FINAL REPORT

eDNA analysis of fungal populations in waxcap fungi from soil samples collected at Severalls Hospital site before and after sward translocation.

GW Griffith and AP Detheridge
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Introduction

The former Severalls Hospital site (Fig. 1A) has been redeveloped for housing and in addition to demolition of the former hospital buildings, and house construction; this also requires landscaping of the site. During ecological surveys, several of the grassland areas were found to contain diverse populations of waxcap fungi. Surveys by Ian Rose in 2001 and more recently by Tony Boniface (three visits in autumn 2015) identified 12 grassland areas with waxcaps present (Table 1). Based on these earlier surveys, several of these grassland areas were home to moderately diverse waxcap populations (6-8 spp.; areas 1,3,5,8,11), whereas less diverse populations were recorded in the other areas (1-5 spp.). These areas are shown in Fig. 1B.

In an attempt to mitigate the destruction of the waxcap populations in the grasslands at the Severalls site, it was decided to explore the possibility that large turves (ca. 100W x 100L x 30D cm) can be removed from the five more promising areas, stored off-site in an adjacent field until the landscaping is complete and then repositioned in the reprofiled grassland areas. This the first rigorous attempt to determine whether the translocation of waxcap fungi is possible and as such is potentially of wider significance for mitigation of loss of important waxcap population and re-establishment of waxcap populations in areas of restored grassland.

Translocation of soil fungi has not previously been tested but the use of DNA-based methodologies allows much more sensitive quantification of changes in the relative biomass of different species that was previously possible by fruitbody surveys. One informal attempt in 2002 (Griffith et al., 2004), using 30x30x30cm turves, was not successful, as judged by the absence of any subsequent fruiting by the transplanted species (*Porpolomopsis calyptriformis*). Griffith et al. (2014) translocated 2x2 m turves (3 cm deep) from waxcap fairy rings but no subsequent fruiting was observed on either the recipient or donor areas. Similar approaches have also been tested for orchids on lawns (e.g. at the National Trust property Tyntesfield House in Somerset, where turves covering a ca. 40 m^2 area (5-10 cm depth) were temporarily translocated in an attempt to preserve a population of *Spiranthes spiralis* (Autumn ladies tresses). However, these orchids did not survive the translocation process (John Bailey, pers. comm., 2017).

More recently Wright (2015) suggested that waxcap population could be translocated by placing excised basidiocarps over the recipient site; however, there is no evidence that this would work and theoretical considerations (mainly relating to the very low amount of inoculum that would be transferred) would suggest that it is highly unlikely to be effective. However, eDNA analysis of the donor and recipient sites at Heysham (as described by Wright) found no evidence of successful translocation of species by this method (Griffith, unpublished report, 2018).

The aim of this study is to determine whether the translocation of larger turves may allow survival of waxcap mycelia in the soil and permit their recolonisation of the re-profiled soil following replacement at the redeveloped Severalls site. The first stage of this process, was the identification of the fungi initially present in the turves prior to their translocation to provide a baseline study of fungal populations in the areas of soil earmarked for

translocation, as reported by Griffith and Detheridge (Griffith and Detheridge, 2017). This was done via DNA metabarcoding of soil fungal populations, using a methodology we have devised at Aberystwyth University. Use of DNA metabarcoding to monitor fungal populations provides a rigorous method for determining mycelial survival (and to monitor changes in wider fungal populations) at the various stages of this process. **This report provides a update to the original report with an analysis of the fungi detected in the translocated swards to determine whether the waxcaps have survived the *ex-situ* storage and subsequent relocation on the Severalls site.**

Timeline and methods summary

Stage1

The original site sampling, prior to turf removal, was undertaken on Monday 10th October 2016 by Dr. Andrew Detheridge, with assistance from Ms. Ella Barnett (now Gibbs) from SES Ltd.. Within each of the five grassland areas, sub areas had been fenced off (Fig. 2) to protect them from construction work in surrounding areas. Six 1x1 m quadrat were marked out (with bamboo stakes, each numbered to identify the quadrat) across the fenced off grassland patches (Fig. 2). These are the turves to be translocated. No waxcaps were present at the time. After marking, quadrat areas were logged with GPS (Fig. 3).

Soil sampling, Oct 2016: For each 1 m^2 quadrat, nine soil cores (15mm diameter x 10 cm deep) were collected on a 3x3 grid pattern and pooled in a sample bag. Thus 30 soil samples in all were taken, each comprising 9 pooled cores from a single 1 m^2 quadrat). Cores were stored cold (4ºC) during transport back to Aberystwyth and frozen at -80ºC.The soil was freeze-dried, homogenised by grinding through a 0.5 mm mesh sieve and then thoroughly mixed before storage at -80ºC. DNA was extracted from a 250 mg sub-sample and the PCR amplification conducted using bespoke PCR primers specific to the large (28S) subunit of the rRNA operon (one of the DNA barcoding loci for Fungi). Next Generation sequencing was conducted using an Ion Torrent PGM sequencer, as described by Detheridge et al. (2016; 2018; 2020).

Stage 2

In spring 2017 turves were removed to an adjacent cricket pitch to the south of the main site (Figs. 3, 7) where they were stored until December 2019. Total of 25x 1m^2 turves were moved and turves from same original area were pushed together (Fig. 7a). It was necessary to move the turves to a second area (Fig. 7B) within the storage site (in January 2018) to make way for other activities. During this process the labelling (red flags) on the turves was lost and there was some loss of integrity of the original monoliths. During the storage period, turves were strimmed annually but otherwise not managed. Occasional waxcaps seen during autumn visits in 2017/2018.

Stage 3

In December 2019, the turves were moved a third time to their final location in the western edge of the site (Fig. 8). The receptor site was an area of undisturbed grassland, partly wooded, where no waxcaps had been observed during earlier surveys (Fig. 9). The turves (ca. 1m^2 area, 15-20cm deep) were placed into pre-excavated holes, in 8 areas, all 15-20m apart However, during storage the labelling of the original sampling quadrats could not be identified and some of the turves had broken into smaller fragments, so it is not possible to say which of the original quadrats were translocated.

A total of 30 quadrats (each 1m^2) were sampled in October 2016. However, only 8 (composite) turves (each 1m^2) were translocated to the recipient sites (Fig. 10). Therefore,

only about a quarter of the originally surveyed soil was relocated so it would be expected that not all of the CHEGD fungi originally identified would be present in the translocated turves.

Soil sampling Oct 2020: On Wed 4th November 2020, approximately 11 months after translocation, 9 cores were taken in a grid at a distance of 40cm apart, across the inserted turves and pooled (Fig. 11). Nine cores were taken in a circle centred on the inserted turf but 2m away from its edge and again pooled. This gave a total of 16 samples in pairs. The soil was stored cold until Fri 6th November when it was transported via courier to Aberystwyth (arrived Mon 9th), frozen and was processed as per the original sampling.

Results

1) eDNA analysis of original turves (Oct16-Apr17)

A total of ca. 160 million basepairs (bp) of sequence data were obtained during the sequence run, corresponding to 650,772 separate DNA barcodes (each barcode is ca. 215 bp long). The raw data from the sequencing run of the sample were first subjected to quality control, removal of incomplete/chimeric reads and removal of unique sequences (potentially the result of sequencing errors). Sequences where then clustered at 97% identity into operational taxonomic units (OTUs), with OTUs containing ≤2 sequences removed. Following clustering there remained a total of 576,127 sequences from the 30 quadrat samples analysed (mean 19204 [range 8915-34283] per quadrat). Of these 96.4% were fungal sequences, the remainder comprising Rhizarians (eg. *Cercozoa*/*Bodomorpha* spp.; flagellate/amoeboid protozoa) or Oomycetes (eg. *Peronospora*/*Pythium*; pseudofungi). Some non-fungal sequences (42-46%) were not identifiable at any taxonomic level, since our reference sample database is focused on Fungi so other eukaryotes are not as well represented.

The fungal sequences from the 30 samples were classified into 1177 OTUs with the number of OTUs in each sample ranging from 85 to 397 (Table. 2). An OTU, based on DNA sequence data (>97% identical to other members of the same OTU), is broadly equivalent to a genus or subgenus. For different fungal groups the genetic similarity (ie % sequence identity) between sister species or genera is variable, so the method used here can provide species level discrimination for some groups (eg. waxcaps/Hygrophoraceae) but only genus level discrimination for others (eg. bracket fungi/Polyporales). However, relative to other loci used for similar metabarcoding (eg ITS locus), the approach used here (D1 region of the LSU locus) is better at providing genus/family/order level identification for less characterised taxa, where reference DNA barcodes are absent.

Only 100,000 of the estimated 1.5 million fungal species have hitherto been named (and many named species do not yet have defined DNA barcode). Therefore, one would not expect to identify all fungal sequences. The bioinformatics ‘pipeline’ which we have designed in order to conduct quality control, clustering and identification of sequences, will designate such unidentified sequence clusters as “OTU[number]”. For example, the 20th most abundant taxon overall across all quadrats (mean abundance 1.2%; present in 9/30 quadrats was identified only to class level and is thus designated Agaricomycetes OTU30 (Table 2). We undertook additional analyses of this sequence and found it to only distantly related to any known (barcoded) fungi, and probably a member of the poorly studied order Trechisporales which are common in temperate soils; the most similar sequences to this (also not linked to any named species) were obtained from forest soils in the USA, so this probably represents a hitherto undiscovered species. Despite the occurrence of unidentified OTUs, >83% of sequences were identified to genus level and >90% to family level. The most abundant 100 taxa accounted for 98.7% of all the sequences.

The more reads per OTU, the more abundant is that particular fungal taxon in the sample. We usually express this as a percentage of the total fungal reads for each sample - the data in Table 2 are ranked in order of decreasing abundance. A total of 22 fungal taxa were present at a mean abundance of >1% per quadrat and 14 of these taxa were CHEG fungi. CHEG fungi together accounted for 51.3% (mostly Hygrophoraceae [waxcaps] and Clavariaceae [fairy clubs]) of all fungal sequences across all samples and were thus the most abundant in all samples. However, there was a high level of variability between quadrats, with waxcaps accounting for 90.7% of all fungal sequences in one quadrat (11-6) but absent in two others (5-5, 5-6); and mean abundance of 24.2% overall. It is important to note that the data presented here are relative abundances.

The data presented here allows identification of which fungi are present and their rank abundance in each quadrat (but not absolute biomass). However, the total amount of fungal DNA present and also total fungal biomass, is likely to vary across quadrats. In order to obtain data for absolute amounts of fungal biomass per quadrat, it would be necessary to quantify total fungal biomass (e.g. using a fungal –specific biomarker such as ergosterol). Then the relative abundance data could be converted to absolute biomass data.

Our initial analyses across all fungi, clustered the sequences into generic or subgeneric groupings. More detailed analysis of the CHEG fungi allows species level identification. In Table 3, the data are presented as numbers of sequences rather than relative percentages. The number of reads (=sequences) per OTU for CHEG species in each samples ranged from 3 (the minimal number, since we discarded smaller clusters during quality control) to 26,610 (*Gliophorus laetus* in quadrat 11-6; Table 3).

The most abundant OTU was *G. laetus* (77% of all reads in sample Q11-6) this species was highly localised in its distribution, mostly in one quadrat. The most common CHEG species across all 30 quadrats was *Calvulinopsis helvola* (mean abundance of 9% of all reads; present in 27/30 quadrats). The second most abundant waxcap (after *Gliophorus laetus*) was *Hygrocybe glutinipes* (mean abundance of 4.6% of all reads; present in 13/30 quadrats) (Table 2).

It is possible to analyse the fungal communities present in each quadrat in order to determine whether different fungal communities occur in different areas of the Severalls sites. Various methods are used in plant or microbial ecology (for instance DCA: detrended correspondence analysis), and we have found NMDS (Non-metric multidimensional scaling) to be the most suitable for comparison on fungal populations. Comparison of the fungal populations present in the 30 quadrats did not indicate any very strong differentiation of quadrats from any particular area. However, fungal populations in area 11 were somewhat divergent from this in other areas of the site, mostly likely due to the abundance of *G. laetus* and *Cuphophyllus pratensis* in this area (both rare/absent elsewhere). Also slightly divergent from other samples was a cluster of samples which contained large amounts of DNA from ectomycorrhizal fungi (Fig. 4; blue polygon). It is likely that these quadrats were located close to trees with whose roots these fungi are associated.

Table 3 shows which CHEG species are present in which quadrats, with summary data for numbers of CHEG spp. and also the numbers of waxcap spp. for each quadrat and also for each area. Care must be taken in interpreting these data, since some species are only represented by small numbers of sequences and this likely to represent only very small mycelial systems. It is unlikely that small mycelial systems would contain enough biomass to form fruitbodies. However, since a conservative approach has already been taken in determining whether a particular species is present (ie the occurrence of >4 corresponding identical DNA barcode sequences per sample), we are confident that the species are present

albeit in potentially small amounts. It is also important to note that the distribution of fungal mycelia is spatially very heterogeneous and that the nine cores taken per quadrat is only a small proportion of the total soil present <0.2%; ie. <20 cm^2 of each 1m^2 quadrat).

2) eDNA analysis of translocated turves and surrounding receptor area (Oct20-Jun21)

Sequencing of environmental DNA from these 16 samples resulted in a total of 67989 fungal sequences with an average of 4249 sequences per sample (minimum: 3174 maximum 6225). Sequence data were processed as summarised above and the data from the original sampling and the current data were combined so that they could be compared.

Substantial changes in the mean abundance of the main phyla in the sequence data were observed (Fig. 5; Table 5). In the original samples, Basidiomycota, the phylum to which most CHEGD fungi apart from earth tongues belong, was dominant, with mean relative abundance of 77%. The other major group of fungi typically found in soils is phylum Ascomycota which was present at a mean relative abundance of 16%. Such a pattern is typical of 'waxcap' grasslands, with two dominant groups within Basidiomycota being Hygrophoraceae (waxcaps) and Clavariacaeae (fairy clubs). However, in samples from 2020, a much lower relative abundance of Basidiomycota was observed. In the both translocated turves (37% B vs. 51% A) and surrounding receptor soils (44% B vs. 44% A) Ascomycota showed higher relative abundance. Mean relative abundance of CHEGD fungi was correspondingly reduced from 54% to 10% (7.6% in inserted turves and 12.6% in receiving turves).

Principal coordinate ordination of both sets of data (Fig. 6) in which most of the original samples ordinated separately from the translocated (IN) samples, suggests that populations of fungi present had changed considerably from the original (pre-translocation) condition. The inserted turves and the receiving turves do not cluster separately suggesting that some colonisation of the inserted turves by fungi in the surrounding receiver area has occurred.

The relative abundance of CHEGD species in the translocated turves was low, ranging from identified 0.9% to 19.6% (mean 6.4%) relative abundance compared to 3.7-94.4% (mean 51.5%) for the original turves pre-translocation (Table 6). For four of the translocated turf locations, CHEGD fungi were more abundant in the surrounding receiver soil (mean 11.3%; range 0.04%-39.3%) than in the translocated turves.

Of the 12 original Hygrophoraceae (Waxcap) species, nine were detected in the inserted turves (*H. chlorophana*, *H. coccinea*, *H. pseudoconica* were absent), and one species not previously detected in the 2016 sampling (*Gliophorus irrigatus*) but reported by Rose from a fruitbody survey in 2001 (Table 1) was found (turf 216I). However, in all cases the numbers of sequences were low (Table 6), with relative abundance of the CHEGD species across all 8 translocated turves being at least 10-fold lower than the average for the original turves prior to translocation. Three waxcap species detected in the receiving soil, in moderate abundance (>250 sequences) across the translocated turves (*Cuphophyllus pratensis*, *Hygrocybe acutoconica*, *Hygrocybe conica*) but for other species, the number of sequences for the waxcap species was very low (<10sequences =ca. 0.05% relative abundance), and it is possible that this represents residual DNA from dead fungal hyphae rather than actual living mycelium. The exception was *H. conica*, found in all the translocated turves. However, *H. conica* is widely recognised as a pioneer species amongst waxcaps, so may potentially have recently colonised the turves.

