by considering the potential ZOI for each receptor. **Table 2.1** summaries the study area used for ecological receptors relating to CHEGD fungi.

Table 2.1. Study area.

Ecological receptor	Study area
Sites designated for nature conservation with fungal qualifying interest and/or reasons for designations	The Site and within 2 km of the Site.
Desk study records	Within 2 km of the Site boundary.
CHEGD eDNA	Within the Site
Fruiting bodies walkover	Within the Site

2.2 Desk study

2.2.1 A desk study was undertaken in December 2025 in accordance with current guidelines for Preliminary Ecological Appraisal (CIEEM, 2017)³ to determine the presence of any designated nature conservation sites for CHEGD fungi, information on CHEGD priority species, and records of CHEGD fungi within the ZOI of the Site.

2.2.2 Information was obtained from the following sources:

- DataMap Wales;
- local council websites (Newport);
- local and regional Nature Recovery Action Plans (Monmouthshire, Torfaen);
- Multi-Agency Geographic Information for the Countryside (MAGIC);
- South-East Wales Biodiversity Centre (SEWBC);
- Wales Biodiversity Partnership.

2.2.3 Species records of CHEGD fungi were obtained from the SEWBC database. All records were considered, regardless of date, although particular interest was given to the most recent records.

³ Chartered Institute of Ecology and Environmental Management. 2017. Guidelines for preliminary ecological appraisal, second edition. Available online: <https://cieem.net/wp-content/uploads/2018/01/Guidelines-for-Preliminary-Ecological-Appraisal-Jan2018-typo-edit.pdf>.

2.3 Field surveys

- 2.3.1 During pre-application email correspondence with Ecology Officers at Torfaen County Borough Council (TCBC) it was advised that *'Although Llanfrechfa Grange SINC site is not within the proposed development boundary it is relatively close by. This SINC was in the past identified as being a site with excellent habitat for notable fungi species. Therefore, given the relatively close proximity, I would recommend that any future ecological assessments include surveys for fungi in addition to the baseline data.'*
- 2.3.2 This pre-application discussion informed the requirement for the CHEGD fungi surveys undertaken. An outline of the methodology detailed below, was presented to Ecology Officers at TCBC, Monmouthshire County Council and Newport City Council and in which the approach was agreed by TCBC Ecology Officers, by email on 29th July 2025.

eDNA

Survey design

- 2.3.3 The eDNA survey was designed by specialists at Nature Metrics Ltd.

Soil sample collection

- 2.3.4 The study area was categorised according to CHEGD habitat suitability⁴. Habitat suitability was sorted into five CHEGD suitability classes (very low suitability, low suitability, medium suitability, high suitability and very high suitability), and the area of each class was calculated. 22 sampling locations were then allocated spatially evenly within each suitability class (but see 'Limitations' below). Any locations on tracks or paths were moved to adjacent less disturbed soil within same habitat suitability patch. Soil sampling locations are shown in **Figure 1**.
- 2.3.5 Soil sample collection was conducted on 6 – 9th October 2025 by personnel from Avian Ecology. At each sampling location, a 10x10m quadrat was demarcated and four (10 ml) subsamples were collected, one at each corner of the quadrat. Subsamples were collected with a corer and placed into a sample pot. Once all four subsamples were collected the sample pot was filled with 50ml of ribonucleic acid (RNA) preservation buffer and the pot was shaken to mix the subsamples and preservation buffer.

Laboratory analysis

- 2.3.6 Laboratory analysis was undertaken by specialists at Nature Metrics using the following methodology:
- After removal of the RNA preservation buffer, soils were rinsed with 10X phosphate buffered saline (PBS), homogenised, and DNA was extracted from approximately 0.5g of the resulting homogenate using a DNeasy PowerSoil Pro Kit (Qiagen) according to the manufacturer's protocol. A negative control was processed with each batch of samples to monitor for

⁴ Nature Metrics utilised their in-house CHEGD habitat suitability model, based on remote sensing data and approximately 2000 soil eDNA samples across the UK.

exogenous DNA contamination. Extraction yields were checked by measuring deoxyribonucleic acid (DNA) concentration using a Qubit fluorometer with the Qubit dsDNA broad range assay kit (Thermo Fisher Scientific).

- Replicate polymerase chain reactions (PCRs) for each sample and extraction blank were amplified via a two-step PCR process, with tails added to the 5' end of taxon specific primers to complement downstream adapter and index primer sequences. Amplification was performed with a commercially available Hot Start DNA polymerase following manufacturers guidelines using the ITS3 5'- GCATCGATGAAGAACGCAGC-3' and ITS4 5'- TCCTCCGCTTATTGATATGC-3' primers targeting the Internal transcribed spacer 2 (ITS2) gene for the target taxa. Indexed PCR products were subsequently purified, quantified, normalised, and pooled in equal volumes. The final pooled library was sequenced on an Illumina MiSeq system using a V3 600 cycle reagent kit (Illumina).

Fruiting Bodies Walkover

- 2.3.7 A walkover by conducted by personnel from Avian Ecology, at the same time as the soil sample collection, on 6 – 9th October 2025. Any fungal fruiting bodies that were encountered within the Survey Area when walking between the soil sampling locations were photographed and the locations recorded.
- 2.3.8 The photographs taken in the field were then assessed by Avian personnel using field guides (Plantlife Cymru, 2024⁵; Wood & Dunkelman, 2025⁶). Those with physical characteristics of CHEGD fungi were included in the reporting. Suggestions as to likely species identity were given where possible.

2.4 Limitations

- 2.4.1 Upon completion of the eDNA sampling undertaken and reported within this baseline report the Site boundary was amended to include additional land for a substation and haul road. This additional land is comparable in nature to the habitats within the wider Site and surveyed during the baseline data collection and therefore, the change to the Site boundary is not deemed to be a significant constraint or likely to result in significant changes to species distribution and/or assemblage.
- 2.4.2 Biological records obtained from third parties and presented in this desk study do not represent a full and complete species list for the area. They are mostly provided by individuals on an ad-hoc basis, meaning while they give a good representation there may be errors or deficiencies in the data.
- 2.4.3 During the soil sample collection, some sampling locations had to be moved from the points selected in the survey design due to the presence of livestock. In these cases, the samples were taken from the

⁵ Plantlife Cymru. 2024. Waxcaps and Grassland Fungi: A guide to identification and management. Plantlife, Salisbury. Available online: <https://www.plantlife.org.uk/wp-content/uploads/2024/08/Plantlife-Wales-Waxcap-ID-guide-2024-WEB.pdf>.

