**Establishing a long-term monitoring scheme: working with citizen scientist beekeepers to monitor the health of the UK countryside**

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**Abstract**

Insect pollinators such as bees depend heavily on flowering plant resources found across complex, and often intensively managed, landscapes. Changes in the availability of these floral resources has been a major contributing factor to pollinator declines and may interact with other environmental stressors, such as climate change or disease, to affect population persistence. Monitoring changes in these resources at national scales provides an opportunity to understanding large scale temporal risks to pollinators posed by land use change and so can inform spatially targeted policy-based practices to minimise these impacts. The National Honey Monitoring Scheme (NHMS) was established in 2018 and aims to use honey bees as a model system for monitoring flowering plant resource in a spatially and temporally resolved manner at national scales. This scheme uses environmental DNA (eDNA) approaches to identify plant DNA (largely pollen grains) suspended in honey collected directly from the comb of hives provided by citizen scientist beekeepers. Honeybees represent a generalist pollinator, and while wild species will have distinct foraging preferences, they provide distinct advantages in terms of the ethics (i.e. no direct sampling of wild bees), their wide national coverage and association with other metadata (e.g. ecotoxicology for pesticides). To-date 5,789 unique honey samples from England, Wales, Scotland and Northern Ireland have been assessed. In addition, the scheme has established an archive of these honey samples that has been used to deliver post regulation monitoring of pesticide exposure risk, quantification of emergent pharmaceuticals contaminants, disease risks and support qualification of commercial honey sugar solution adulteration assessments. In this paper, we describe how the NHMS was established and give an overview of data generated thus far. By providing insights at national scale, we hope this scheme can provide key evidence for policy decisions associated with the management of intensively managed systems, such as agricultural and urban environments.

**Keywords: h**oney, eDNA, pollinator, landscape, honey bee, *Apis mellifera*

**Introduction**

Insect pollinators provide critical ecosystem services worldwide, with an estimated contribution to UK crop yields of *c.* £500 million annually provided by a range of insect taxa, although honey bees and wild bees are likely to be a dominant contributor to this service [1]. There is clear evidence for widespread declines across all insects, with van Klink *et al.* [2] identifying a 9% per decade decline in global abundance, and more specifically for wild insect pollinators with Powney *et al.* [3] identifying a 33% since 1980 in Great Britain. The causes for pollinator declines are thought to be diverse, and include pesticides, diseases, invasive species and climate change, although in many cases the consequences of these factors are underpinned by habitat loss and landscape simplification critically impacting access to floral foraging resources and nesting sites [4, 5]. This can be particularly problematic in many agricultural systems, where intensive arable and pasture management promotes low wild plant abundance and diversity [6-8]. There is evidence that many environmental factors associated with pollinator declines interact with reductions in diet quality, including exposure to pesticides and susceptibility to disease [9, 10]. The European honey bee (*Apis mellifera* L.), while representing a managed domesticated species, has also undergone widescale declines often associated with a diaspora of factors leading to colony collapse disorder [11-13].

Although the expansion of earth observation approaches to land use mapping have dramatically improved our understanding of landscape scale resources quality for pollinators, at a fundamental level these represent surrogates for actual floral resource availability [14, 15]. These floral resources can be dramatically impacted upon by local management or environmental conditions, such that relatively coarse landscape scale habitat classification fail to capture the diversity of local floral resources resulting from management, regional species pools and historical legacy effects [6, 7]. Attempts to understand distributions of foraging resources at national scales by inference are valuable but are prone to biases linked to assumptions dictated by the resolution of the underlying data [15, 16]. Spatially and temporally explicit monitoring at national scales of the availability of foraging plants and their utilisation by pollinators has important utility for targeted conservation measures [17]. The honey bee provides an opportunity to act as a model system for understanding impacts of many of these drivers of wild pollinators, in particular wild bees. This is because: 1) honey bees are managed as livestock, disease control and supplementary feeding means that they are kept in almost every environment with c. 288,000 hives [18] in the UK. As a result a very comprehensive geographical cover exists that in practice is not seen for wild bee species. This is particularly true in the UK where there is a dramatic longitudinal shift with the result that many wild species are very spatially restricted [6]; 2) beekeepers represent an engaged community willing to participate in citizen scientist projects with a demonstrated track record in the UK of providing stored hive products like honey for analysis scientific studies [19, 20]. Importantly, this community is trained in the safe extraction of stored hive products and is used to systematic record-keeping as part of good hive management practices; 3) there are limited ethical considerations for the collection of stored products from hives compared to comparable sampling from wild bee species. This is particularly true where sampling involves killing wild pollinators; 4) honey bees provide insight into pollinator resource utilisation. Although each species of wild pollinators may differ to honey bees in their foraging preferences (e.g. oligolectic or polylectic species) [21], local competitive interactions [22] or differences in foraging range [23], as a generalist forager honey bees will provide information on the range of plant species likely to be in flower. This provides an indication of wider resource available for foraging by wild bee species, even if that range may not be fully realised on a species-by-species basis; 5) honey bees integrate information on foraging resources over large areas, with mean foraging distances reported to be on average 1.4 km from hives [24].