In a third of cases (10/29), waxcap species present both in either the translocated or adjacent receiving soils were present in both (Table 5), so it is possible that colonisation one way or the other had occurred in the 11 months since turf insertion. Six species were present in translocated turves and the original soils but not detected in receiver soils

(*Cuphophyllus pratensis*, *Gliophorus irrigatus*, *Gliophorus laetus*, *Gliophorus psittacinus*, *Hygrocybe ceracea*, *Hygrocybe glutinipes*), though often at low sequence abundance and it is more likely that these illustrate survival of the translocation process (as opposed to in-growth from the receiving soils).

Of the other CHEGD fungi (except Entolomataceae [pink gills], where there is great taxonomic uncertainty and poor coverage by reliable DNA barcodes), most of the Clavariaceae (16/21 spp.) and all the Geoglossaceae detected in the original soils were found in translocated turves but as with waxcaps at much lower relative abundance (only *Hodophilus foetens* found with >100 sequences). Two species (*Trichoglossum hirsutum*, *Dermoloma cuneifolium*)were detected in translocated turves but not in the original soils. Since *D. cuneifolium* was found in two receiving soil samples, it is likely that the translocated turves were colonised during 2020 after final relocation of the turves.

The general decrease in abundance of CHEGD fungi in the translocated turves is clear, as is the increase in relative abundance of Ascomycota. However, without quantification of fungal biomass (eg. via ergosterol analysis; (Detheridge et al., 2018)), it is not possible determine whether other species have expanded to fill the 'gap' left by the declining CHEGD fungi or whether has been a general decline in fungal biomass. Perusal of the most abundant species (Table 6) does not reveal any consistent pattern across the translocated turves but it was noteworthy that a *Mycena* sp., and Typhula sp., often associated with decaying roots and litter, was present at high abundance in turves 216I and 218I respectively.

With regard to the receiving soils, some samples contained high levels of wood decay fungi, for example *Gymnopus*, Marasmius, *Parasola*, *Coprinellus* in 221O and *Endoperplexa*, *Calyptella* in 220O. This suggests the presence of buried woody debris or roots, consistent with the presence nearby of trees. Similarly, ectomycorrhizal fungi (*Inocybe*, *Cortinarius*, *Scleroderma*, Thelephoraceae) were abundant in 218O suggesting that living tree roots were present in the soil. The presence of *Microdochium* and *Limonomyces*, found on senescent grass tissues was observed in 214O and 220O.

Conclusion

Waxcaps and other fungi characteristically found in undisturbed grasslands dominated the fungal populations in all five donor sites. The numbers of waxcap species present in each area was similar to the numbers found in earlier fruitbody surveys and there was good (but not exact) overlap in the species detected and where they were found. This is to be expected since the quadrats themselves comprised only a small part of each area so it would be expected that some species would be missed (since their mycelia would not be present in the quadrat). This likely explains the instances where waxcaps species were found in surveys but not in the DNA (red cells in Table 4).

Of the three species found in DNA but not by fruitbody surveys, two of these (*Hygrocybe acutoconica* [formerly *H. persistens*] and *H. pseudoconica*) were likely missed because they are morphologically very similar to *H. conica*, and often fruit rather early in the season (July/August). From the perspective of the translocation experiment, the original sampling provided baseline data as to which CHEG (and other) fungi are present in the turves. From this set of baseline data, we were able to determine whether the abundance of waxcap mycelia was altered by the translocation.

The difference in the community structure between the original samples of the turves in situ and after translocation (Fig. 5) indicates that the fungal population in the turves has changed considerably, most likely during the 30 months of storage. There was evidence of invasion of

translocated cores by species absent from the donor site but only limited evidence of possibly spread of the CHEGD fungi into the recipient soils.

Many of the original CHEG species have disappeared or exist at very low sequence abundance. It is not possible to exclude the possibility that the eDNA detected was from relict (i.e. dead) mycelia. Overall, the sequence data indicate that the translocation has not been successful in re-establishing the original populations of CHEGD fungi in the receiving location. Longer term sampling (e.g. resampling in late 2023/24) would determine whether the CHEGD fungi still present in late 2020 will recover or are in terminal decline.

Recommendations for future translocation trials

This translocation experiment met with limited success, in part due to its complexity. It is likely that the survival of CHEGD fungi would have been greater had the donor turves been moved directly to the final receiving site. The storage for 30 months at two storage sites exposed the turves to drought and physical disruption which would have negatively impacted on the CHEGD fungi which are biotrophic and rely on living host plants for nutrition. Ideally translocation should be undertaken with a single handling to minimise physical deterioration of the turves and the risk of excessive droughting/waterlogging in storage.

With regard to timing, translocation in winter (as was done) when plants and soil organisms are less active would reduce disturbance, although the higher water content of soils in winter and problems of heavy machinery moving over sensitive soils, risks logistical problems. Late spring, before the growing season is in full swing, would be preferable to autumn when the grassland fungi are fruiting.

The ultimate destination of the turves was undisturbed (‘retained’) grassland with nearby trees. It is possible that fungi already present in receiver soils might outcompete the fungi in the turves at such locations. In hindsight, translocation into newly created (reprofiled) grassland might have been preferable, if possible, but in this case it is unlikely that this would have made a difference.

The most widely deployed wildlife translocations in Europe are for amphibians and reptiles and in many cases these fail or the translocated population shows continued decline (Edgar et al., 2005). However, translocations of larger populations are found to be more successful (Germano and Bishop, 2009). Analogous to this in the case of grassland fungi would be the translocation of larger soil areas, attempting where possible to avoid break-up of the monoliths in transit. Specialised earthmoving equipment capable of moving 2x2x0.25 m monoliths intact likely do exist but are not regularly to hand on building sites. However, diggers equipped with a wide scoop should permit the moving on 1.5x1m turves would be more readily available but the operator would likely need some training /practice (e.g. when creating the holes at the receiver site) in order to undertake the delicate turf transfer operation effectively.

From a monitoring perspective, eDNA analysis should be ideally conducted immediately before the translocation from the donor site and include sampling of the removed monoliths at the receiver area, as well as the areas surrounding the receiver site. Translocation inevitably causes disturbance to the organisms involved and whilst changes in fungal populations can be sensitively monitored using eDNA metabarcoding, it would also be informative to monitor changes in total fungal biomass and also in vegetation over the months/years following translocation.

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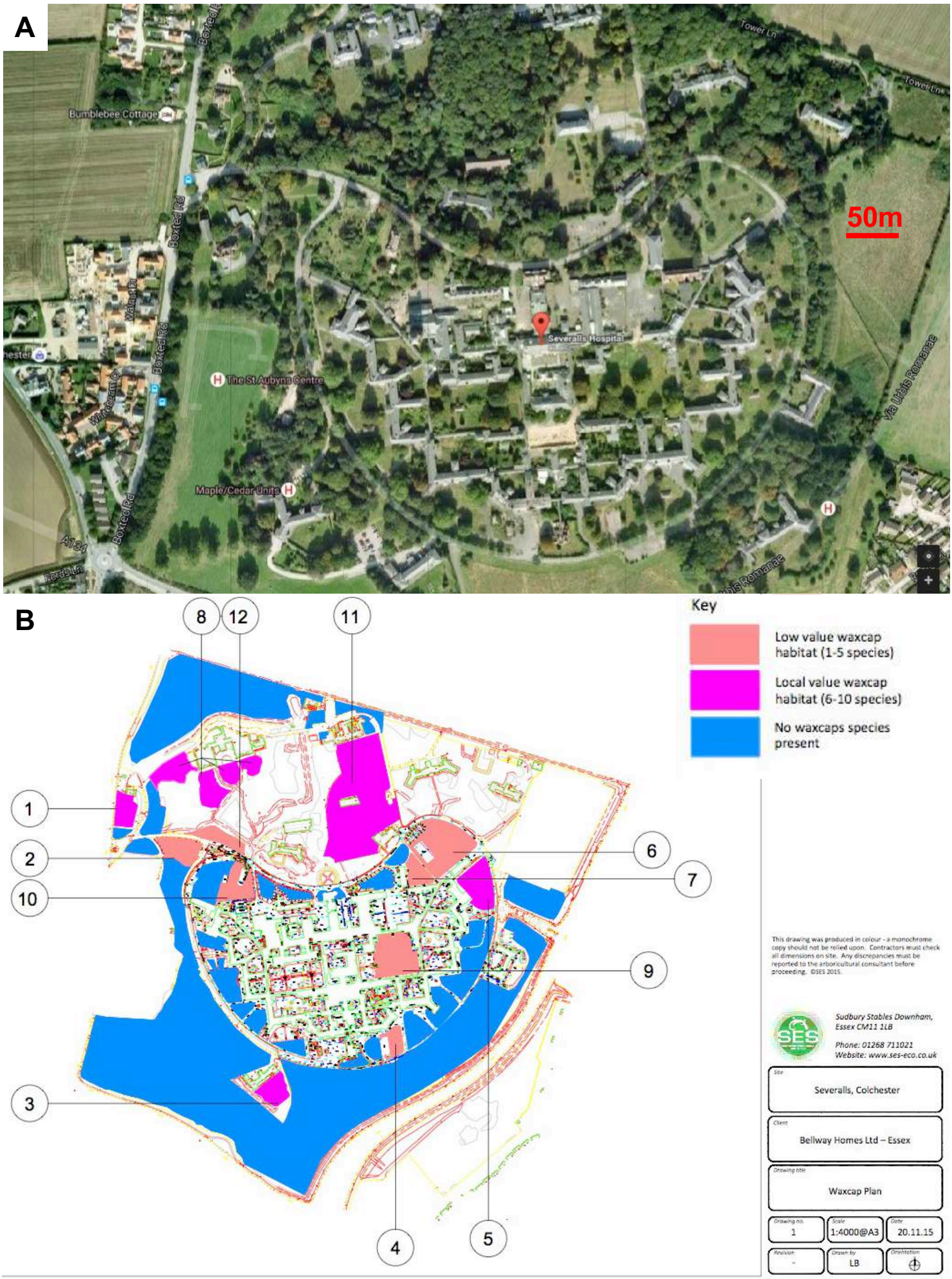

Fig. 1. **A**. Aerial photograph (Googlemaps) of the Severalls site. **B.** Map of the Severalls site indicating th egrassland areas with no waxcaps (**blue**), 1-5 waxcap species (fawn) or 6-10 waxcap species (**bright pink**) based on survey data from Tony Boniface in 2015.

Table 1. Summary of the waxcap survey undertaken by Tony Boniface and Lucy Addison (29th Oct/4th Nov/12th Nov 2015) indicating which species were found in which areas. Three species are highlighted in pink, indicating those found during an earlier survey by Ian Rose (Andrew Martin Associates) in 2001 but not by Boniface & Addison; the exact location of these was not reported. Those highlighted in blue indicate three species found by Boniface but not by Rose. Of the 12 sub-areas defined by Boniface & Addison, the five most species-rich are highlighted in green and these were the areas studied during the current investigation. Note that current Latin names are used here (specific names are unchanged, but we now know that 'waxcaps' fall into 6 different genera within the family Hygrophoraceae. Note also that *C. berkeleyi* is now considered a separate species (no longer a subspecies of *C. pratensis*). Only Latin names are used here since use of English names is prone to cause confusion.

	SPECIES	Three Gardens 1	Driveway 2	Behind Birchwood 3	Garden 4	Garden 5	Garden 6	Garden 7	Myland Court 8	Courtyard 9	Garden bh. Larch House 10	Behind Medway 11	Near the Church 12	TOTAL
2	Cuphophyllus berkleyi										1			1
3	Cuphophyllus fornicatus							1				1		2
4	Cuphophyllus pratensis	1	1	1		1	1	1	1		1	1		9
1	Cuphophyllus russocoriaceus	Recorded by Rose (2001) but no location given												1
5	Cuphophyllus virgineus	1	1	1		1	1	1	1	1		1		9
6	Gliophorus irrigatus	1		1					1					3
7	Gliophorus psittacinus	1		1		1	1	1				1		6
8	Hygrocybe ceracea	1		1	1	1			1	1		1	1	8
9	Hygrocybe chlorophana			1		1			1	1		1	1	6
10	Hygrocybe coccinea	Recorded by Rose (2001) but no location given												1
11	Hygrocybe conica	1		1			1		1					4
12	Hygrocybe glutinipes												1	1
13	Hygrocybe insipida			1		1								2
14	Hygrocybe miniata	Recorded by Rose (2001) but no location given												1
		6	2	8	1	6	4	4	6	3	2	6	3	

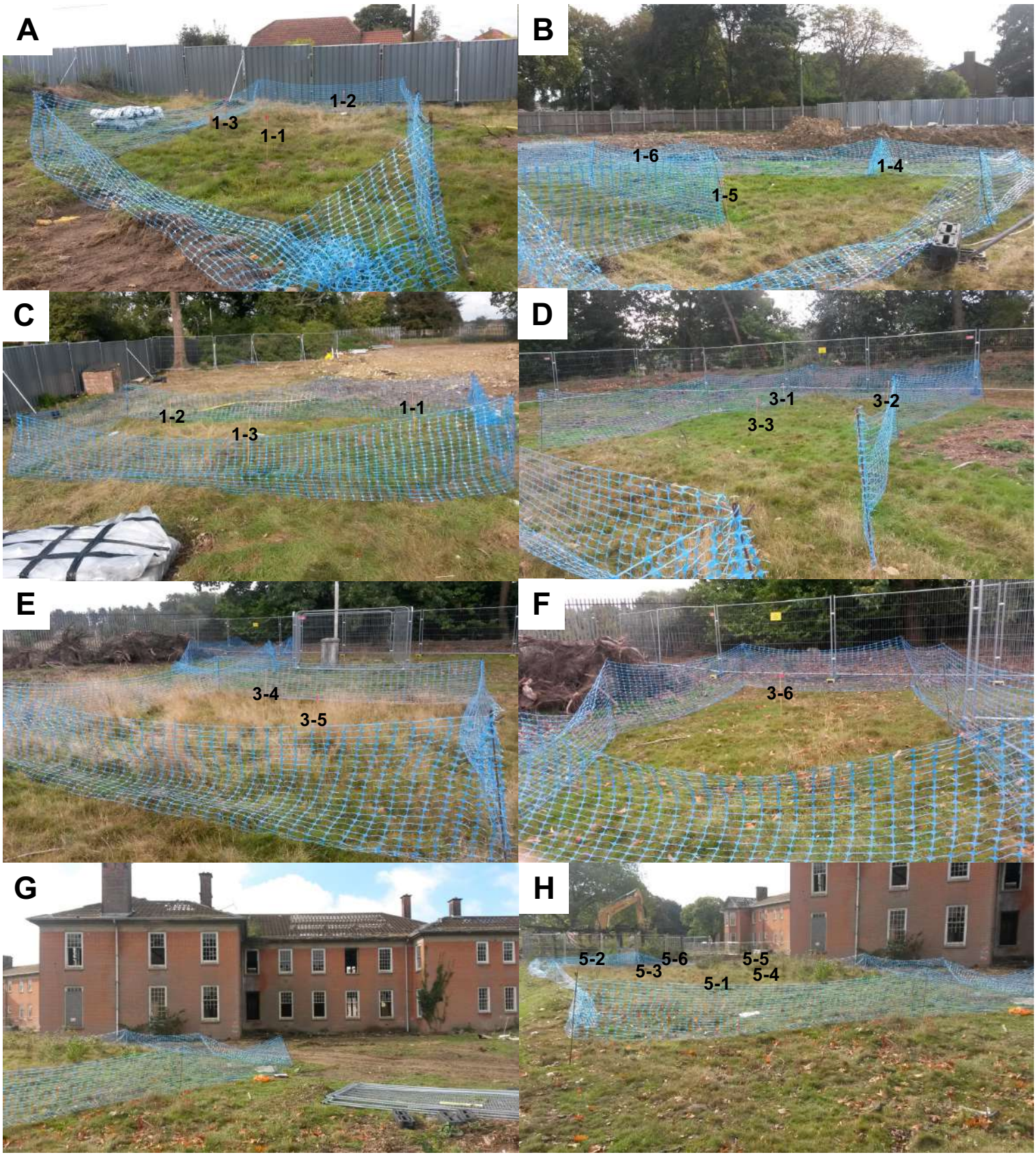

Fig. 2. Photographs of the five sampling areas. A,B,C: Area1(Three Gardens), D,E,F: Area 3 (Behind Birchwood) and G,H: Area 5 (Garden). Bamboo stakes with red flags indicate the quadrat locations