⁶ Wood, E. Dunkelman, J. 2025. Grassland Fungi: a field guide 3rd ed. Monmouthshire Meadows Group. Monmouth.

same field but in an area away from the livestock. Grid references for these locations were updated accordingly.

- 2.4.4 eDNA analysis was able to identify a certain number of OTUs⁷ associated with CHEGD fungi, however the majority of OTUs could not be assigned to a named species. Information from Nature Metrics states that 'there are multiple reasons that an OTU is not assigned to a species, including that the species is not in the reference databases or there could be multiple species in the databases with very similar DNA barcode'.
- 2.4.5 Identification of fruiting bodies to species using photographs must be considered as a 'best guess'. Confirmation of species identity requires more detailed investigation of physical features of the specimen, by a mycologist, in the field.

3 RESULTS

3.1 Desk study

Designated sites

- 3.1.1 There are no statutory designated sites located within study area that are designated specifically for fungi.
- 3.1.2 In review of MAGIC, Datamap Wales and SEWBRC, the survey area contains one non-statutory designated site with fungi listed as a reason for designation. This is shown in **Table 3.1** below.

Table 3.1. Non-Statutory designated sites within 2km of the Site with CHEGD fungi as a reason for designation.

Site	Designation(s)	Distance from Site	Reason for designation
Llanfrechfa Grange	SINC	0.75 km	Ancient mown grassland, parkland trees, scrub, species-rich hedgerows. The site is mown extensively, and the clippings are taken away. This management contributes to the low fertility of the underlying soil, providing ideal conditions for a wide range of grassland fungi. Many of the trees and most of the habitats on site also provide ideal conditions for fungi.

Biological records

⁷ 'Operational Taxonomic Unit'. A DNA sequence found in a sample. Broadly equivalent to species.

- 3.1.3 The data from SEWBC includes multiple records of CHEGD fungi within the study area, from between 2008 and 2024, although none are from within the Site. The records represent 36 species: six Clavarioids, 19 Hygrocybe, six Entoloma and five Geoglossoids.
- 3.1.4 The most recent records, from 2024, are of seven different species (one Clavarioid, six Hygrocybe):
- White spindles *Clavaria fragilis*
 - Spangle waxcap *Hygrocybe insipida* Glutinous waxcap *Hygrocybe glutinipes* var. *glutinipes*
 - Pink waxcap *Porpolomopsis calyptriformis*
 - Golden waxcap *Hygrocybe chlorophana*
 - Orange waxcap *Hygrocybe aurantiosplendens*
 - White spindles *Clavaria fragilis*
 - Meadow waxcap *Cuphophyllus pratensis* var. *pratensis*.
- 3.1.5 Amongst the historical records are two species listed as priority species on Section 7 of the Environment (Wales) Act 2016. One record is for date waxcap *Hygrocybe spadicea* in 2008, and three records of olive earthtongue *Microglossum olivaceum* agg from between 2008 and 2010. Olive earthtongue is also a priority species in the Monmouthshire Nature Recovery Action Plan.
- 3.1.6 The Torfaen Nature Recovery Action Plan includes waxcaps (Hygrocybe) as protected species which will benefit from grassland restoration. Newport City Council list fungi as priority species in Newport.

3.2 eDNA

- 3.2.1 A summary of the results of the eDNA analysis, relating specifically to CHEGD fungi, is presented in **Annex 1** at the end of this report. The full report from Nature Metrics, relating to all fungal diversity, is presented in **Annex 3**.
- 3.2.2 These results should be read with reference to **Figure 1**.
- 3.2.3 The results of the eDNA analysis indicate that CHEGD fungi are present in soil samples of 18 of the 22 sampling locations. The sampling locations with the highest CHEGD fungal richness (10 OTUs) occur in the southeast of the study area, and are composed of Clavarioid, Hygrocybe and Geoglossoid OTUs. Sampling locations in the northeast of the study area also have relatively high richness of 7 – 8 OTUs. See **Table 3.2**.

Table 3.2. Results of the eDNA analysis: number of CHEGD fungi detected in soil from each sampling location.

Sampling location (Refer to 'S' on Figure 1)	Grid reference	CHEGD fungal richness (number of OTUs)	Number of CHEGD OTUs named at species level	Which CHEGD groups
Point 13	ST3358892528	10	3	CHG
Point 18	ST3392592787	10	2	CG
Point 19	ST3399193887	8	3	CHGD

Point 3	ST3242393596	7	4	CHE
Point 21	ST3409493999	7	1	CHG
Point 22	ST3431193801	7	1	CHD
Point 11	ST3357892924	6	1	CH
Point 12	ST3361293241	6	0	C
Point 5	ST3261493725	5	1	CD
Point 6	ST3284894363	5	1	CD
Point 9	ST3312194551	4	1	CH
Point 16	ST3379393050	4	0	C
Point 20	ST3400593572	4	1	CG
Point 14	ST3364493109	3	0	CHG
Point 15	ST3365692668	3	0	C
Point 2	ST3225694137	1	0	H
Point 4	ST3248793876	1	1	D
Point 17	ST3387893570	1	0	H
Point 1	ST3224394494	0	0	
Point 7	ST3273094056	0	0	
Point 8	ST3295494146	0	0	
Point 10	ST3309893700	0	0	

3.2.4 In total, 37 different OTUs were detected: 26 Clavaroids, five Hygrocybe, one Entoloma, three Geoglossoids and two Dermoloma.

3.2.5 There were 10 detected OTUs which correspond to a named CHEGD species, these are shown in **Table 3.3** below.

Table 3.3. Results of the eDNA analysis: named CHEGD fungi detected in the soil samples.

Species		CHEGD Group	Sampling Locations Where OTU Occurs
Yellow fairy club fungus	<i>Clavaria amoenoides</i> *	Clavarioid	Point 18
Straw club	<i>Clavaria flavipes</i>	Clavarioid	Point 3 Point 9 Point 13 Point 18

White spindles	<i>Clavaria fragilis</i>	Clavarioid	Point 3
Fairy club	<i>Clavaria tenuipes</i>	Clavarioid	Point 11 Point 20
Yellow club	<i>Clavulinopsis helvola</i>	Clavarioid	Point 19
Parrot waxcap	<i>Gliophorus psittacinus</i> *	Hygrocybe	Point 3 Point 13
species of pinkgill	<i>Entoloma velenovskyi</i> *	Entoloma	Point 3
species of earth tongue	<i>Geoglossum barlae</i> *	Geoglossoid	Point 19
species of glutinous earth tongue	<i>Glutinoglossum pseudoglutinosum</i>	Geoglossoid	Point 13 Point 21
Black magic	<i>Dermoloma magicum</i>	Dermoloma	Point 4 Point 5 Point 6 Point 19 Point 22

* There is lower support for this taxonomic identification as it is based on fewer than three matches to sequences in the reference database.

3.3 Fruiting bodies walkover

- 3.3.1 During the walkover, two small clusters of fruiting bodies were identified which have features typical of Hygrocybe fungi. Both of these clusters were located in grazing pasture in the northeast of the survey area, as shown in **Figure 1**.
- 3.3.2 One cluster of fruiting bodies was found next to a hedgerow near to sampling location 22 (ST 34287 93865). These fruiting bodies could not be identified to species but have a flattened cap, with thick irregular and sticky-looking gills, and have emerged in a vague ring. See **Photos 1** and **2** in **Annex 2**.
- 3.3.3 **Photos 3, 4** and **5** show a cluster of small orange fruiting bodies with a distinctive sticky appearance. These are likely to be glutinous waxcap *Hygrocybe glutinipes*. They were located in the field between sampling locations 19 and 20 (ST 33904 93704).

4 CONCLUSION

4.1 eDNA

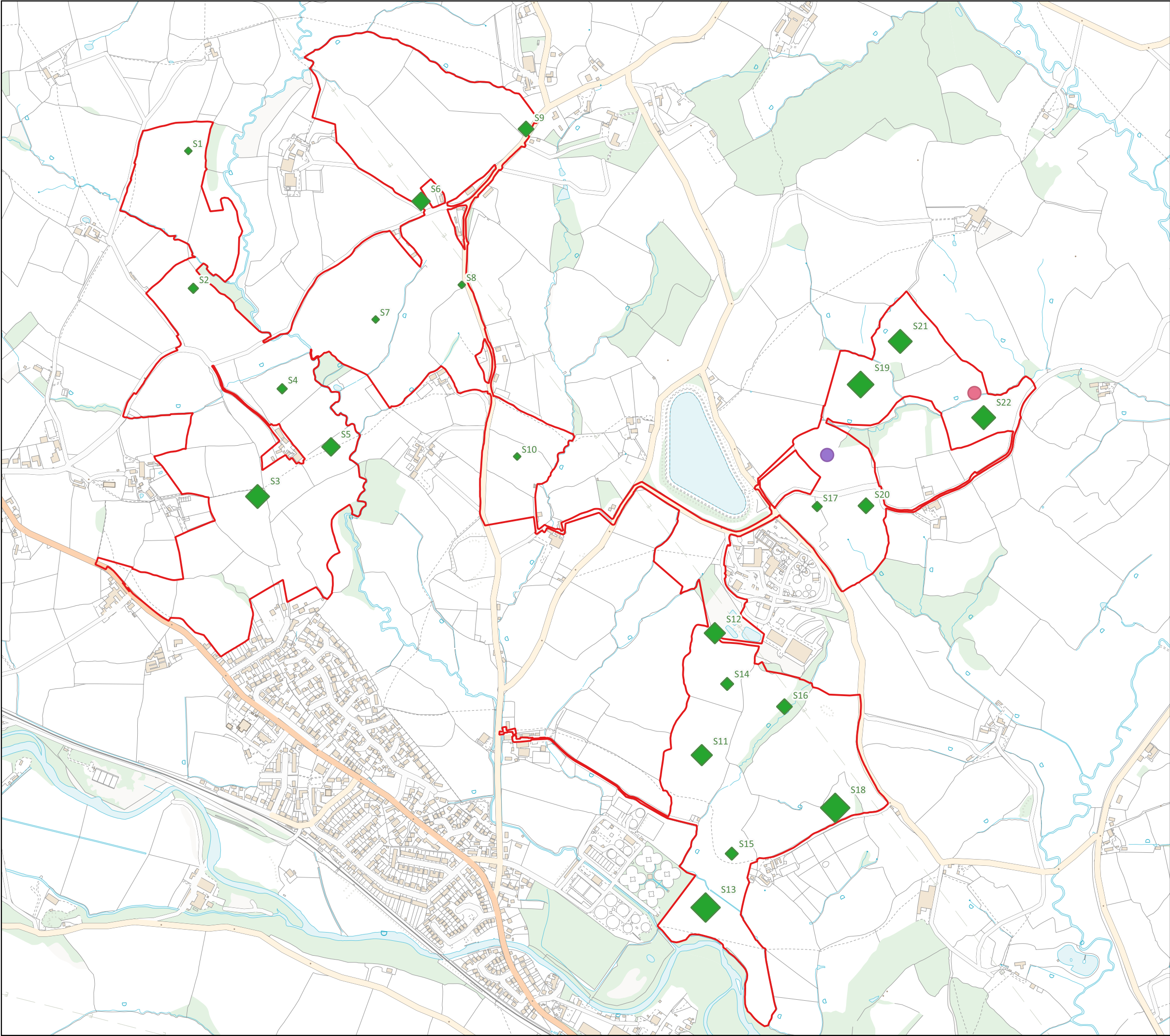
- 4.1.1 Of the named CHEGD species identified within the study area via eDNA sampling (see **Table 3.3**) none are listed on Section 7 of the Environment Act (Wales), on Schedule 8 of the Wildlife and Countryside Act 1981 or on a relevant Nature Recovery Action Plan.

4.2 Fruiting bodies walkover

- 4.2.1 The fruiting bodies walkover identified CHEDG species (*Hygrocybe*). No identified species are listed on Section 7 of the Environment Act (Wales), on Schedule 8 of the Wildlife and Countryside Act 1981 or on a relevant Nature Recovery Action Plan.

Figure 1: CHEGD Fungal Richness and Fruiting Body Locations





Site

CHEGD Fungal Richness (number of OTUs)



Fruiting Body Locations

- Glutinous waxcap *Hygrocybe glutinipes*
- Hygrocybe fungi

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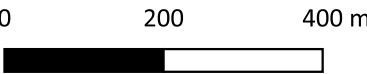
CHEGD Fungal Richness and Fruiting Body Locations

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Co-ordinate System : British National Grid
Projection: Traverse Mercator
Datum: OSGB 1936
Units: Metres



This map contains data from the following sources:

Ordnance Survey (2024)
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1 licence number 010031673.