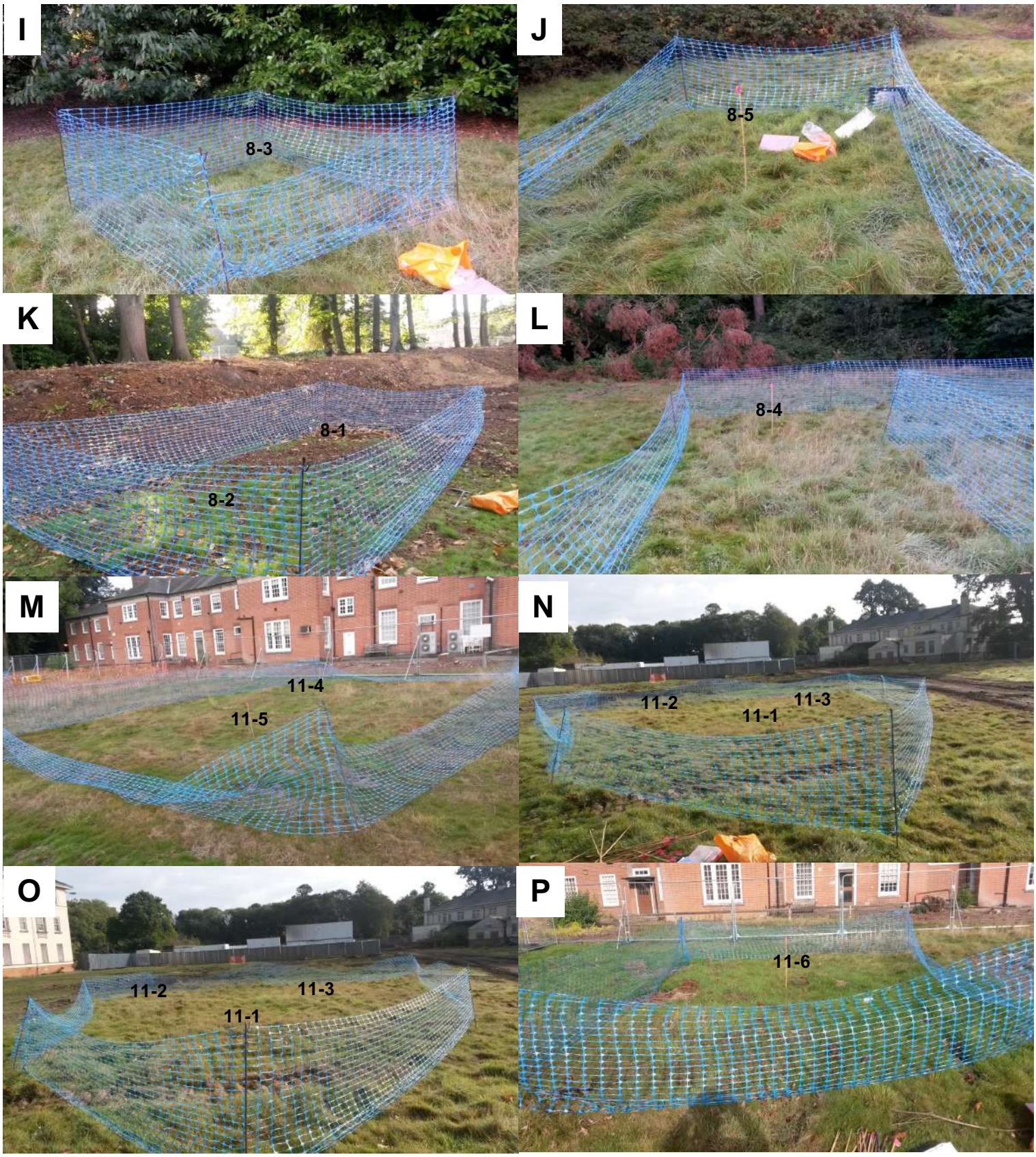

Fig. 2 (Continued). Photographs of the five sampling areas. I,J,K,L: Area 8 (Myland Court); M,N,O,P: Area 11 (Behind Medway). Bamboo stakes with red flags indicate the quadrat locations.

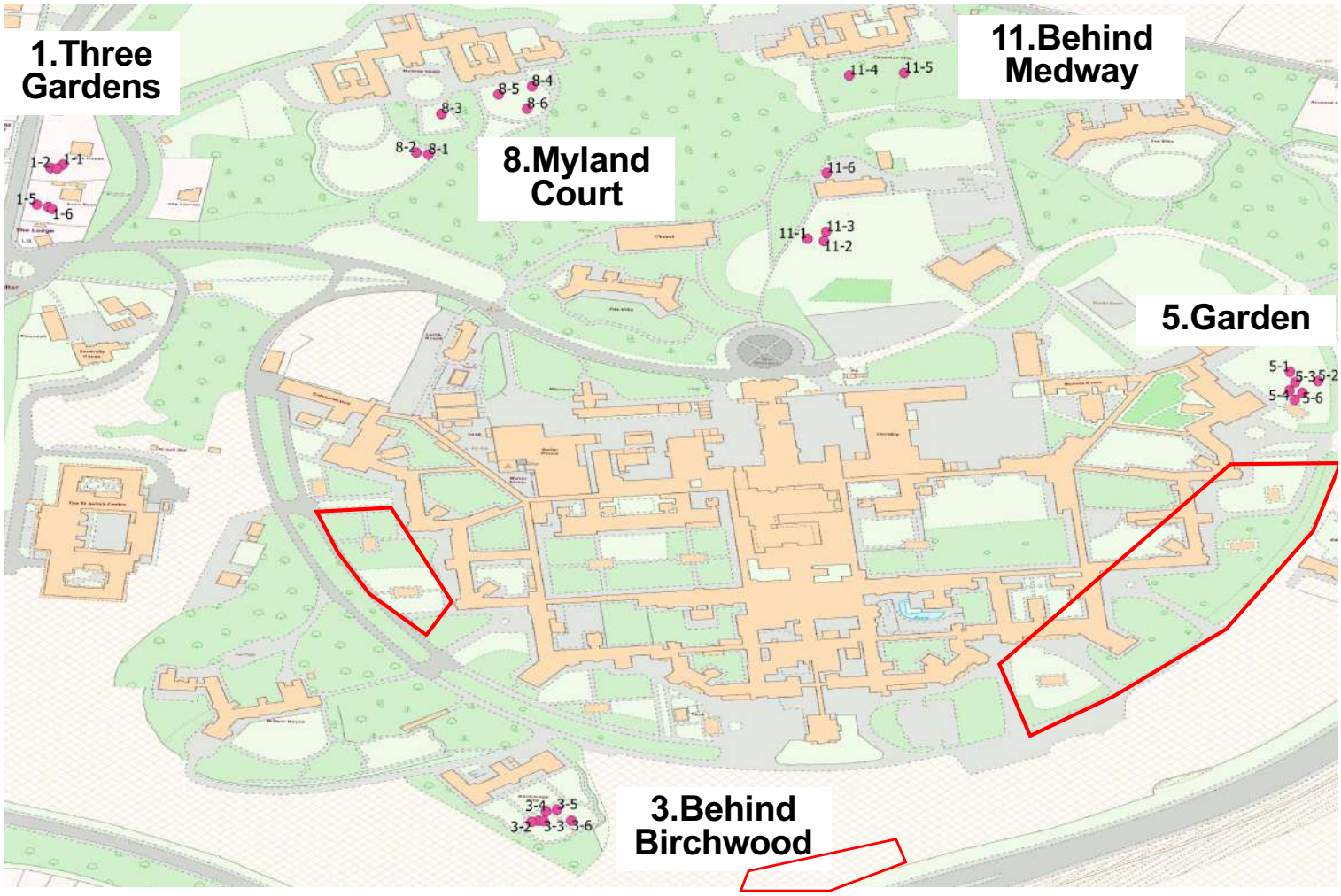

Fig. 3. GIS layer showing the locations of the original quadrats across the Severalls site. At the southern end is the approximate location of the storage sites and to the west the two final destination areas.

Table 2. Output from the RDP classifier showing the relative abundance of each fungal taxon in each of the 30 quadrats sampled at the Severalls site. More abundant taxa are highlighted in green (>5%) and less abundant taxa (<0.01%) in pink. On the left are the taxonomic descriptions, with CHEG taxa highlighted in yellow. Summary data are presented at the bottom of the the table. Dark pink cells show total abundance for each of the CHEG families