Annex 1: Laboratory results for CHEGD fungi

Table A1.1: A summary of the results from the eDNA analysis showing all detected CHEGD OTUs. The numeric values under 'Sampling location number' refer to the number of DNA sequences detected per sample.

Family	Genus	Species	CHEGD fungal group	No. samples in which OTU occurs	Sampling location number																						
					1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	
Clavariaceae	<i>Clavaria</i>	<i>Clavaria amoenoides</i>	Clavarioid fungi*	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	29	0	0	0	0	
Clavariaceae	<i>Clavaria</i>	<i>Clavaria flavipes</i>	Clavarioid fungi	4	0	0	25	0	0	0	0	0	410	0	0	0	30	0	0	0	0	4742	0	0	0	0	
Clavariaceae	<i>Clavaria</i>	<i>Clavaria fragilis</i>	Clavarioid fungi	1	0	0	18 24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Clavariaceae	<i>Clavaria</i>	<i>Clavaria tenuipes</i>	Clavarioid fungi	2	0	0	0	0	0	0	0	0	0	0	45	0	0	0	0	0	0	0	0	0	82	0	0
Clavariaceae	<i>Clavulinopsis</i>	<i>Clavulinopsis helvola</i>	Clavarioid fungi	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	587	0	0	0	
Clavariaceae	<i>Clavaria</i>		Clavarioid fungi*	10	0	0	0	0	151	23	0	0	0	0	179	268	91	0	54	0	0	109	0	84	83	92	
Clavariaceae	<i>Clavaria</i>		Clavarioid fungi*	7	0	0	0	0	132	1762	0	0	111	0	0	212	652	0	0	0	0	0	32	0	0	451	
Clavariaceae	<i>Clavaria</i>		Clavarioid fungi*	7	0	0	0	0	29	319	0	0	0	0	91	33	38	0	0	0	0	85	0	0	0	55	

Clavariaceae	<i>Clavaria</i>		Clavarioid fungi	9	0	0	0	0	318	776	0	0	0	0	35	121	0	0	74	32	0	228	0	127	0	113
Clavariaceae	<i>Clavaria</i>		Clavarioid fungi	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	28	0	0	0	0	0	0	
Clavariaceae	<i>Clavaria</i>		Clavarioid fungi*	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	31	0	0	0	0	0	0	
Clavariaceae	<i>Clavaria</i>		Clavarioid fungi*	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82	0	0	0	0	
Clavariaceae	<i>Clavaria</i>		Clavarioid fungi*	1	0	0	0	0	0	0	0	0	0	0	0	0	94	0	0	0	0	0	0	0	0	
Clavariaceae	<i>Clavaria</i>		Clavarioid fungi*	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	34	0	0	0	0	0	
Clavariaceae	<i>Clavulinopsis</i>		Clavarioid fungi	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	322	0	59	0	
Clavariaceae	<i>Clavulinopsis</i>		Clavarioid fungi*	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2014 8	0	
Clavariaceae	<i>Clavulinopsis</i>		Clavarioid fungi	4	0	0	22 9	0	0	0	0	0	0	0	1939 3	9729	0	0	0	0	2439	0	0	0	0	
Clavariaceae	<i>Ramariopsis</i>		Clavarioid fungi	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	153	0	
Clavariaceae	<i>Ramariopsis</i>		Clavarioid fungi	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	235	29	
Clavariaceae	<i>Ramariopsis</i>		Clavarioid fungi*	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	46	0	0	0	0	
Clavariaceae			Clavarioid fungi	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	185	0	0	0	0	0	0	

Clavariaceae			Clavarioid fungi*	1	0	0	0	0	0	0	0	0	0	0	0	0	407	0	0	0	0	0	0	0	0	0
Clavariaceae			Clavarioid fungi*	1	0	0	0	0	0	0	0	0	0	0	0	29	0	0	0	0	0	0	0	0	0	0
Clavariaceae			Clavarioid fungi*	2	0	0	0	0	0	0	0	0	0	0	0	0	19760	0	4517	0	0	0	0	0	0	0
Clavariaceae			Clavarioid fungi	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	280	0	0	0	0
Clavariaceae			Clavarioid fungi*	2	0	0	0	0	0	0	0	0	18	0	0	0	0	46	0	0	0	0	0	0	0	0
Tricholomataceae	<i>Dermoloma</i>	Dermoloma magicum	Dermoloma	5	0	0	0	326	26772	262	0	0	0	0	0	0	0	0	0	0	0	14575	0	0	13220	0
Tricholomataceae	<i>Dermoloma</i>		Dermoloma	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	32	0	0	0	0
Entolomataceae	<i>Entoloma</i>	Entoloma velenovskyi	Entoloma*	1	0	0	27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Geoglossaceae	<i>Geoglossum</i>	Geoglossum barlae	Geoglossoid fungi*	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58	0	0	0	0
Geoglossaceae	<i>Glutinoglossum</i>	Glutinoglossum pseudoglutinosum	Geoglossoid fungi	2	0	0	0	0	0	0	0	0	0	0	0	0	709	0	0	0	0	0	0	0	441	0
Geoglossaceae			Geoglossoid fungi	3	0	0	0	0	0	0	0	0	0	0	0	0	0	170	0	0	0	1712	0	8051	0	0
Hygrophoraceae	<i>Gliophorus</i>	Gliophorus psittacinus	Hygrocybe*	2	0	0	2738	0	0	0	0	0	0	0	0	0	105	0	0	0	0	0	0	0	0	0
Hygrophoraceae	<i>Arrhenia</i>		Hygrocybe	1	0	0	0	0	0	0	0	0	0	0	36	0	0	0	0	0	0	0	0	0	0	0

Hygrophoraceae	<i>Hygrocybe</i>		Hygrocybe*	7	0	0	17 77 6	0	0	0	0	0	4177	0	0	0	355	3954 9	0	0	2056 4	0	0	0	88	1205
Hygrophoraceae	<i>Hygrocybe</i>		Hygrocybe*	1	0	37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
Hygrophoraceae			Hygrocybe	2	0	0	17 73 6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5390	0	0	0

* There is lower support for this taxonomic identification as it is based on fewer than three matches to sequences in the reference database.

Annex 2: Fruiting bodies photographs



Photo 1. Hygrocybe fruiting bodies. Grid reference: ST 34287 93865.



Photo 2. Hygrocybe fruiting bodies. Grid reference: ST 34287 93865.



Photo 3. Glutinous waxcap *Hygrocybe glutinipes*. Grid reference: ST 33904 93704.



Photo 4. Glutinous waxcap *Hygrocybe glutinipes*. Grid reference: ST 33904 93704.

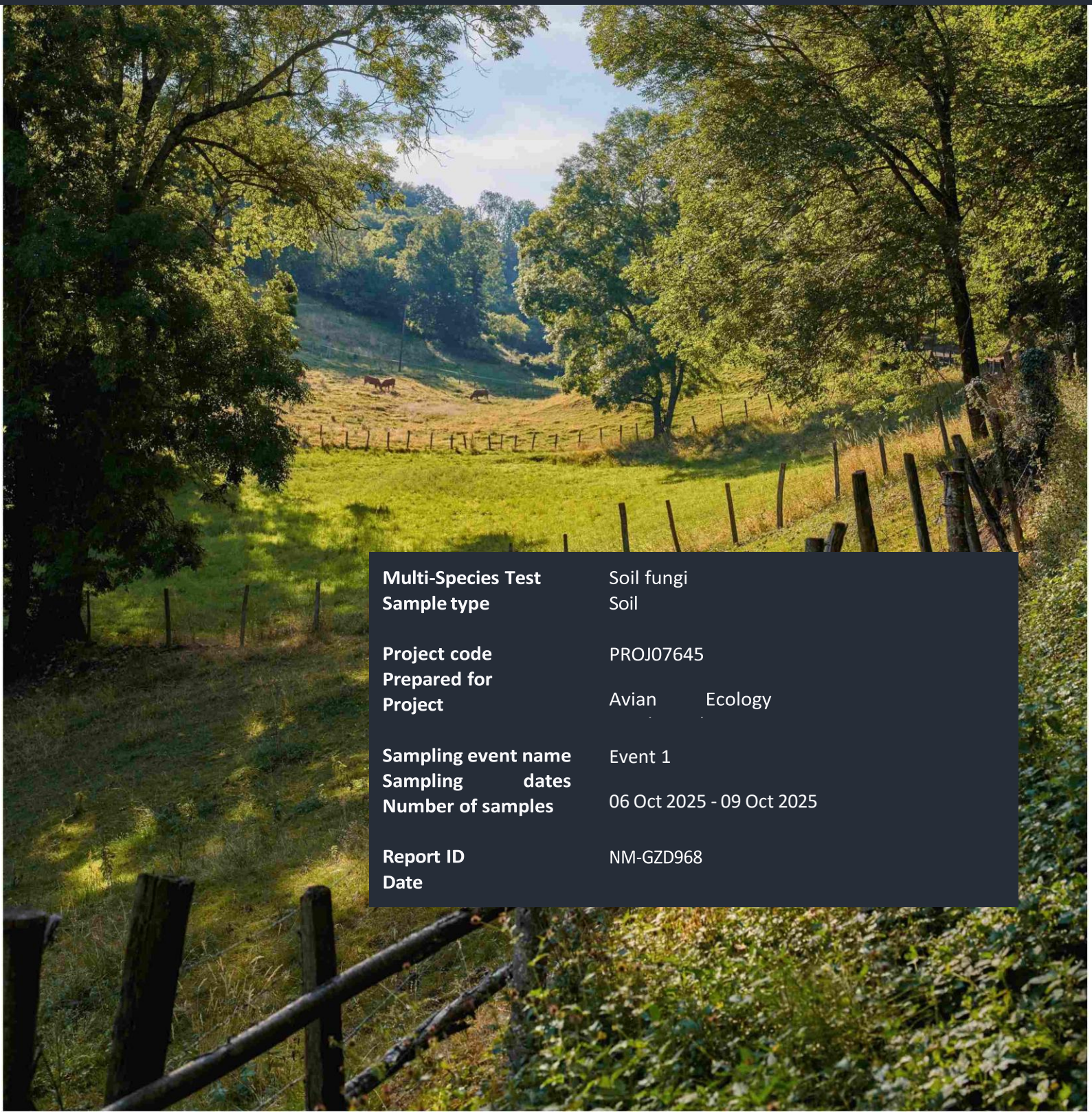


Photo 5. Glutinous waxcap *Hygrocybe glutinipes*. Grid reference: ST 33904 93704.

Annex 3: Nature Metrics report

Environmental DNA Report

Soil fungi



Multi-Species Test
Sample type

Soil fungi
Soil

Project code
Prepared for
Project

PROJ07645
Avian Ecology

Sampling event name
Sampling dates
Number of samples

Event 1
06 Oct 2025 - 09 Oct 2025

Report ID
Date

NM-GZD968



THANK YOU FOR CHOOSING NATUREMETRICS

Your Nature Intelligence Partner

Welcome to your report

Your report consists of:

This document: Providing you with our world class insights and metrics.

Data Tables: Accompanying spreadsheet with results at the individual sample level: species detected, metrics and quality control: NM-GZD968 - PROJ07645 - Soil fungi - Results.xlsx

Data Description

Species Data Table: Percentages

Species Data Table: Read Counts

Metrics by Sample Table

Quality Control Table

If you have purchased metrics and they are not featured in this document, please see the 'Metrics by Sample Table' tab of the Data Tables spreadsheet.

OTU: Throughout the report you'll see reference to 'OTU'. This stands for Operational Taxonomic Unit; an OTU is broadly equivalent to a species in most cases.

EXECUTIVE SUMMARY

Field Samples submitted:	22
Field Samples reported:	22
Field Blanks submitted:	0
Species Richness:	758
Average Species Richness per sample:	135
Total number of CHEGD OTUs:	37
Total number of IUCN Red List Species:	0

Reported samples are those that passed Quality Control and are included in the Species Data Table



Please be careful when sharing this report, it contains biodiversity information that may be sensitive, particularly with respect to endangered or protected species. Please share responsibly. If the report is shared, we kindly ask that the report is shared in its entirety - to limit the possibility of any information being taken out of context.