Phylum	Class	Order	Family	Genus	Ecology	Coun	mulative T	Mean	Max	Min	1-1	1-2	1-3	1-4	1-5	1-6	3-1	3-2	3-3	3-4	3-5	3-6	5-1	5-2	5-3	5-4	5-5	5-6	8-1	8-2	8-3	8-4	8-5	8-6	11-1	11-2	11-3	11-4	11-5	11-6
Basidior	Agaricr	Agarica	Clavariacea	Clavulinopsis_CPLA	MR CHEG	27	269.44%	8.98%	49.58%	0.00%	5.68%	3.21%	18.14%	1.36%	0.09%	1.08%	36.35%	16.26%	3.96%	0.11%	22.86%	0.09%	18.80%	0.00%	26.53%	11.89%	0.08%	0.14%	0.04%	2.81%	5.00%	49.58%	16.55%	17.18%	0.06%	11.22%	0.05%	0.33%	0.00%	0.00%
Basidior	Agaricr	Trechis	Trechispora	Trechispora	SAP SOIL	30	192.34%	6.41%	21.98%	0.29%	4.37%	5.37%	17.16%	3.77%	12.42%	16.53%	16.97%	4.48%	21.98%	1.27%	6.81%	5.46%	2.27%	3.60%	5.88%	10.92%	13.17%	5.71%	4.31%	1.34%	4.53%	0.60%	1.85%	10.73%	0.29%	3.51%	0.35%	0.81%	5.58%	0.29%
Basidior	Agaricr	Agarica	Hygrophora	Gliophorus	MR CHEG	8	149.56%	4.99%	77.77%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.42%	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.02%	0.02%	0.00%	3.55%	63.71%	77.77%
Basidior	Agaricr	Agarica	Clavariacea	Camarophyllopsis C/	MR CHEG	15	142.25%	4.74%	52.14%	0.00%	0.00%	0.00%	0.00%	52.14%	3.58%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.63%	0.00%	0.15%	0.00%	0.01%	0.00%	6.83%	0.00%	4.49%	2.00%	26.04%	32.00%	0.09%	0.02%	0.00%	14.21%	0.00%	0.00%
Basidior	Agaricr	Agarica	Hygrophora	Hygrocybe_HY5	MR CHEG	13	137.77%	4.59%	73.07%	0.00%	73.07%	0.55%	0.00%	0.00%	4.57%	4.21%	0.02%	0.02%	0.00%	0.01%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%	55.12%	0.02%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.09%	0.00%
Basidior	Agaricr	Agarica	Hygrophora	Hygrocybe_HY2	MR CHEG	15	123.78%	4.13%	49.53%	0.00%	0.00%	0.00%	0.12%	12.54%	0.29%	0.24%	0.04%	0.00%	0.00%	49.53%	23.48%	11.88%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.16%	0.02%	0.02%	0.67%	6.52%	16.24%	0.00%	0.00%	0.00%
Basidior	Agaricr	Agarica	Hygrophora	OTU 6	MR CHEG	8	94.70%	3.16%	39.36%	0.00%	0.00%	0.00%	0.00%	11.77%	0.00%	1.61%	0.06%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	4.09%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.04%	39.36%	0.00%	37.75%	0.00%	0.00%	0.00%
Basidior	Agaricr	Agarica	Hygrophora	Cuphophyllus_CU1	MR CHEG	9	88.79%	2.96%	75.53%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.03%	0.00%	0.00%	0.18%	0.00%	0.00%	0.02%	0.00%	75.53%	0.03%	12.94%
Basidior	Agaricr	Russule	Russulacea	uncultured Russulace	MR EM	11	72.74%	2.42%	53.69%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.87%	0.02%	0.26%	0.00%	2.62%	0.05%	14.04%	53.69%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	1.10%	0.00%
Ascomy	Geoglc	Geoglo	Geoglossa	Geoglossum	MR CHEG	20	67.89%	2.26%	19.34%	0.00%	1.25%	0.93%	0.00%	0.43%	0.00%	12.45%	0.00%	0.00%	0.22%	0.19%	5.05%	1.36%	7.98%	7.90%	19.34%	1.81%	0.00%	3.55%	0.04%	0.00%	0.00%	0.00%	0.04%	0.00%	0.80%	0.00%	0.50%	0.06%	2.00%	2.00%
Basidior	Agaricr	Agarica	Hygrophora	Hygrocybe_PS1	MR CHEG	11	67.55%	2.25%	35.64%	0.00%	0.00%	0.00%	0.04%	0.00%	0.00%	0.02%	0.00%	0.29%	35.64%	15.12%	0.00%	0.00%	0.00%	0.21%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	16.03%	0.08%	0.02%	0.02%	0.07%	0.00%	0.00%	0.00%
Fungi in	Mortier	Mortiere	Mortierellac	Mortierella	SAP SOIL	30	63.63%	2.12%	6.04%	0.13%	1.25%	2.02%	4.84%	0.48%	2.10%	1.06%	2.99%	4.29%	1.88%	2.13%	2.10%	4.97%	0.89%	1.84%	2.84%	3.53%	4.35%	2.08%	1.16%	0.63%	0.13%	0.80%	0.54%	0.87%	4.90%	6.04%	1.22%	0.46%	1.03%	0.17%
Basidior	Agaricr	Russule	Russulacea	Russula	MR EM	14	60.42%	2.01%	16.73%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	16.73%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.45%	4.23%	10.09%	2.11%	13.96%	0.04%	2.74%	6.21%	0.00%	2.59%	0.00%	0.00%	0.00%	0.00%	0.00%	0.11%	1.03%	0.09%
Ascomy	Eurotic	Chaeto	Herpotrichi	Sorocybe	MR DSE	30	53.02%	1.77%	6.57%	0.23%	0.40%	4.21%	5.67%	0.68%	0.63%	1.16%	0.48%	0.23%	0.48%	0.86%	4.44%	1.59%	2.77%	0.77%	2.06%	6.57%	0.24%	2.28%	2.29%	0.33%	0.80%	1.46%	0.88%	3.00%	2.98%	2.80%	1.57%	0.27%	0.88%	0.24%
Basidior	Agaricr	Agarica	Tricholoma	Gymnopus	SAP	13	50.04%	1.67%	41.45%	0.00%	0.00%	0.04%	0.00%	0.00%	0.03%	0.00%	4.75%	0.02%	0.12%	0.00%	0.02%	0.04%	41.45%	0.04%	0.08%	0.49%	2.93%	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Basidior	Agaricr	Agarica	Clavariacea	Clavaria_CVAC	MR CHEG	23	47.33%	1.58%	11.53%	0.00%	0.00%	0.11%	0.22%	1.16%	0.00%	0.06%	0.05%	0.00%	0.12%	0.00%	1.57%	0.00%	0.14%	3.51%	2.11%	3.48%	5.71%	2.76%	1.50%	0.02%	0.36%	0.65%	0.10%	0.48%	11.53%	8.12%	3.33%	0.26%	0.00%	0.00%
Basidior	Agaricr	Agarica	Clavariacea	Clavulinopsis_CPFU	MR CHEG	11	45.76%	1.53%	16.93%	0.00%	0.00%	0.00%	0.03%	0.00%	4.24%	0.01%	0.00%	0.02%	11.94%	0.00%	0.00%	0.00%	0.07%	0.00%	0.00%	0.00%	0.00%	16.93%	0.00%	0.00%	0.00%	0.07%	0.00%	0.03%	0.00%	0.00%	10.23%	0.00%	2.19%	0.00%
Basidior	Agaricr	Agarica	Clavariacea	Clavaria_CVFR	MR CHEG	7	44.42%	1.48%	42.95%	0.00%	0.00%	0.00%	0.07%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	42.95%	0.52%	0.00%	0.04%	0.77%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Basidior	Agaricr	Agarica	Clavariacea	Clavulinopsis_CPCO	MR CHEG	5	38.71%	1.29%	22.74%	0.00%	0.01%	0.00%	0.00%	0.00%	15.55%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	22.74%	0.38%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%
Basidior	Agaricr	X	X	OTU 30		9	34.67%	1.16%	31.58%	0.00%	0.00%	31.58%	0.15%	0.07%	0.00%	0.00%	0.62%	0.00%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.04%	0.00%	0.70%	0.00%	0.00%	0.00%	0.00%	0.00%	1.41%
Basidior	Tremel	Tremell	Trimorphon	Saitozyma		30	30.57%	1.02%	2.41%	0.09%	0.23%	2.41%	1.61%	0.46%	0.74%	1.85%	1.28%	2.01%	0.72%	0.51%	0.97%	1.80%	1.51%	1.07%	1.28%	1.37%	0.72%	0.55%	0.73%	0.34%	0.89%	0.42%	1.08%	1.20%	1.48%	1.43%	0.32%	0.41%	1.11%	0.09%
Basidior	Agaricr	Agarica	Clavariacea	Clavaria_CVAR	MR CHEG	28	30.32%	1.01%	5.95%	0.00%	0.01%	0.49%	0.39%	4.39%	0.11%	4.94%	0.05%	0.06%	0.94%	0.00%	0.38%	0.02%	0.42%	0.25%	0.59%	4.01%	5.95%	1.87%	0.22%	0.24%	0.12%	0.51%	0.76%	0.04%	0.97%	0.50%	1.41%	0.35%	0.30%	0.00%
Basidior	Agaricr	Agarica	Hygrophora	Hygrocybe_PS4	MR CHEG	4	29.39%	0.98%	28.71%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	28.71%	0.64%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Basidior	Agaricr	Agarica	Tricholoma	Laccaria	MR EM	23	29.07%	0.97%	10.52%	0.00%	0.21%	0.26%	0.05%	0.02%	0.01%	0.71%	0.02%	0.07%	0.00%	0.00%	1.62%	0.00%	0.38%	0.32%	1.32%	4.42%	10.52%	0.65%	7.74%	0.03%	0.00%	0.00%	0.01%	0.14%	0.02%	0.04%	0.00%	0.06%	0.41%	0.00%
Basidior	Agaricr	Agarica	Clavariacea	Ramariopsis_RMKU	MR CHEG	12	28.36%	0.95%	10.92%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.41%	1.06%	0.00%	0.00%	1.05%	0.00%	4.70%	0.00%	0.41%	0.00%	0.00%	0.56%	1.57%	4.99%	2.11%	10.92%	0.00%	0.55%	0.03%
Basidior	Agaricr	Agarica	Clavariacea	Ramariopsis_RMPU	MR CHEG	12	26.74%	0.89%	5.47%	0.00%	0.00%	0.00%	3.89%	0.45%	0.00%	0.32%	0.00%	0.00%	0.00%	5.47%	0.00%	0.14%	4.09%	0.00%	0.00%	0.07%	0.00%	2.84%	0.00%	0.00%	5.04%	0.00%	0.00%	0.00%	0.59%	2.62%	1.22%	0.00%	0.00%	0.00%
Basidior	Agaricr	Agarica	Psathyrella	Coprinellus	SAP SOIL	20	26.10%	0.87%	25.37%	0.00%	0.00%	0.04%	0.00%	0.02%	0.02%	0.00%	0.02%	25.37%	0.02%	0.02%	0.00%	0.04%	0.02%	0.03%	0.00%	0.00%	0.01%	0.02%	0.02%	0.01%	0.00%	0.01%	0.02%	0.00%	0.02%	0.12%	0.16%	0.12%	0.00%	0.00%
Ascomy	Leotior	Helotial	X	OTU 32		30	25.26%	0.84%	3.37%	0.01%	0.24%	0.31%	0.29%	0.65%	1.03%	1.08%	0.32%	1.65%	0.73%	1.21%	1.09%	1.43%	1.04%	1.47%	0.85%	1.05%	0.66%	2.71%	0.44%	0.11%	0.11%	3.37%	0.77%	0.96%	0.74%	0.19%	0.28%	0.07%	0.42%	0.01%
Basidior	Agaricr	Agarica	Tricholoma	Lepista	SAP SOIL	11	24.89%	0.83%	13.42%	0.00%	0.00%	2.12%	0.07%	0.00%	3.54%	0.83%	0.04%	0.00%	0.00%	2.59%	0.04%	0.00%	0.00%	1.77%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	13.42%	0.00%	0.45%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Basidior	Agaricr	Agarica	Marasmiac	Marasmius	SAP	3	23.74%	0.79%	23.70%	0.00%	0.01%	0.00%	0.00%	0.00%	23.70%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%	0.00%	0.00%
Basidior	Agaricr	Agarica	Tricholoma	Mycena	SAP SOIL	27	20.92%	0.70%	6.37%	0.00%	0.80%	0.27%	0.34%	1.49%	1.61%	0.07%	0.25%	0.13%	0.92%	0.02%	0.04%	0.02%	0.03%	0.08%	2.35%	0.85%	1.83%	6.37%	0.37%	0.62%	0.00%	0.56%	0.01%	0.11%	0.49%	1.09%	0.00%	0.00%	0.14%	0.09%
Basidior	Agaricr	Agarica	Entolomata	Nolanea	MR CHEG	29	20.71%	0.69%	5.69%	0.00%	0.08%	0.47%	0.57%	0.06%	0.15%	0.22%	0.10%	0.08%	0.06%	0.19%	0.40%	0.09%	0.11%	3.76%	1.26%	0.27%	1.01%	3.21%	1.33%	0.09%	0.16%	0.16%	0.04%	5.69%	0.27%	0.59%	0.15%	0.00%	0.11%	0.01%
Basidior	Agaricr	Agarica	Hygrophora	Cuphophyllus_CU4	MR CHEG	6	20.01%	0.67%	9.46%	0.00%	0.00%	0.00%	0.00%	0.00%	0.57%	0.16%	0.00%	0.00%	0.01%	0.47%	0.00%	0.00%	0.00%	9.33%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	9.46%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Basidior	Tremel	Filobas	Piskurozym	Solicoccozyma		30	19.63%	0.65%	1.86%	0.08%	0.19%	1.86%	1.22%	0.23%	0.40%	1.33%	0.33%	0.44%	0.39%	0.27%	0.64%	0.30%	0.41%	0.48%	1.00%	1.45%	1.26%	0.53%	1.39%	0.86%	0.45%	0.08%	0.19%	1.25%	0.78%	0.76%	0.36%	0.18%	0.52%	0.08%
Ascomy	Eurotic	Eurotial	Trichocome	Eupenicillium	SAP SOIL	30	17.64%	0.59%	1.60%	0.05%	0.14%	0.27%	0.53%	0.16%	0.45%	0.31%	1.02%	1.04%	0.49%	0.43%	1.26%	1.27%	0.79%	1.59%	0.36%	0.48%	0.47%	1.60%	1.46%	0.68%	0.17%	0.11%	0.05%	0.18%	0.36%	0.35%	0.22%	0.13%	0.88%	0.40%
Ascomy	Leotior	Helotial	Helotiaceae	Cudoniella	MR DSE	30	17.49%	0.58%	1.61%	0.03%	0.17%	1.16%	0.63%	0.07%	0.88%	1.16%	1.46%	1.61%	0.94%	1.16%	0.12%	0.82%	0.29%	0.82%	0.78%	1.24%	0.19%	0.85%	0.64%	1.14%	0.16%	0.30%	0.03%	0.19%	0.10%	0.15%	0.21%	0.05%	0.12%	0.06%
Ascomy	Eurotic	Eurotial	Trichocome	Penicillium	SAP SOIL	29	17.12%	0.57%	2.08%	0.00%	0.12%	0.27%	0.17%	0.09%	0.49%	0.69%	1.86%	1.19%	0.73%	0.30%	0.59%	1.90%	0.92%	2.08%	0.38%	0.34%	0.30%	1.80%	0.74%	0.86%	0.13%	0.08%	0.05%	0.03%	0.11%	0.35%	0.15%	0.00%	0.32%	0.06%
Basidior	Agaricr	Agarica	Hygrophora	Hygrocybe_HY1	MR CHEG	2	13.92%	0.46%	13.90%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	13.90%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Basidior	Agaricr	Agarica	Clavariacea	Clavaria_CVX5	MR CHEG	3	13.86%	0.46%	12.99%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.33%	12.99%	0.54%	0.00%	0.00%	0.00%
Basidior	Agaricr	Agarica	X	OTU 39		3	13.28%	0.44%	5.32%	0.00%	0.00%	0.00%	5.32%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	3.30%	0.00%	0.00%	0.00%	0.00%	4.66%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Ascomy	Dothid	Pleospor	Pleosporac	Pyrenochaeta	SAP	27	13.15%	0.44%	1.48%	0.00%	0.22%	0.47%	0.22%	0.00%	0.70%	0.05%	1.01%	1.48%	0.07%	0.32%	0.59%	1.19%	0.21%	1.19%	0.24%	0.43%	0.61%	1.00%	0.47%	0.27%	0.00%	0.06%	0.03%	0.03%	0.87%	0.78%	0.19%	0.00%	0.40%	0.04%
Basidior	Agaricr	Thelepl	Thelephora	uncultured Thelephor	MR EM	21	12.92%	0.43%	6.74%	0.00%	0.00%	0.00%	0.00%	0.04%	0.00%	6.74%	0.04%	0.07%	0.03%	0.00%	0.23%	0.00%	0.06%	0.04%	0.05%	0.89%	0.89%	0.08%	2.05%	0.12%	0.54%	0.00%	0.02%	0.19%	0.00%	0.03%	0.00%	0.04%	0.72%	0.03%
Basidior	Agaricr	Agarica	Cortinariac	Inocybe	MR EM	14	12.62%	0.42%	3.46%	0.00%	0.00%	0.00%	0.00%	0.13%	0.00%	0.03%	0.18%	0.76%	1.24%	0.00%	0.16%	0.00%	0.03%	0.02%	0.00%	2.16%	1.72%	0.00%	3.46%	0.00%	1.92%	0.00%	0.00%	0.47%	0.00%	0.00%	0.00%	0.00%	0.34%	0.00%
Fungi in	Mucorr	Endogc	Endogonac	Endogone		29	12.54%	0.42%	3.33%	0.00%	0.55%	3.33%	1.24%	0.13%	0.11%	0.06%	0.07%	0.08%	0.12%	0.05%	0.11%	0.05%	0.15%	0.00%	0.05%	0.34%	0.56%	0.04%	1.61%	0.05%	0.64%	0.08%	0.10%	2.26%	0.15%	0.24%	0.05%	0.15%	0.17%	0.01%
Ascomy	Eurotic	Chaeto	Herpotrichi	Veronaea	MR DSE	28	11.72%	0.39%	1.84%	0.00%	0.15%	0.22%	0.11%	0.11%	0.28%	0.46%	0.41%	0.50%	0.18%	0.26%	0.62%	0.18%	0.16%	0.59%	0.97%	0.54%	1.70%	1.84%	0.28%	0.18%	0.00%	0.00%	0.01%	0.02%	0.42%	0.59%	0.40%	0.08%	0.42%	0.04%
Ascomy	Leotior	Helotial	Hyaloscyph	Lachnum	MR DSE	30	11.46%	0.38%	1.23%	0.02%	0.15%	0.48%	0.23%	0.13%	0.75%	0.37%	0.57%	1.23%	0.39%	0.45%	0.32%	0.31%	0.53%	0.87%	0.85%	0.21%	0.39%	0.69%	0.08%	0.04%	0.06%	0.30%	0.13%	0.16%	1.11%	0.29%	0.04%	0.03%	0.25%	0.02%
Ascomy	Leotior	Helotial	Dermateac	Mollisia	MR DSE	30	11.38%	0.38%	1.73%	0.06%	0.43%	1.73%	0.62%	0.12%	0.58%	0.56%	0.15%	0.53%	0.36%	0.14%	0.39%	0.50%	0.12%	0.46%	0.34%	0.56%	0.13%	0.41%	0.18%	0.11%	0.33%	0.32%	0.31%	0.27%	0.31%	0.87%	0.06%	0.08%	0.37%	0.06%
Basidior	Agaricr	Agarica	Tricholoma	OTU 48		8	11.06%	0.37%	7.42%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	7.42%	0.00%	0.36%	0.12%	0.15%	0.11%	2.08%	0.00%	0.80%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Basidior	Microb	Microbc	Microbotryc	Kriegeria	PATH SMU	30	10.76%	0.36%	1.97%	0.04%	0.13%	1.97%	1.05%	0.04%	0.17%	0.46%	0.19%	0.24%	0.32%	0.09%	0.10%	0.27%	0.12%	0.19%	0.32%	0.31%	0.22%	0.15%	1.58%	0.73%	0.08%	0.21%	0.27%	0.59%	0.17%	0.23%	0.08%	0.06%	0.29%	0.16%
Basidior	Agaricr	Agarica	Tricholoma	OTU 34		10	10.01%	0.33%	6.21%	0.00%	0.00%	0.00%	0.00%	0.00%	0.15%	0.01%	0.18%	0.00%	0.07%	0.00%	0.39%	0.00%	0.00%	0.00%	0.00%	0.31%	0.00%	0.07%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	2.60%	6.21%	0.00%	0.00%	0.00%	0.00%
Basidior	Agaricr	Russule	Russulacea	Lactarius	MR EM	5	8.81%	0.29%	6.75%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.06%	0.00%	0.00%	0.00%	0.00%	0.00%	6.75%	1.95%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.00%
% Fungi identified to family								90.2%	99.0%	52.4%	96.3%	52.4%	76.6%	97.1%	92.9%	94.4%	89.3%	85.3%	93.1%	94.6%	90.6%	91.6%	95.1%	90.5%	93.8%	89.1%	88.1%	84.8%	86.5%	94.5%	98.7%	89.7%	95.5%	84.9%	86.9%	87.2%	95.4%	99.0%	94.2%	97.1%
% Fungi identified to genus								83.5%	98.3%	43.0%	95.4%	47.2%	73.1%	83.6%	87.8%	90.3%	84.0%	81.1%	90.6%	85.7%	87.6%	88.0%	92.3%	88.1%	91.4%	79.5%	84.5%	80.1%	81.6%	87.8%	98.2%	87.5%	94.3%	82.6%	43.0%	76.2%	56.2%	98.3%	91.8%	96.1%
Ascomycota								16.0%	34.6%	1.5%	6.2%	20.3%	22.6%	5.6%	12.9%	24.4%	15.8%	23.1%	9.8%	9.9%	21.8%	23.4%	20.6%	29.7%	34.6%	22.5%	14.0%	34.2%	22.4%	12.0%	3.3%	12.9%	5.7%	9.9%	18.4%	17.6%	7.9%	1.5%	12.2%	4.9%
Basidiomycota								77.1%	96.9%	59.4%	89.5%	62.8%	61.9%	93.2%	80.9%	71.9%	72.7%	61.2%	84.4%	85.5%	71.0%	66.9%	76.4%	65.0%	59.8%	69.1%	72.4%	59.4%	70.3%	84.5%	95.3%	84.3%	91.5%	83.2%	71.5%	67.2%	88.8%	96.9%	82.1%	94.1%
Blastocladiomycota								0.00%	0.04%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.04%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.03%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Chytridiomycota								0.93%	3.47%	0.06%	0.65%	3.47%	3.09%	0.15%	0.54%	0.45%	2.40%	1.11%	1.09%	0.66%	1.13%	0.93%	0.51%	0.65%	0.75%	1.74%	1.24%	1.28%	0.66%	0.29%	0.24%	0.37%	0.21%	0.77%	0.73%	1.45%	0.33%	0.08%	0.76%	0.06%
Fungi incertae sedis								3.45%	9.99%	0.29%	2.01%	5.96%	6.69%	0.73%	3.82%	1.50%	4.43%	9.99%	2.81%	2.80%	2.99%	6.10%	1.40%	2.48%	3.39%	5.10%	6.48%	2.64%	4.50%	1.51%	0.77%	1.09%	0.91%	3.28%	6.73%	8.84%	1.61%	0.97%	1.69%	0.29%
Glomeromycota								0.77%	2.53%	0.03%	0.60%	2.53%	0.61%	0.07%	0.55%	0.54%	1.41%	0.51%	0.32%	0.41%	0.78%	0.55%	0.47%	0.79%	0.63%	0.61%	2.18%	0.69%	0.72%	0.74%	0.03%	0.26%	0.86%	0.99%	0.76%	1.53%	0.46%	0.36%	1.71%	0.38%
Neocallimastigomycota								0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
X								1.72%	5.09%	0.20%	1.04%	4.97%	5.09%	0.24%	1.30%	1.21%	3.28%	4.04%	1.50%	0.66%	2.31%	2.19%	0.62%	1.37%	0.74%	0.96%	3.65%	1.74%	1.44%	0.92%	0.38%	1.04%	0.85%	1.80%	1.83%	3.35%	0.89%	0.20%	1.62%	0.31%
Fungi Total								19204	34283	8915	21370	11127	9640	24564	21173	25668	17139	17518	22803	21614	14168	16880	18512	17034	14869	13107	22704	14664	13698	27872	8915	31164	29630	18741	12745	26061	19729	11593	17142	34283
Non Fungi Total								685	2746	55	559	1051	614	189	956	702	1021	911	673	684	763	980	428	873	475	635	1389	708	310	375	55	474	558	369	779	2746	483	70	560	161
Taxa Count								201	331	65	152	210	187	142	228	205	272	271	230	183	213	227	179	238	197	213	327	260	201	272	69	206	174	160	165	331	161	65	175	117
Inverse Simpson Index (OTU)								10.43	34.081	1.678	1.9238	9.1918	20.3	3.3491	10.207	16.389	6.842	10.368	6.2855	5.5286	11.041	5.1573	4.6914	9.7492	8.4791	28.64	34.081	31.705	24.824	3.4076	3.12	3.642	9.0261	7.1282	5.737	20.699	5.1875	1.8499	2.5918	1.6778
OTU Count								251.6	397	85	200	249	234	176	292	257	329	324	287	229	259	278	233	286	247	265	389	331	253	336	88	284	230	207	218	397	200	85	226	160
Shannon Index (OTU)								3.072	4.3918	1.165	1.7339	3.7368	4.0413	2.0947	3.3994	3.5909	3.4544	3.7203	2.976	2.7703	3.478	3.0946	2.6838	3.5968	3.2866	4.1481	4.3049	4.3918	4.1205	2.8292	2.0157	2.4277	2.8197	3.0033	3.0596	4.0685	2.5857	1.216	2.3582	1.165
				Clavariaceae		30		23.7%	76.46%	0.16%	6.39%	4.81%	23.73%	59.69%	23.90%	7.69%	38.71%	16.39%	16.97%	5.70%	25.08%	43.72%	26.85%	5.21%	30.09%	28.60%	12.34%	30.89%	9.42%	3.60%	15.11%	76.46%	44.55%	52.08%	20.78%	38.52%	27.93%	15.27%	4.78%	0.16%
				Hygrophoraceae		28		24.2%	90.71%	0.00%	73.07%	0.55%	0.17%	24.31%	5.43%	10.70%	0.12%	0.33%	35.70%	65.17%	23.51%	11.88%	0.02%	38.26%	0.64%	4.11%	0.00%	0.00%	0.07%	0.05%	55.12%	0.18%	39.59%	0.14%	40.07%	6.59%	56.06%	79.08%	63.83%	90.71%
				Entolomataceae		30		0.9%	5.77%	0.03%	0.16%	1.26%	0.75%	0.14%	0.95%	0.70%	0.37%	0.27%	0.18%	0.34%	0.64%	0.25%	0.18%	3.76%	1.56%	1.44%	1.61%	3.38%	1.43%	0.27%	0.16%	0.27%	0.17%	5.77%	0.27%	0.61%	0.15%	0.03%	0.22%	0.04%
				Geoglossaceae		23		2.5%	19.89%	0.00%	1.25%	1.26%	0.58%	1.27%	0.00%	12.45%	0.25%	0.34%	0.74%	0.19%	5.34%	1.36%	8.03%	7.90%	19.89%	1.81%	0.00%	5.05%	0.04%	0.00%	0.00%	0.00%	0.32%	0.00%	1.07%	0.00%	0.57%	0.06%	2.00%	2.00%
				CHEGtot		30		51.3%	94.44%	3.91%	80.88%	7.88%	25.23%	85.41%	30.28%	31.54%	37.44%	17.34%	53.59%	71.40%	54.57%	57.22%	34.09%	55.13%	52.18%	35.97%	13.95%	39.31%	10.97%	3.91%	70.39%	76.91%	84.62%	58.00%	62.20%	45.72%	84.71%	94.44%	70.79%	92.91%