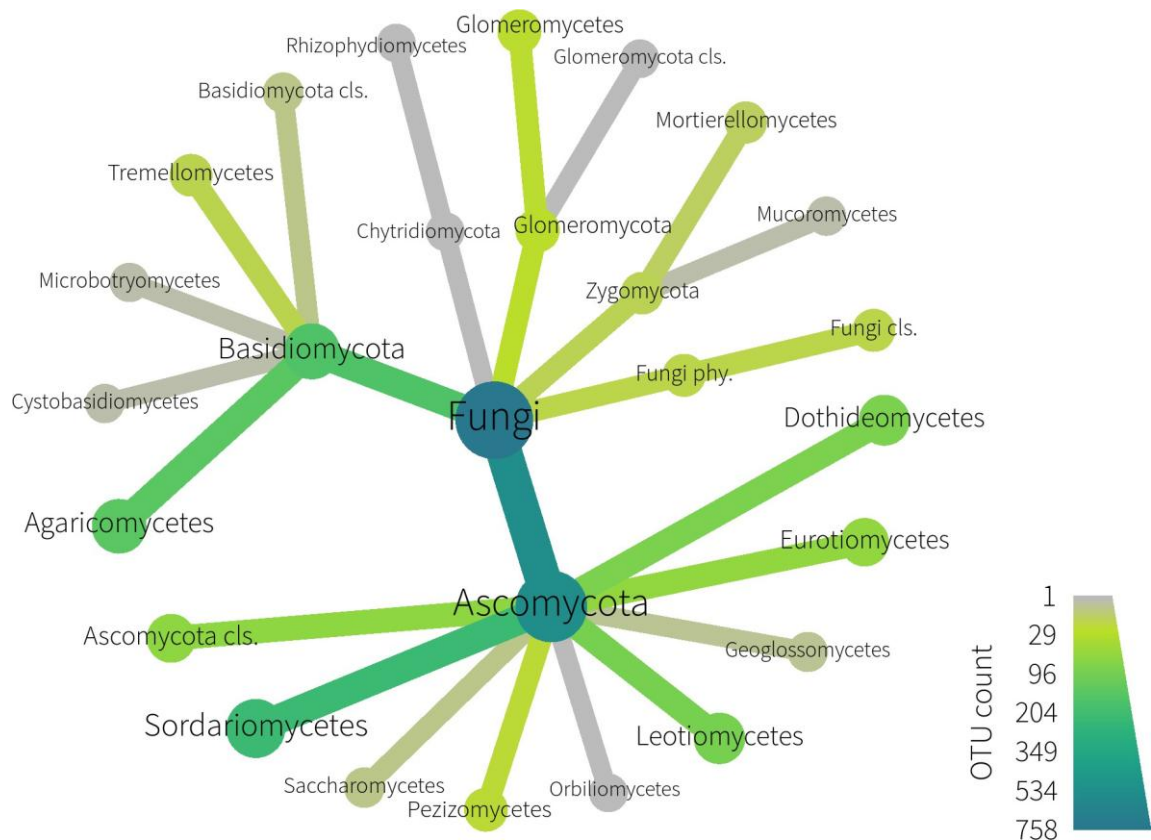
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www.naturemetrics.co.uk/report-interpretation-guide



REPORT

Taxonomic Comparison

This chart provides a view of the species detected in your samples and their taxonomic relationship, (names on the same branch are more similar than those on different branches). The chart is structured with the highest taxonomic rank at the centre (e.g., kingdom, phylum, class), moving through the ranks of order, family, genus, species as you move to the outer edge. Note that the centre and outer ranks will change depending on the [test](#) applied and the number of species detected. The legend in the bottom right of the chart indicates how to relate the colour in the branches to the number of species. The colour scale goes from grey - indicating very few species, to blue - indicating a lot of species.



Taxonomic Resolution

This table provides the number of **OTUs** detected and the percentage of OTUs identified to each taxonomic level.

Depending on completeness of **reference databases** for the region where you sampled, some OTUs may not match to a reference at species level. Global DNA reference databases contain millions of barcodes, but gaps remain, particularly in regions and taxonomic groups that are more diverse and less studied. Coverage is expected to improve over time and data tables can be updated to include new information at a future date.

Number of OTUs	Phylum	Class	Order	Family	Genus	Species
758	98.02%	89.31%	80.87%	63.06%	31.66%	13.46%

Want to increase the number of species named to species level? If you have specimens of species you have identified, we can sequence the DNA and add the species to our reference databases. We will then be able to enhance the reference library and report if the species is detected. Please contact us about this service and we can send you our barcoding kits, but note that we only offer these kits for fish and amphibians.

IUCN Red List Species

These are the IUCN (International Union for Conservation of Nature) Red List species detected in your samples. These are detected species that are designated as one of the IUCN Red List Threatened Categories (Vulnerable, Endangered and Critically Endangered). An increase in the number of threatened species is generally associated with a positive trend in **biodiversity** or habitat condition. The Data Tables may also include designations for non-target species* (species that are not targeted by the selected test, but were detected in your samples). These do not appear in this table and do not contribute to summaries or counts in this report.

No species designated Vulnerable, Endangered or Critically Endangered were detected in the samples.

CHEGD Species

This is a summary of the CHEGD (*Clavariaceae*, *Hygrophoraceae*, *Entolomataceae*, *Geoglossaceae*, and *Dermoloma*) fungi detections. CHEGD fungi are of conservation interest as indicators of grassland soil health; the frequency of their detection is a reliable indicator of grasslands that have not been heavily modified or degraded.

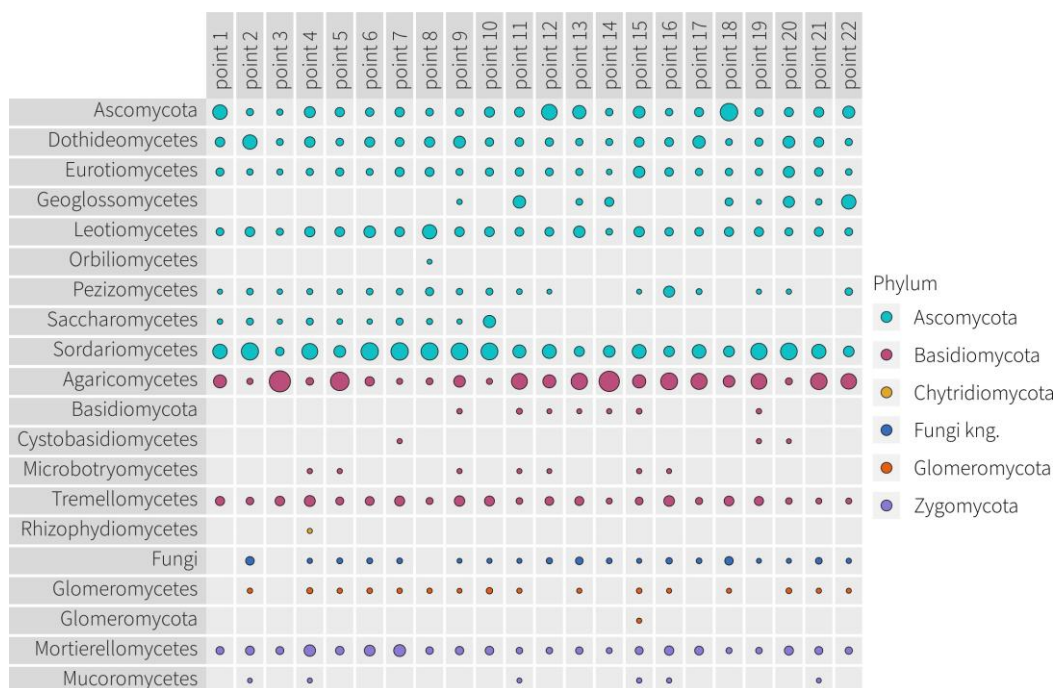
There was a total of 37 CHEGD fungi detected. Of these, 10 were named at species level.

Species	CHEGD Fungal Group	CHEGD Group common name
<i>unclassified Arrhenia</i>	Hygrocybe	Waxcaps
<i>Gliophorus psittacinus</i>	Hygrocybe	Waxcaps
<i>unclassified Hygrocybe</i>	Hygrocybe	Waxcaps
<i>unclassified Hygrophoraceae</i>	Hygrocybe	Waxcaps
<i>Clavaria amoenoides</i>	Clavarioid fungi	Clavarioid fungi fanvaults and meadowcaps
<i>Clavaria flavipes</i>	Clavarioid fungi	Clavarioid fungi fanvaults and meadowcaps
<i>Clavaria fragilis</i>	Clavarioid fungi	Clavarioid fungi fanvaults and meadowcaps
<i>Clavaria tenuipes</i>	Clavarioid fungi	Clavarioid fungi fanvaults and meadowcaps
<i>unclassified Clavaria</i>	Clavarioid fungi	Clavarioid fungi fanvaults and meadowcaps
<i>Clavulinopsis helvola</i>	Clavarioid fungi	Clavarioid fungi fanvaults and meadowcaps
<i>unclassified Clavulinopsis</i>	Clavarioid fungi	Clavarioid fungi fanvaults and meadowcaps
<i>unclassified Ramariopsis</i>	Clavarioid fungi	Clavarioid fungi fanvaults and meadowcaps
<i>unclassified Clavariaceae</i>	Clavarioid fungi	Clavarioid fungi fanvaults and meadowcaps
<i>Entoloma velenovskyi</i>	Entoloma	Pinkgills
<i>Dermoloma magicum</i>	Dermoloma	Crazed caps, fanvaults and meadowcaps
<i>unclassified Dermoloma</i>	Dermoloma	Crazed caps, fanvaults and meadowcaps
<i>Geoglossum barlae</i>	Geoglossoid fungi	Earthtongues
<i>Glutinoglossum pseudoglutinosum</i>	Geoglossoid fungi	Earthtongues
<i>unclassified Geoglossaceae</i>	Geoglossoid fungi	Earthtongues
Number of OTUs		37

Community Composition

This chart lists the species found in each sample. The presence of a bubble means a species was detected in that sample. The chart displays at species level, unless the number of species detected is too great to display clearly in the document. In these cases, the chart displays at a higher taxonomic level. The full species level chart is provided as an appendix.

The size of the bubbles represents the proportion of DNA sequences within a sample. A larger bubble size can indicate a stronger eDNA signal. This signal may be linked to abundance of species in the environment but should be interpreted only as a coarse measure because the signal is also impacted by biological (e.g., biomass, life stage, activity, body condition), environmental (e.g., temperature, pH, salinity, conductivity), and technical factors (e.g., primer bias, PCR stochasticity).





Species Richness

This is the total count of OTUs detected in each sample. The blue portion of each bar indicates the number of OTUs identified to a species.