Table 3. Summary of the number of sequences of each CHEG species detected in DNA from each quadrat sampled at the Severalls site. Cells highlighted in pink show area totals (sum of sequenced from each quadrat). Cells highlighted in green show the more abundant sequences (>100 sequences). Note that for Clavariaceae (fairy clubs), the molecular taxonomy of the family is less well studied than for Hygrophoraceae (waxcaps); as a result, several putative species shown here have not been formally named. At the bottom of the table the total number of CHEG and also waxcap species are shown for each quadrat/area.

		Summary data -per area																																No. Quads where	Total No.
Code	Species	Area1	Area3	Area5	Area8	Area11	Q1-1	Q1-2	Q1-3	Q1-4	Q1-5	Q1-6	Q3-1	Q3-2	Q3-3	Q3-4	Q3-5	Q3-6	Q5-1	Q5-2	Q5-3	Q5-4	Q5-5	Q5-6	Q8-1	Q8-2	Q8-3	Q8-4	Q8-5	Q8-6	Q11-1	Q11-2	Q11-3	Q11-4	Q11-5	Q11-6	present	Seqs
C1	Camarophyllopsis schulzeri	13546	8	140	15671	1664				12788	758							8	117		23				935		400	623	7716	5997	12	5		1647			13	31029
C2	Clavaria acuta	335	257	2965	476	1934		12	21	286		16	8		27		222		25	598	314	456	1296	276	174	5	29	192	27	49	1416	216	272	30			23	5967
C3	Clavaria roseaAFF			121	80	2571																		121	31			8		41	42	2009	520				7	2772
C4	Clavaria straminea	2487	304	2401	531	292		54	38	1079	48	1268	16	11	215		54	8	77	86	88	525	1351	274	60	66	11	160	226	8	56	131	13	41	51		27	6015
C5	Clavaria sp. JMB10061001	40		19	206	213					40											19						197	9		213						5	478
C6	Clavaria fragilis	47	7262	229		47			7	10		30	5					7257	96	14	9	110									19		28				11	7585
C7	Clavaria incarnata				162																								162								1	162
C8	Clavulinopsis sulcata			581															17			564															2	581
C9	Clavaria guilleminii	27	8	116	30	75				16	5	6						8	5	10		79		22	6			12	12		66		9				13	256
C10	Clavaria sp. BRACR 16032					3533																									42	3385	106				3	3533
C11	Clavaria amoenoides	268				156						268																				127	29				3	424
C12	Clavulinopsis corniculata	3286			7292						3286																	7180	112								3	10578
C13	Clavulinopsis luteoalba	1485	4291	55	25	421	337		37		897	214			2708		1583		5	5	12	33						25				21		24	376		14	6277
C14	Clavulinopsis helvola	3369	11683	11496	24790	2043	876	357	1715	334	20	67	6226	2847	917	24	1653	16	3484		3942	1559	18	2493	5	782	446	15433	4899	3225	8	10	2025				26	53381
C15	Clavulinopsis laeticolor					2924																										2913		11			2	2924
C16	Ramariopsis sp. JMB-2011	266	81	372	574	1148	147	38	31			50	38	7		19		17			38	145		189		109			171	294	569		459		110	10	18	2441
C17	Ramariopsis crocea	75	6	474	449	608		12	58	5						6				212	41	36	133	52			449				35	261	241		41	30	15	1612
C18	Ramariopsis kunzei		53	883		2334												53	192			13		678							67	550	1696		21		8	3270
C19	Ramariopsis pulchella	564	1206	1171		557			371	111		82				1182		24	758			9		404							40	517					10	3498
C20	Clavulinopsis corallinorosacea	22	100	29	233	366	6	7	9				53		5		42		12	6		5		6		10		101		122		114	10	8	218	16	18	750
H1	Cuphophyllus pratensis	5			60	13204						5														7			53			6		8756	5	4437	7	13269
H2	Cuphophyllus russocoriaceus	149	96	169	2804						107	42				96				169									2804								5	3218
H3	Cuphophyllus virgineus	13	6	1421							13					6				1421																	3	1440
H4	Gliophorus laetus		9		7	37778									9											7								409	10759	26610	5	37794
H5	Gliophorus psittacinus	1135				135						1135																							135		2	1270
H6	Hygrocybe acutoconica	3307	11	536	8	12474				2894		413	11									536								8	5019		7455				7	16336
H7	Hygrocybe ceracea	6	11405	4986	4761	13						6		51	8116	3238				4891	95							4746	15			13				9	21171
H8	Hygrocybe chlorophana				4120																							4120								1	4120
H9	Hygrocybe coccinea			36																36																1	36
H10	Hygrocybe conica	3206	6455		55	5368			12	3074	58	62	6		12	1597	3315	1525										50	5		85	1692	3591				14	15084
H11	Hygrocybe glutinipes	17666			4920	15	15561	61			967	1077													7		4907	6							15		8	22601
H12	Hygrocybe pseudoconica	7	9557			8				7						9067	9	481														8				5	9572
G1	Geoglossum fallax	3672	1036	6459	17	1238	267	103		106		3196			51	41	715	229	1478	1345	2878	237		521	6				11		102		98	7	342	689	20	12422
G2	Geoglossum simile				79																							79								1	79
G3	Glutinoglossum glutinosum	300	260	309	83	49		37	56	207			43	59	117		41		8		82			219					83		35		14				13	1001
"G"4	Microglossum spp.	421	24	154	20	8	128		19	53		221					24		32	17		105				6	7		7			8				12	627
	Total No. Sequences	128023	128059	117173	142502	135015	23477	13330	11395	26709	24205	28907	19975	20932	25377	24995	16649	20131	20587	20018	17198	14870	26463	18037	15051	31475	9586	34430	31868	20092	14657	31021	21358	12267	18783	36929		
	No. CHEG Sequences	55704	54118	35122	67453	91176	17322	681	2374	20970	6199	8158	6406	2975	12177	15276	7658	9626	6306	8810	7522	4431	2798	5255	1224	992	6249	23987	25242	9759	7826	11965	16587	10933	12073	31792		
	%CHEG	44%	42%	30%	47%	68%	74%	5%	21%	79%	26%	28%	32%	14%	48%	61%	46%	48%	31%	44%	44%	30%	11%	29%	8%	3%	65%	70%	79%	49%	53%	39%	78%	89%	64%	86%		
	No. CHEG Species	26	22	23	25	28	7	9	12	14	11	18	9	5	10	10	10	11	14	13	11	16	4	12	8	8	7	12	18	9	17	16	18	9	11	6		
	No. Waxcap Species	9	7	5	8	8	1	1	1	3	4	7	2	1	3	5	2	2	0	4	1	1	0	0	1	2	1	2	5	2	2	2	4	2	4	2		

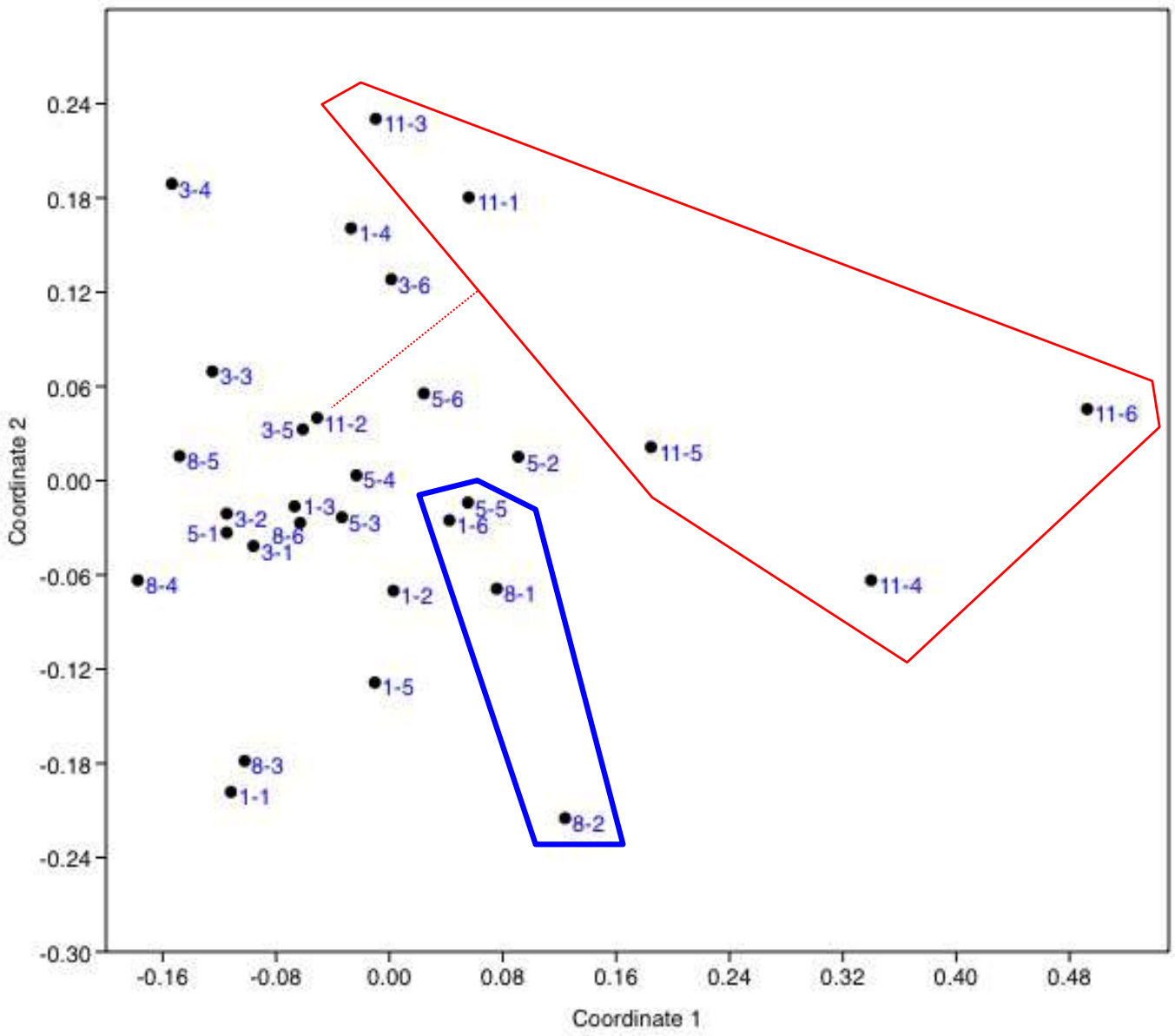

Fig. 4. Non-metric multidimensional scaling ordination of the fungal populations in the Severalls quadrats. The samples from area 11 (red polygon) form a broadly distinct cluster suggesting the presence of a distinctive fungal population (in large part dominated by the waxcap *G. laetus*). Four quadrats (blue polygon) contained large amounts (27-70%) of DNA from ectomycorrhizal basidiomycetes (*Laccaria*, *Lactarius*, *Russula*, *Thelephora*; Table 2). This suggests the nearby presence of suitable host trees (oak, beech, birch, conifers).

Table 4. Summary of the quadrats where waxcap species were detected, correlated with the results of earlier fruitbody surveys (Table 1).Columns highlighted in green indicate those areas sampled in the present investigation and the numbers in these cells show the number of sequences of each species detected.
Cells highlighted pink/red indicate where species were found in previous surveys, with red boxes surrounded by black line showing those areas where a particular species had been found during FB surveys but not detected in the DNA from any of the quadrats in that area.
DNA metabarcoding detected the presence of twelve waxcap species, including three species not previously recorded from Severalls (*Gliophorus laetus*, *Hygrocybe acutoconica*, *Hygrocybe pseudoconica*) whereas four species previously detected in the areas sampled here were not detected (*Cuphophyllus fornicatus*, *Gliophorus irrigatus*, *Hygrocybe insipida*, *Hygrocybe miniata*).