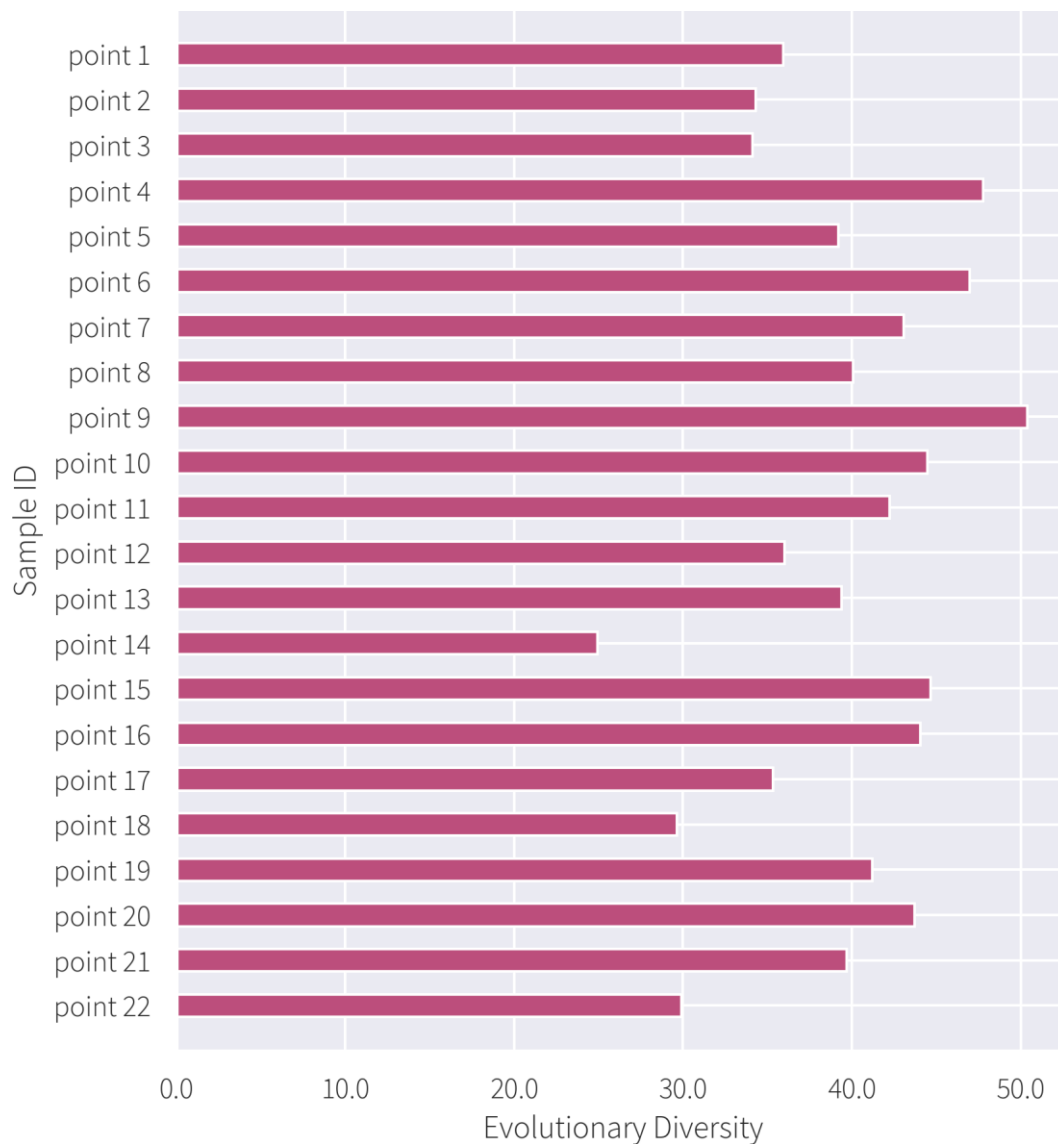


High Species Richness generally indicates a healthier and functioning ecosystem and is the simplest biodiversity metric that is consistently reported in biodiversity monitoring.



Evolutionary Diversity

Evolutionary Diversity calculated for each sample. This is a measure of the variety of species types that occurred in your samples.

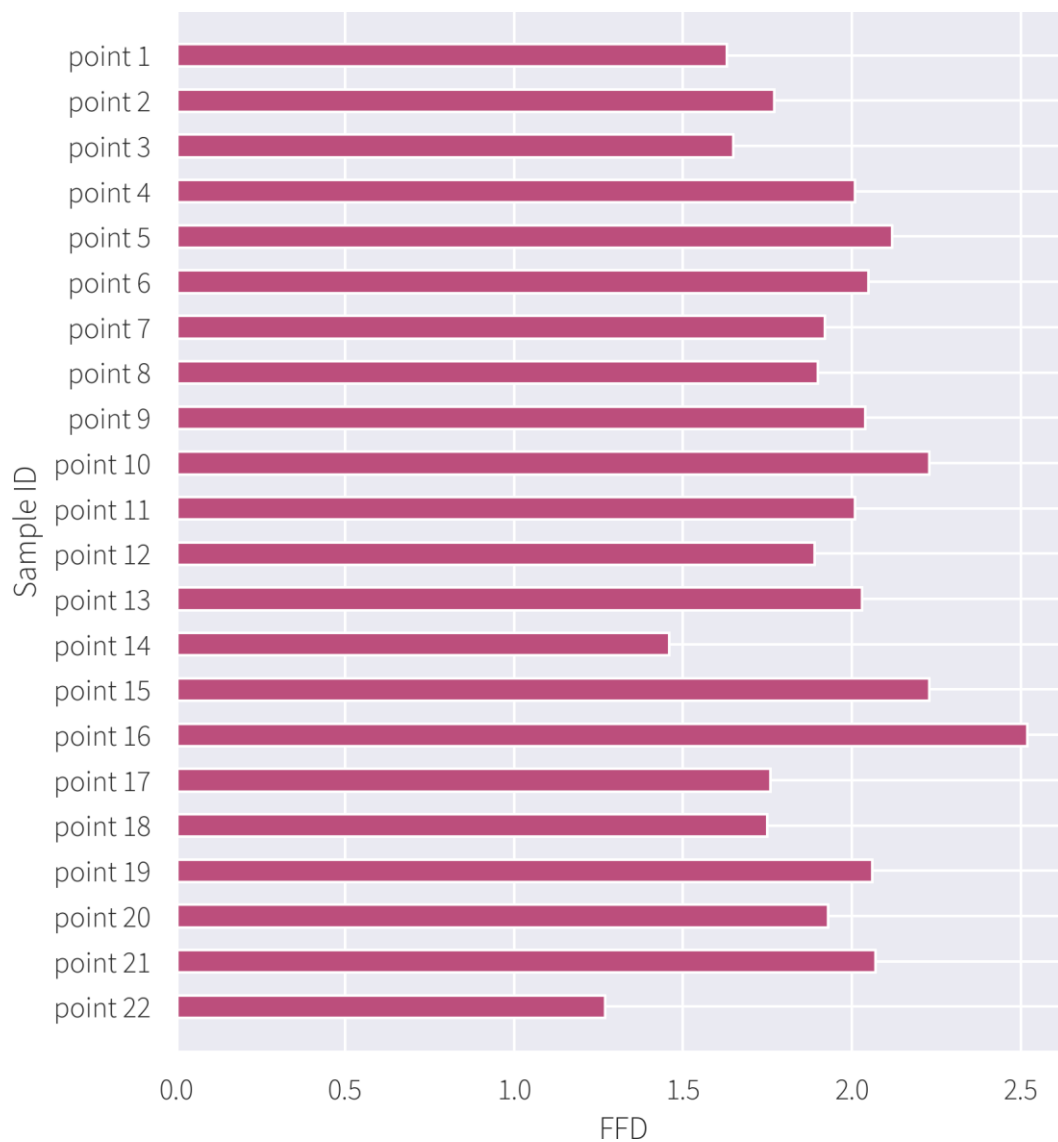


Evolutionary Diversity is a strong complementary indicator of biodiversity progress alongside Species Richness. Increasing Evolutionary Diversity can indicate an increasing resilience of the community.



Fungal Functional Diversity

Fungal Functional Diversity (FFD) calculated for each sample. This is an overall measure of the different functions performed by all the fungal species detected in a sample.



The breadth of functions that fungal species perform in ecosystems, such as nutrient cycling, decomposition, and symbiotic interactions. Greater functional diversity indicates a more resilient and stable ecosystem.

Looking for something more?

We also offer comparative reporting. This includes statistical comparison of metrics and communities according to categories that you define. For instance, these might include waterbody, Site, Management Regime, or anything else that is a focus of your project. Please contact us for further details.

END OF REPORT

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