	Waxcap Species	Three Gardens 1	Driveway 2	Behind Birchwood 3	Garden 4	Garden 5	Garden 6	Garden 7	Myland Court 8	Courtyard 9	10	Behind Medway 11	Near the Church 12	TOTAL
1	Cuphophyllus berkleyi	0	*	0	*	0	*	*	0	*	*	0	*	**0**
2	Cuphophyllus fornicatus	0	*	0	*	0	*	*	0	*	*	**0**	*	**0**
3	Cuphophyllus pratensis	5	*	**0**	*	**0**	*	*	60	*	*	13204	*	**13269**
4	Cuphophyllus russocoriaceus	149	*	96	*	169	*	*	2804	*	*	0	*	**3218**
5	Cuphophyllus virgineus	13	*	6	*	1421	*	*	**0**	*	*	**0**	*	**1440**
6	Gliophorus irrigatus	**0**	*	**0**	*	0	*	*	**0**	*	*	0	*	**0**
7	Gliophorus laetus	0	*	9	*	0	*	*	7	*	*	37778	*	**37794**
8	Gliophorus psittacinus	1135	*	**0**	*	**0**	*	*	0	*	*	135	*	**1270**
9	Hygrocybe acutoconica	3307	*	11	*	536	*	*	8	*	*	12474	*	**16336**
10	Hygrocybe ceracea	6	*	11405	*	4989	*	*	4761	*	*	13	*	**21174**
11	Hygrocybe chlorophana	0	*	**0**	*	**0**	*	*	4120	*	*	**0**	*	**4120**
12	Hygrocybe coccinea	0	*	0	*	36	*	*	0	*	*	0	*	**36**
13	Hygrocybe conica	3206	*	6455	*	3	*	*	55	*	*	5368	*	**15087**
14	Hygrocybe glutinipes	17666	*	14	*	0	*	*	4920	*	*	15	*	**22615**
15	Hygrocybe insipida	0	*	**0**	*	**0**	*	*	0	*	*	0	*	**0**
16	Hygrocybe miniata	0		0		0			0			0		**0**
17	Hygrocybe pseudoconica	7	*	9557	*	0	*	*	0	*	*	8	*	**9572**
		25494	*	**27553**	*	**7154**	*	*	**16735**	*	*	**68995**	*	**145931**

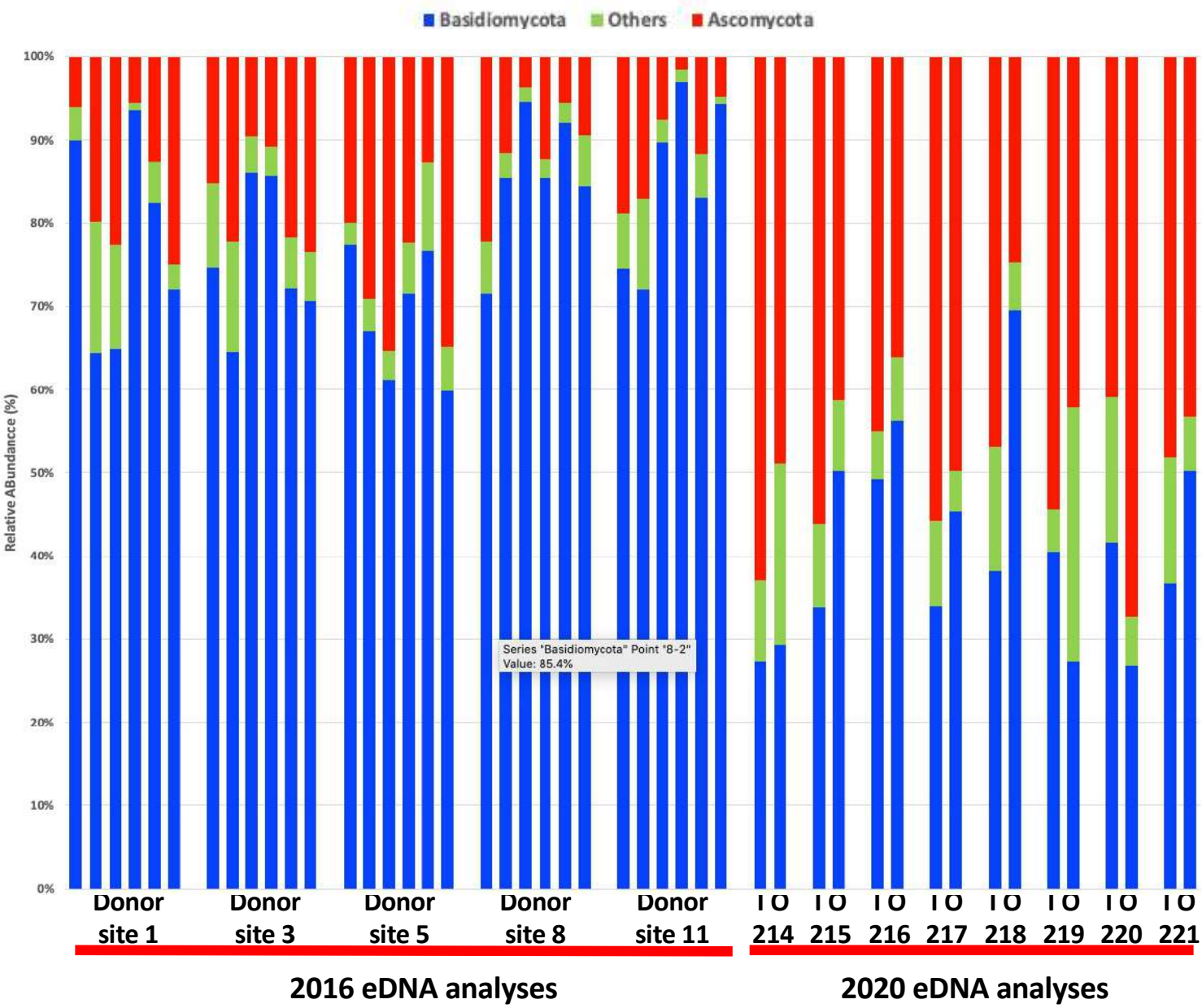

Fig. 5. Stacked barchart showing the relative abundance of Basidiomycota, Ascomycota and other fungal phyla in the soils samples from 2016 and 2020.

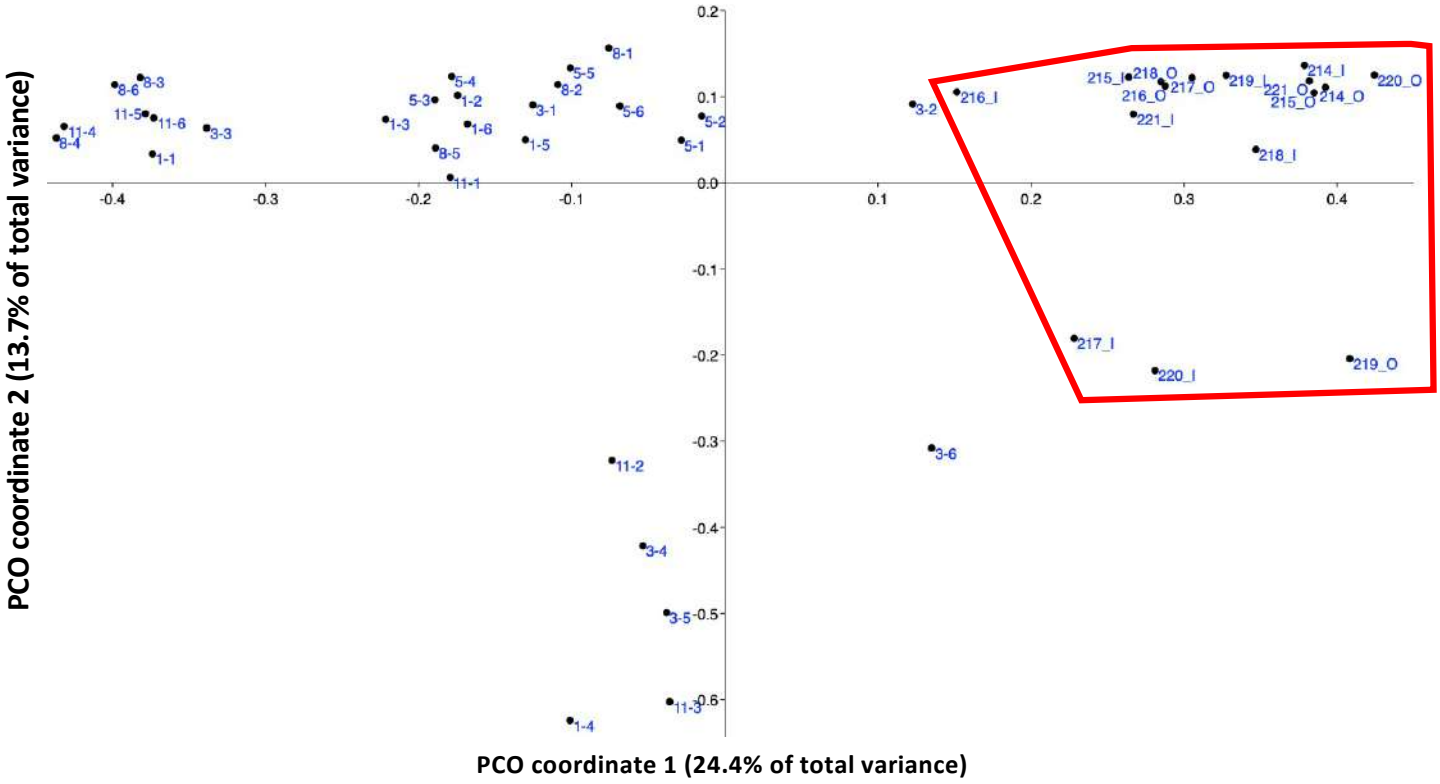

Fig. 6. Principal coordinate ordination of the new samples taken in 2020 (red polygon) after translocation and the original samples before translocation taken in 2016. The clear separation between the two sampling points indicates distinct fungal populations

		phylum	class	order	family	genus	Count	nulative T	Mean	Max	Min	214_I	214_O	215_I	215_O	216_I	216_O	217_I	217_O	218_I	218_O	219_I	219_O	220_I	220_O	221_I	221_O	Ave2016	AveIN20	AveOUT20
1	Fun	Basidiomyc	Agaricomycetes	Agaricales	Tricholoma	Mycena	35	56.4%	1.23%	32.7%	0.01%	2.62%	0.00%	0.95%	0.00%	34.71%	0.17%	0.06%	0.47%	0.05%	0.00%	0.27%	0.00%	0.00%	0.00%	0.18%	0.00%	0.65%	4.86%	0.08%
2	Fun	Ascomycot	Dothideomycet	Pleosporal	Pleosporac	Pyrenochaeta	43	40.1%	0.87%	7.0%	0.01%	2.25%	1.87%	1.39%	2.22%	0.31%	0.28%	1.15%	1.37%	8.43%	0.84%	4.32%	2.02%	2.14%	4.09%	2.16%	1.27%	0.28%	2.77%	1.74%
3	Fun	Basidiomyc	Agaricomycetes	Trechispor	Trechispor	Trechispora	44	148.6%	3.23%	20.2%	0.04%	0.07%	0.00%	2.27%	1.06%	0.61%	0.54%	3.37%	1.67%	0.24%	0.50%	0.64%	0.68%	0.25%	0.00%	12.68%	0.14%	4.30%	2.52%	0.57%
4	Fun	Ascomycot	Dothideomycet	Capnodiale	Davidiellac	Cladosporium co	44	44.9%	0.98%	4.0%	0.01%	3.84%	3.87%	1.29%	2.09%	1.88%	2.79%	0.87%	2.52%	3.58%	2.37%	3.25%	1.81%	1.46%	4.20%	2.39%	1.78%	0.30%	2.32%	2.68%
5	Fun	Basidiomyc	Agaricomycetes	Agaricales	Hygrophor	Hygrocybe_sgH2	28	101.6%	2.21%	24.0%	0.01%	0.07%	0.00%	0.38%	0.54%	0.28%	0.00%	5.97%	0.19%	1.76%	0.17%	0.52%	5.73%	6.67%	0.00%	0.18%	0.06%	2.80%	1.98%	0.84%
6	Fun	Ascomycot	Dothideomycet	Dothideale	Dothiorace	Columnosphaeri	35	22.2%	0.48%	3.2%	0.01%	3.35%	0.59%	1.20%	0.98%	3.22%	1.32%	1.57%	0.61%	2.24%	0.34%	1.95%	0.24%	0.11%	0.33%	0.57%	0.37%	0.16%	1.78%	0.60%
7	Fun	Ascomycot	Leotiomycetes	Helotiales	Helotiacea	OTU 151	12	16.1%	0.35%	6.6%	0.04%	1.94%	0.37%	0.19%	2.60%	6.98%	0.26%	2.83%	0.27%	1.15%	0.65%	0.25%	0.00%	0.00%	0.04%	0.00%	0.00%	0.00%	1.67%	0.52%
8	Fun	Ascomycot	Eurotiomycetes	Chaetothyr	Herpotrichi	OTU 30	46	33.2%	0.72%	3.8%	0.01%	1.15%	0.26%	1.64%	1.60%	2.78%	4.06%	3.56%	2.31%	0.72%	0.57%	1.07%	0.92%	1.24%	0.10%	0.68%	0.48%	0.42%	1.60%	1.29%
9	Fun	Pseudofun	Oomycetes	Saprolegni	Saprolegni	OTU 96	43	17.0%	0.37%	4.1%	0.01%	0.21%	0.13%	0.91%	0.34%	0.63%	0.50%	0.42%	0.10%	2.64%	0.38%	0.11%	3.41%	2.62%	0.06%	4.68%	0.00%	0.08%	1.53%	0.61%
10	Fun	Basidiomyc	Tremellomycete	Tremellales	Trimorphon	Saitozyma	45	47.7%	1.04%	2.5%	0.08%	0.91%	0.78%	2.05%	1.03%	2.41%	1.38%	2.05%	1.75%	1.95%	0.23%	1.39%	0.48%	0.68%	0.00%	0.68%	0.08%	1.08%	1.51%	0.72%
11	Fun	Ascomycot	Sordariomycete	Sordariales	Lasiospha	Schizothecium	21	18.4%	0.40%	2.9%	0.01%	2.88%	0.70%	1.76%	1.16%	0.15%	0.24%	0.53%	1.46%	1.44%	0.97%	2.16%	1.04%	0.70%	3.01%	0.62%	1.21%	0.00%	1.28%	1.22%
12	Fun	Basidiomyc	Tremellomycete	Filobasidial	Piskurozym	Solicoccozyma	46	38.8%	0.84%	4.0%	0.04%	0.47%	0.26%	1.48%	1.68%	1.49%	4.34%	1.91%	2.36%	0.91%	0.04%	1.59%	0.24%	1.75%	0.90%	0.42%	0.28%	0.69%	1.25%	1.26%
13	Fun	Ascomycot	Leotiomycetes	Thelebolal	Thelebolac	Thelebolus	46	23.6%	0.51%	3.9%	0.01%	0.54%	0.37%	0.79%	0.49%	4.16%	1.71%	2.13%	1.53%	0.35%	0.15%	0.43%	0.89%	0.53%	0.49%	1.01%	0.65%	0.30%	1.24%	0.78%
14	Fun	Ascomycot	Eurotiomycetes	Eurotiales	Trichocom	Penicillium	45	27.3%	0.59%	3.1%	0.02%	0.84%	0.39%	2.21%	0.21%	0.70%	0.61%	3.42%	0.92%	0.24%	0.11%	0.23%	0.74%	0.68%	0.47%	0.47%	0.54%	0.54%	1.10%	0.50%
15	Fun	Ascomycot	Sordariomycete	Xylariales	Amphispha	Sarcostroma	9	9.0%	0.20%	3.7%	0.11%	0.12%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.27%	0.15%	4.00%	0.15%	2.34%	0.18%	2.05%	0.82%	0.00%	1.10%	0.16%
16	Fun	Basidiomyc	Agaricomycetes	Agaricales	Clavariacea	Hodophilus_varia	3	7.4%	0.16%	7.2%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	8.47%	0.08%	0.00%	0.17%	0.00%	1.06%	0.03%
17	Fun	Ascomycot	Leotiomycetes	Helotiales	Helotiacea	Cudoniella	46	28.6%	0.62%	2.2%	0.03%	2.30%	0.59%	0.69%	0.18%	0.20%	0.74%	0.14%	0.08%	1.76%	0.46%	1.66%	1.04%	0.76%	0.51%	0.91%	1.38%	0.56%	1.05%	0.62%
18	Fun	Basidiomyc	Agaricomycetes	Cantharella	Ceratobasi	Thanatephorus	13	14.4%	0.31%	6.9%	0.01%	0.80%	8.05%	0.13%	0.00%	0.00%	0.00%	0.00%	0.00%	7.31%	0.08%	0.05%	0.00%	0.00%	0.16%	0.00%	0.00%	0.01%	1.03%	1.04%
19	Fun	Ascomycot	X	X	X	OTU 154	21	20.7%	0.45%	4.1%	0.01%	0.59%	0.74%	1.45%	2.55%	0.00%	0.48%	0.84%	1.64%	1.36%	0.78%	0.55%	2.55%	3.21%	4.30%	0.21%	1.55%	0.01%	1.02%	1.82%
20	Fun	Fungi incer	Mortierellomyco	Mortierellal	Mortierellac	OTU 436	28	14.1%	0.31%	2.1%	0.01%	0.70%	0.54%	0.79%	0.95%	0.55%	1.32%	1.15%	0.55%	1.07%	0.59%	0.45%	2.70%	2.45%	0.16%	0.91%	0.90%	0.01%	1.01%	0.96%
21	Fun	Basidiomyc	Agaricomycetes	Thelephor	Typhulacea	Typhula	5	7.0%	0.15%	6.5%	0.05%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	7.90%	0.00%	0.00%	0.18%	0.00%	0.00%	0.00%	0.25%	0.00%	0.99%	0.05%
22	Fun	Basidiomyc	Pucciniomycete	Pucciniales	Pucciniace	Puccinia	29	15.0%	0.33%	6.9%	0.01%	0.00%	0.26%	7.40%	1.19%	0.00%	0.00%	0.22%	0.79%	0.21%	0.23%	0.00%	0.12%	0.00%	0.06%	0.00%	0.17%	0.18%	0.98%	0.35%
23	Fun	Basidiomyc	Agaricomycetes	Cantharella	Ceratobasi	Waitea	4	7.8%	0.17%	7.2%	0.04%	0.00%	0.00%	0.00%	0.46%	0.00%	0.00%	0.00%	0.05%	0.00%	0.00%	7.82%	0.12%	0.00%	0.00%	0.00%	0.00%	0.00%	0.98%	0.08%
24	Fun	Basidiomyc	Agaricomycetes	Trechispor	Trechispor	OTU 10	39	73.2%	1.59%	10.0%	0.01%	0.19%	0.00%	2.39%	0.00%	0.09%	0.41%	0.87%	0.84%	0.19%	0.00%	0.11%	0.00%	0.45%	0.00%	3.14%	0.00%	2.22%	0.93%	0.16%
25	Fun	Basidiomyc	Agaricomycetes	Agaricales	Hygrophor	Hygrocybe_sgH3	17	109.0%	2.37%	41.0%	0.01%	0.00%	0.00%	0.22%	0.00%	0.11%	0.00%	0.00%	3.63%	0.43%	0.00%	0.00%	0.00%	4.81%	0.00%	1.77%	0.06%	3.39%	0.92%	0.46%
26	Fun	Basidiomyc	Agaricomycetes	Agaricales	Strophariac	Tubaria	9	6.9%	0.15%	4.4%	0.01%	1.52%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.03%	5.36%	0.04%	0.18%	0.80%	0.00%	0.04%	0.00%	0.00%	0.00%	0.88%	0.11%
27	Fun	Basidiomyc	Agaricomycetes	Agaricales	Hygrophor	Cuphophyllus1_	15	94.8%	2.06%	75.4%	0.01%	0.00%	0.00%	0.00%	0.00%	0.07%	0.00%	5.05%	0.00%	0.00%	0.00%	0.84%	0.00%	0.00%	0.00%	0.96%	0.00%	2.96%	0.86%	0.00%
28	Fun	Fungi incer	Mortierellomyco	Mortierellal	Mortierellac	OTU 777	44	15.2%	0.33%	2.0%	0.02%	0.30%	1.15%	0.44%	0.59%	0.63%	0.54%	0.73%	0.48%	1.44%	0.88%	0.59%	2.58%	1.41%	0.39%	1.25%	0.59%	0.10%	0.85%	0.90%
29	Fun	Basidiomyc	Agaricomycetes	X	X	OTU 295	3	6.3%	0.14%	6.1%	0.06%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	6.64%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.83%	0.00%
30	Fun	Ascomycot	Dothideomycet	Pleosporal	Phaeosphi	OTU 118	41	18.3%	0.40%	2.4%	0.01%	1.97%	2.74%	0.60%	1.37%	0.31%	0.24%	0.22%	0.64%	1.33%	0.65%	1.02%	0.15%	0.39%	1.80%	0.78%	0.20%	0.18%	0.83%	0.97%
31	Fun	Ascomycot	X	X	X	OTU 217	18	8.5%	0.18%	5.1%	0.01%	0.00%	0.33%	0.06%	0.00%	0.50%	1.58%	0.06%	0.13%	0.00%	0.06%	0.07%	0.45%	0.00%	0.00%	5.84%	0.08%	0.01%	0.82%	0.33%
32	Fun	Ascomycot	Dothideomycet	Pleosporal	Didymellac	OTU 60	42	15.5%	0.34%	1.5%	0.01%	0.54%	0.15%	1.58%	0.82%	0.26%	0.93%	0.34%	1.00%	1.07%	0.50%	1.45%	0.74%	0.59%	0.45%	0.57%	0.28%	0.18%	0.80%	0.61%
33	Fun	Ascomycot	Sordariomycete	Hypocreale	Clavicipitac	Paecilomyces	32	11.3%	0.24%	2.1%	0.01%	0.30%	0.15%	0.60%	0.90%	0.94%	1.27%	2.36%	1.98%	0.43%	0.23%	0.27%	0.80%	0.42%	0.08%	1.01%	0.25%	0.02%	0.79%	0.71%
34	Fun	Basidiomyc	Agaricomycetes	Trechispor	X	OTU 346	12	7.4%	0.16%	2.5%	0.04%	2.44%	0.26%	0.16%	0.49%	0.04%	0.00%	0.00%	0.00%	0.35%	0.04%	2.73%	0.74%	0.20%	0.00%	0.05%	0.65%	0.00%	0.74%	0.27%
35	Fun	Ascomycot	Dothideomycet	Pleosporal	Pleosporac	Cochliobolus	45	17.2%	0.37%	1.8%	0.03%	0.94%	0.24%	0.47%	0.28%	0.39%	0.54%	1.60%	1.93%	1.15%	0.42%	0.61%	0.50%	0.59%	0.14%	0.16%	0.28%	0.27%	0.74%	0.54%
36	Fun	Ascomycot	Leotiomycetes	Helotiales	Helotiales i	Spirosphaera	21	9.8%	0.21%	2.1%	0.01%	0.19%	0.15%	2.27%	1.57%	0.39%	0.26%	0.25%	0.14%	0.53%	0.08%	0.25%	2.64%	1.24%	0.12%	0.75%	0.20%	0.01%	0.73%	0.65%
37	Fun	Ascomycot	Leotiomycetes	Helotiales	Helotiacea	Tricladium	43	12.4%	0.27%	1.6%	0.01%	0.28%	0.04%	1.70%	0.31%	0.48%	0.47%	0.53%	0.56%	0.69%	0.29%	0.75%	0.36%	0.59%	0.00%	0.47%	0.17%	0.19%	0.69%	0.28%
38	Fun	Ascomycot	Leotiomycetes	Helotiales	X	OTU 32	41	30.7%	0.67%	2.9%	0.05%	0.30%	0.00%	1.01%	0.41%	0.39%	0.39%	2.50%	2.14%	0.35%	0.38%	0.25%	0.00%	0.59%	0.00%	0.08%	0.00%	0.77%	0.68%	0.41%
39	Fun	Ascomycot	Leotiomycetes	Helotiales	Hyaloscypl	Lachnum	45	24.2%	0.53%	4.1%	0.02%	2.25%	2.26%	0.44%	0.23%	0.24%	0.06%	0.17%	1.09%	0.24%	0.19%	0.14%	0.00%	1.63%	4.32%	0.23%	0.11%	0.40%	0.67%	1.03%
40	Fun	Pseudofun	Oomycetes	Pythiales	Pythiaceae	Pythium_B	12	6.9%	0.15%	3.3%	0.01%	3.42%	1.39%	0.00%	0.00%	0.00%	0.30%	1.54%	0.03%	0.00%	0.06%	0.00%	0.36%	0.14%	0.18%	0.08%	0.00%	0.00%	0.65%	0.29%
41	Fun	Ascomycot	Sordariomycete	Xylariales	Amphispha	Microdochium	13	31.9%	0.69%	11.8%	0.05%	2.11%	12.92%	1.04%	0.80%	0.00%	0.00%	0.62%	0.06%	0.67%	0.57%	0.00%	2.26%	0.34%	12.26%	0.05%	1.69%	0.00%	0.60%	3.82%
42	Fun	Basidiomyc	Agaricomycetes	Agaricales	Tricholoma	Calyptella	9	16.4%	0.36%	7.9%	0.05%	0.49%	0.44%	0.00%	0.21%	0.00%	0.06%	0.00%	0.00%	0.00%	0.61%	4.27%	0.00%	0.00%	8.25%	0.00%	3.02%	0.00%	0.60%	1.57%
43	Fun	Basidiomyc	Agaricomycetes	Agaricales	X	OTU 207	21	12.4%	0.27%	3.1%	0.01%	0.00%	0.00%	0.00%	0.49%	0.00%	2.09%	1.01%	2.47%	0.00%	0.21%	3.34%	1.45%	0.00%	0.00%	0.23%	0.11%	0.07%	0.57%	0.85%
44	Fun	Basidiomyc	Agaricomycetes	Agaricales	Psathyrella	Coprinopsis	23	5.8%	0.13%	2.6%	0.01%	0.35%	0.39%	0.47%	0.00%	0.00%	0.00%	0.11%	0.10%	0.37%	0.04%	0.09%	0.53%	3.04%	0.31%	0.08%	0.20%	0.02%	0.56%	0.20%
45	Fun	Ascomycot	Sordariomycete	Hypocreale	Nectriacea	Calonectria	16	6.2%	0.13%	0.9%	0.06%	0.94%	0.09%	0.47%	0.36%	0.72%	0.67%	0.93%	0.50%	0.21%	0.08%	0.25%	0.50%	0.28%	0.06%	0.68%	0.08%	0.00%	0.56%	0.29%
46	Fun	Basidiomyc	Agaricomycetes	X	X	OTU 31	11	39.0%	0.85%	31.9%	0.02%	0.00%	0.00%	4.25%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	1.19%	0.53%	0.00%
47	Fun	Ascomycot	Leotiomycetes	Helotiales	X	OTU 160	34	7.7%	0.17%	1.4%	0.01%	0.07%	0.00%	0.79%	0.05%	0.00%	0.63%	0.39%	0.26%	0.32%	0.11%	0.52%	1.75%	0.90%	0.00%	1.14%	0.25%	0.05%	0.52%	0.38%
48	Fun	Ascomycot	Dothideomycet	Capnodiale	Davidiellac	OTU 1866	20	6.5%	0.14%	0.9%	0.01%	0.66%	0.28%	0.16%	0.39%	0.44%	0.41%	0.39%	0.53%	0.99%	0.61%	0.93%	0.09%	0.28%	0.57%	0.23%	0.20%	0.00%	0.51%	0.38%
49	Fun	Fungi incer	Zoopagomycot	Zoopagale	Piptocepha	Piptocephalis	20	6.3%	0.14%	1.9%	0.02%	0.00%	0.13%	0.13%	0.05%	0.68%	0.00%	0.20%	0.03%	1.31%	0.44%	0.00%	2.38%	1.35%	0.00%	0.36%	0.14%	0.01%	0.50%	0.40%
50	Fun	Basidiomyc	Agaricomycetes	Agaricales	X	OTU 459	1	3.5%	0.08%	3.5%	3.51%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	4.00%	0.00%	0.00%	0.50%	0.00%
51	Fun	Ascomycot	Leotiomycetes	Helotiales	Dermateac	Neofabraea	12	9.4%	0.20%	3.9%	0.02%	1.64%	0.80%	1.07%	0.00%	0.50%	0.41%	0.00%	0.00%	0.05%	0.00%	0.00%	0.95%	0.14%	0.04%	0.49%	4.18%	0.00%	0.49%	0.80%
52	Fun	Pseudofun	Oomycetes	Pythiales	Pythiaceae	Pythium_F	32	6.7%	0.15%	1.1%	0.01%	0.44%	0.54%	0.28%	0.23%	0.57%	0.37%	0.17%	0.14%	0.85%	0.17%	0.09%	1.43%	0.84%	0.04%	0.60%	0.37%	0.02%	0.48%	0.41%
53	Fun	Ascomycot	Sordariomycete	X	X	OTU 294	18	5.2%	0.11%	1.4%	0.01%	0.75%	0.00%	0.19%	0.05%	0.44%	0.17%	1.43%	1.51%	0.45%	0.00%	0.05%	0.00%	0.51%	0.00%	0.00%	0.00%	0.01%	0.48%	0.22%
54	Fun	Ascomycot	X	X	X	OTU 279	9	5.9%	0.13%	2.4%	0.09%	0.14%	0.00%	0.00%	0.18%	0.00%	0.09%	0.00%	0.19%	1.09%	1.87%	2.57%	0.00%	0.00%	0.10%	0.00%	0.31%	0.00%	0.48%	0.34%
55	Fun	Ascomycot	Leotiomycetes	Helotiales	Helotiales i	Tetracladium	24	7.8%	0.17%	1.4%	0.01%	0.84%	0.74%	0.50%	0.64%	0.35%	0.32%	0.34%	0.29%	0.05%	0.61%	0.80%	0.12%	0.51%	1.45%	0.36%	0.37%	0.01%	0.47%	0.57%
56	Fun	Basidiomyc	Agaricomycetes	Agaricales	Strophariac	Stropharia	9	8.9%	0.19%	4.2%	0.01%	3.75%	0.00%	0.00%	4.67%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.04%	0.47%	0.58%
57	Fun	Basidiomyc	Agaricomycetes	Auricularial	X	OTU 519	4	3.3%	0.07%	3.1%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.09%	3.69%	0.00%	0.05%	0.06%	0.00%	0.47%	0.02%
58	Fun	Fungi incer	Mortierellomyco	Mortierellal	Mortierellac	OTU 2532	14	4.4%	0.10%	0.7%	0.07%	0.12%	0.09%	0.38%	0.13%	0.55%	0.24%	0.53%	0.16%	0.43%	0.08%	0.18%	0.74%	0.62%	0.00%	0.75%	0.00%	0.00%	0.44%	0.18%
59	Fun	Ascomycot	Dothideomycet	Pleosporal	Melanomm	OTU 161	38	6.6%	0.14%	1.3%	0.01%	0.16%	0.07%	0.35%	0.41%	0.17%	0.15%	1.43%	0.45%	0.32%	0.06%	0.45%	0.39%	0.17%	0.14%	0.49%	0.06%	0.06%	0.44%	0.21%
60	Fun	Basidiomyc	Agaricomycetes	Auricularial	X	OTU 375	7	5.4%	0.12%	1.7%	0.04%	0.00%	0.00%	1.80%	0.15%	0.00%	1.69%	0.00%	0.00%	0.13%	0.00%	0.00%	0.00%	0.00%	0.04%	1.53%	0.54%	0.00%	0.43%	0.30%

Table 5. Output from the RDP classifier showing the relative abundance of each fungal taxon in each of the 8 translocated turves (grey columns) and 8 receiver site quadrats sampled at the Severalls site. The top 60 most abundant taxa across the translocated turves are shown here. On the left are the taxonomic descriptions, with CHEG taxa highlighted in orange (waxcaps) or yellow (fairy clubs). Summary data are presented on the right.

Table 6. List of CHEGD species detected via eDNA at the Severalls site, with species only detected in 2020 surveys listed in red font. Data for the original 2016 samples are shown in light blue and translocated soils from 2020 in light green. Summary data for the original soils, the translocated turves and receiving soils are shown in pink highlight. For species present in either the translocated or receiving soils, boxes shaded dark green indicated turves where a given species was found in both translocated and receiving soils and yellow boxes indicate were a given species was found only in the translocated soil.

		SUMMARY			2020 soil sampling														2016 soil sampling (grouped by area)				
	Species	Tot2016	TotIN20	TotOUT20	214_I	214_O	215_I	215_O	216_I	216_O	217_I	217_O	218_I	218_O	219_I	219_O	220_I	220_O	221_I	221_O	Area1	Area3	Area5	Area8	Area11
C1	*Camarophyllopsis schulzeri*	29802																			13158	9	143	14862	1630
C2	*Clavaria acuta*	5637	41	110				2	3	7	9	65	18	36			8		3		319	251	2740	424	1903
C3	*Clavaria amoenoides*	418	16										16								264	0	0	0	154
C4	*Clavaria fragilis*	7247	31				11				9						11				41	6999	205	2	0
C5	*Clavaria guilleminii*	178	11						2						9						18	6	77	2	75
C6	*Clavaria incarnata*	157		3				3													0	0	0	157	0
C7	*Clavaria roseaAFF*	2622	14		2						2				10						0	0	113	88	2421
C8	*Clavaria sp. BRACR 16032*	3438	3						3												0	0	0	2	3436
C9	*Clavaria sp. JMB10061001*	455	11								9						2				41	0	13	187	214
C10	*Clavaria straminea*	5527	52	29	10	2		8	2		38	7	2	12							2319	280	2195	475	258
C11	*Clavulinopsis corallinorosace*	589																			22	84	28	219	236
C12	*Clavulinopsis corniculata*	9857	130	2			2	2	18		39				69		2				3182	0	0	6672	3
C13	*Clavulinopsis helvola*	50574	27	29	4		15		5	9		20							3		3291	11223	10605	23935	1520
C14	*Clavulinopsis laeticolor*	2882	31						2		29										0	0	0	0	2882
C15	*Clavulinopsis luteoalba AFF*	6038	5	23							3	23			2						1404	4074	49	89	422
C16	*Clavulinopsis sulcata*	566																			0	2	564	0	0
C17	*Hodophilus foetens*	12	301	10													301	4		6	0	0	0	10	2
C18	*Ramariopsis crocea*	1906	4												2		2				297	71	639	448	451
C19	*Ramariopsis kunzei AFF*	4153	36	114											11	114	25				0	51	896	6	3200
C20	*Ramariopsis pulchella*	3261	25	179				68		78	23	31			2					2	544	1148	1048	0	521
C21	*Ramariopsis sp. JMB-2011*	784																			0	21	14	540	209
G1	*Geoglossum fallax*	12194	8	128					3	33		95			3		2				3601	1017	6339	17	1220
G2	*Geoglossum simile*	75	17												6		6		5		0	0	0	75	0
G3	*Glutinoglossum glutinosum*	941	104	24	19		4	3			26			21	55						293	251	276	74	47
G4	***Trichoglossum hirsutum***		8												8						0	0	0	0	0
G5	***Trichoglossum octopartitum***			50				43												7	0	0	0	0	0
D1	***Dermoloma cuneifolium***		26	686			15	508	11			178									0	0	0	0	0
H1	*Cuphophyllus pratensis*	12804	257						3		180				37				37		5	7	0	64	12728
H2	*Cuphophyllus russocoriacea*	77	2	253						169	2	84									6	6	3	62	0
H3	*Cuphophyllus virgineus*	6577	16	2999			2	35	2	1974	3	990			9						1159	687	1918	2811	2
H4	***Gliophorus irrigatus***		7						7												0	0	0	0	0
H5	*Gliophorus laetus*	36911	55												5				50		4	11	2	9	36885
H6	*Gliophorus psittacinus*	1250	8						2								6				1118	0	0	0	132
H7	*Hygrocybe ceracea*	20567	2														2				14	11052	4865	4617	19
H8	*Hygrocybe acutoconica*	16267	267	228			7		5			226	16				171		68	2	3248	16	527	8	12468
H9	*Hygrocybe chlorophana*	4040																			3	0	0	4037	0
H10	*Hygrocybe coccinea*	32																			0	0	32	0	0
H11	*Hygrocybe conica*	16684	594	236	3		12	21	33		213	12	66	8	23	193	237		7	2	3619	6432	2	1354	5277
H12	*Hygrocybe glutinipes*	22064	71										19				52				17235	14	4	4793	18
H13	*Hygrocybe pseudoconica*	6565																			16	6540	0	0	9
	Total No .Fungal Sequences	544408	34583	40796	4443	5348	3421	4321	4854	5772	3971	6694	4545	5242	4748	4250	4209	5331	4392	3838	108888	102252	94388	122459	116421
	Total No. CHEGD Sequences	293151	2180	5103	38	2	68	693	101	2270	585	1731	137	77	251	307	827	4	173	19	55221	50252	33297	66039	88342
	%CHEGD	53.8%	6.3%	12.5%	0.9%	0.0%	2.0%	16.0%	2.1%	39.3%	14.7%	25.9%	3.0%	1.5%	5.3%	7.2%	19.6%	0.1%	3.9%	0.5%	50.7%	49.1%	35.3%	53.9%	75.9%
	No. CHEGD species	36	31	17	5	1	8	10	15	6	14	11	6	4	15	2	14	1	7	5	26	24	25	29	29
	No. waxcap species	12	10	4	1	0	3	2	6	2	4	4	3	1	4	1	5	0	4	2	11	9	8	9	9

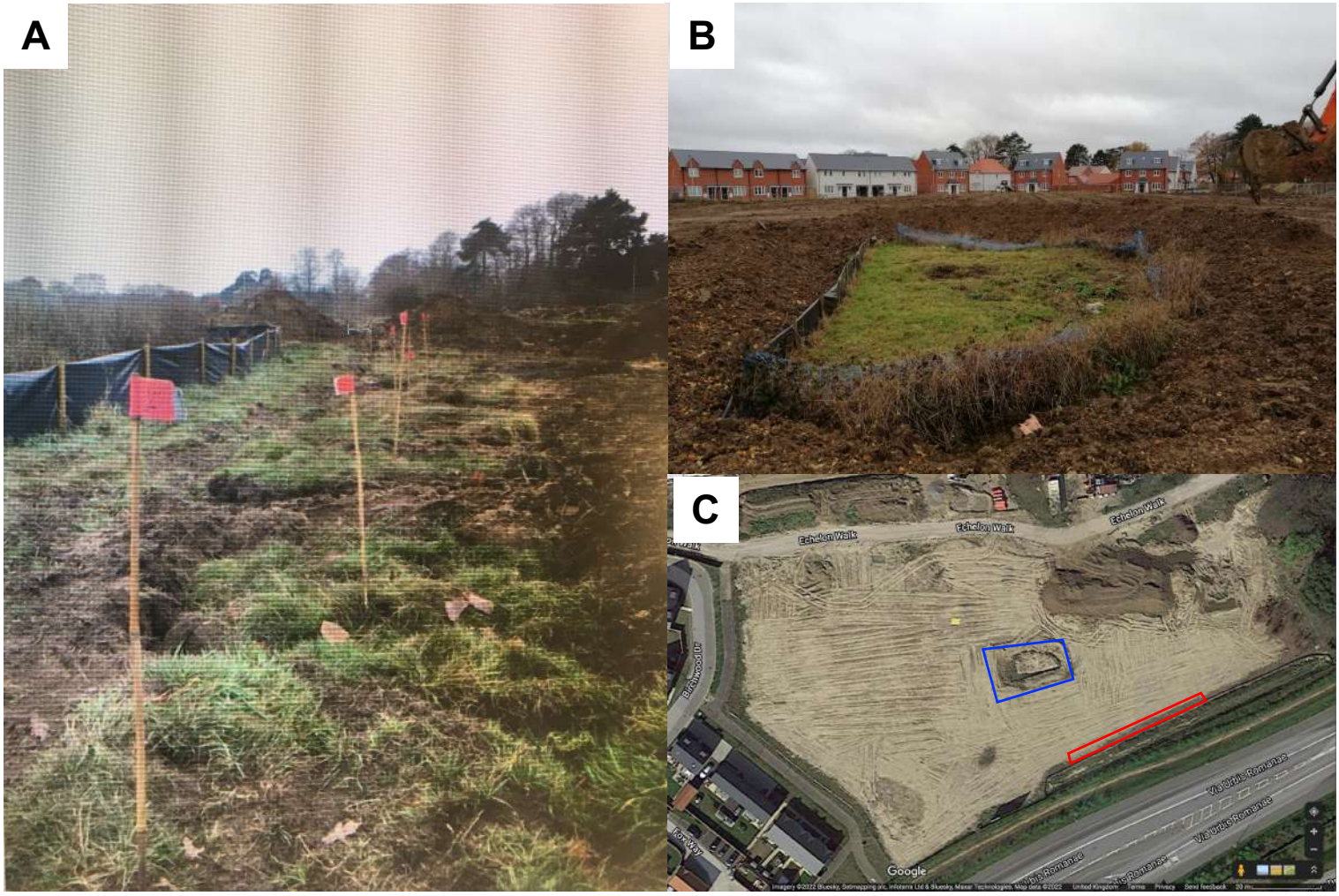

Fig. 7. Red flags (A) indicate the initial storage site area from XX 2017(black fence is reptile receptor site boundary). The cores were later moved to storage site 2 in XX 2018. The red flags which initially identified each monolith were lost in transit. The map (C) shows the relative locations of the two storage sites on the former cricket pitch at the south of the site (now levelled as a recreational area).

<u>Severalls translocation timeline</u>:

1) 10th Oct 2016: APD/EB initial sampling of marked 1m^2 turves in five areas (1,3,5,8,11; 5 turves per area)

2) Spring 2017: Turves translocated to storage site 1 (south end of cricket pitch) at south of site (51.9163,0.8975).

3) Turves had to be relocated in January 2018 to 2nd storage area.

4) Turves moved to final locations in December 2019 -into retained (undisturbed) grassland areas around the three Airing shelters.

5) Soil cores taken on 4th November 2020 for 2nd eDNA analysis of waxcaps

Fig. 8. Stage (3) of turf monolith translocation process: transfer from the storage area. Turves were excavated from the storage site using a large digger bucket (ca. 100 cm wide; A) used to translocate the intact turf monoliths. Initial attempts involved placing the turf directly ono wooden pallet (B,C) with the pallets located on adjacent hardstanding. A smaller tipper truck was used for final placement of some turves (E) and a digger bucket for others (F).

Fig. 9. Stage 3 of turf monolith translocation process: final placement on the turves in the destination area. The receptor site is at the SE end of the site (A,B,C). A hole (1m x 1m 1m deep) was dug(D) and the monolith fragments transported to the receptor site in a digger bucket and dropped into the hole. As can be seen the structure of the monoliths had degraded during storage.

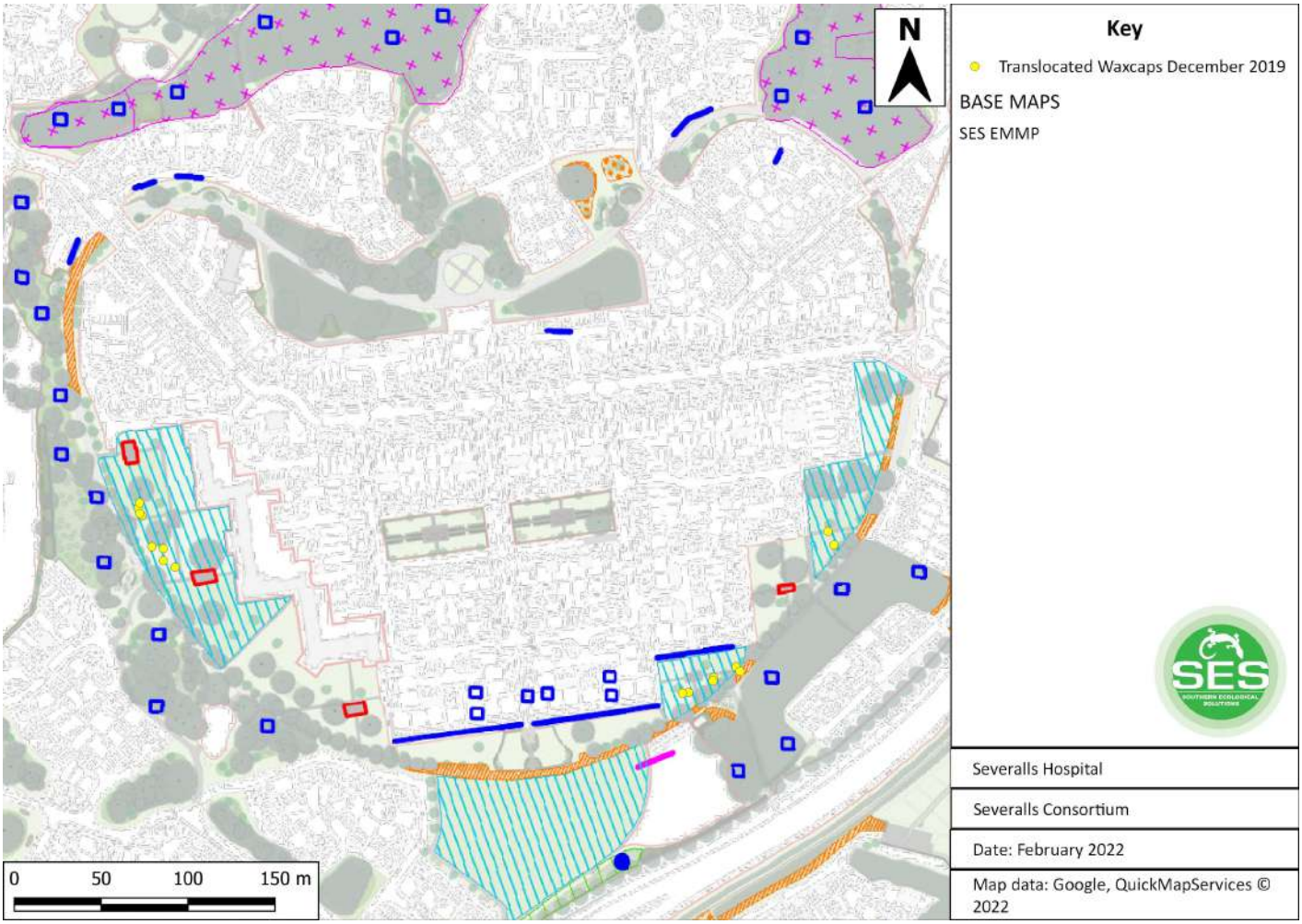

Fig. 10. Final location of the translocated turves in the peripheral retained grassland areas.

Fig. 11. Sampling of the receptor site on 4th November 2020, 11 mths after the placement of the monolith. Cores were taken as outlined above (A-D). Some mushrooms (nn-waxcap) were observed at the receptor site during sampling but not directly on the translocated turves (E).


2000
© 2021 Infoterra Ltd & Bluesky
Google Earth
Imagery Date: 1/1/2000 51°55'24.43" N 0°53'18.28" E elev 47 m eye alt 1.12 km


10Sept 2006
© 2021 Infoterra Ltd & Bluesky
Google Earth
Imagery Date: 9/10/2006 51°55'28.28" N 0°53'25.81" E elev 48 m eye alt 1.12 km


2009
Image © 2021 Getmapping plc
Google Earth
Imagery Date: 1/1/2009 51°55'28.24" N 0°53'27.55" E elev 49 m eye alt 1.12 km


2May/2017
Google Earth
Imagery Date: 5/2/2017 51°54'57.80" N 0°53'24.91" E elev 51 m eye alt 1.12 km


26 June 2018
Google Earth
Imagery Date: 6/26/2018 51°55'28.33" N 0°53'32.61" E elev 48 m eye alt 1.12 km


10 April 2020
Google Earth
Imagery Date: 4/10/2020 51°55'09.11" N 0°53'51.14" E elev 50 m eye alt 1.12 km