Filling this knowledge gap at the national scales is a daunting task and one likely to be beyond the resources of most research projects relying on professional field monitoring. However, engagement with such beekeeper citizen scientists provides an opportunity to address this in a cost-effective manner. Existing or planned citizen science projects involving pollinators have focussed predominantly on wild pollinator populations, either in terms of assessing their presence at a location (i.e. occupancy) determined through ad hoc sightings or via more systematic structure monitoring programs. Systematic monitoring of populations includes the various European Butterfly Monitoring Schemes as well as proposed or implemented UK and European Pollinator Monitoring Schemes [25, 26] or the US National Native Bee Monitoring Network [27]. Distributional data describing occupancy of species in locations is also widely collected, including those from the UK Bees Wasps & Ants Recording Society (BWARS). While these schemes often include information on associations between pollinators and wild plants, these represent single interactions capturing only one of many unobserved foraging events of that pollinator. Such observations are prone to failing to understand the full spectrum of foraging interactions seen over the course of weeks due to limitations in sampling effort [17, 28]. As such they provide only limited insight into the scope of foraging resources available for generalist species at landscape scales. Information on longer-term foraging patterns has the potential to provide critical insights into foraging resource utilisation over time periods likely to impact on population level processes [29, 30].

Here we report on the National Honey Monitoring Scheme (NHMS) which attempts to address this current knowledge gap in resource availability and utilisations by pollinators at a national scale, while also providing an archive of samples for targeted questions on the impacts of land use and environmental change. In the following we will report how advances in an environmental DNA (eDNA) based approach for plant identification can be used to analyse DNA derived from honey (majority from pollen) to identify foraging plants utilised by the colony linked to explicit spatial, temporal and other beekeeper provided metadata [31-35]. Pollen is ideally suited to this process as it is both ubiquitous and robust to degradation, with DNA markers that differ between species but being relatively conserved within species [36]. In this paper we describe in detail how the NHMS was established, give an overview of data generated to-date and focus on the value of citizen scientist beekeeper and honey bees as a cost-effective means of monitoring the status and change in floral resources for pollinators (and other insects) at the national scale.

**Materials & Methods**

From its inception the NHMS aimed to establish the first UK-wide, long-term monitoring program of managed pollinators. The scheme relies upon citizen scientist beekeepers collecting honey samples throughout the beekeeping season (April to October) from across the UK. Honey collected by the scheme was initially intended as a resource for tracking foraging preferences of honey bees using plant metabarcoding of honey DNA, but has become a resource for future studies by establishing an archive of honey samples which has potential to address future research priorities over inter-annual timescales.

*Establishment of the scheme*

The scheme was initiated by the UK Centre for Ecology & Hydrology (UKCEH) and was officially launched on 1st July 2018 after consultation with the UK’s national apicultural bodies for amateur (the British Beekeepers Association - BBKA) and professional (Bee Farmers Association - BFA) beekeepers. This initial consultation phase was used to identify limiting factors to uptake of the scheme, key approaches to publicising and acquiring beekeeper participants, expectations from participants of data dissemination, as well as approaches to limit participation fatigue and membership loss rates over time. Stakeholders were also critical in the scope of additional metadata that may be collected from beekeepers including information on hive productivity, management and diseases and their treatment. Stakeholder engagement was also critical in the decision to focus on honey stored in combs as opposed to pollen that is actively collected and stored as beebread. It was advised that largescale collection either directly from combs or using pollen traps would be less appealing to beekeepers and reduce both participation and retention in the scheme. Stakeholder consultation was also used to design user-friendly web-based portals as well as subsequent type and frequency result dissemination. This included proposals for email updates, member web portals for accessing results and newsletters. The stakeholder groups also supported development of ‘how to’ videos to standardise sample collection methodology.

*Recruitment of beekeepers*

Advertising the scheme was achieved though the BBKA newsletters as well as other industry targeted magazine articles and promotion though attendance at apicultural conventions. A website (Supplementary Figure 1) and Twitter/X account were created to publicise and explain the scientific aims of the scheme, enabling enquiries from interested beekeepers and updates to be posted on the scheme. The website was also used as the portal for members to participate and order sampling packs. After consultation with the BBKA and BFA outreach to the beekeeping community was integrated into the project so that regular presentations at national or regional beekeeping shows were provided, as well as presentations to regional or local beekeeping societies. Further publicity to promote interest in the scheme was sought by providing articles for specialist beekeeping publications (e.g. [37, 38]) as well as placing adverts in trade magazines.

*Honey sample collection by beekeepers*

Figure 1 gives an overview of the process by which beekeepers request a sampling pack and receive notifications of sample receipt and processing. Briefly, beekeepers create an account on the online portal – accessed *via* the NHMS website – and provide the location of the hive they intend to sample from (Supplementary Figure 2) in order to request a sample pack. Sample packs are posted to the beekeeper and contain sampling instructions (Supplementary Figure 3) and links to online tutorial demonstrations by a professional beekeeper. Beekeepers are asked to label the sample tubes with the date that the sample was collected, and this is updated in the online portal when the sample arrives at UKCEH. The beekeeper receives an email update each time the status of their sample changes (e.g. arrives at UKCEH) or information is added to the online portal. Further details of sample pack requests, initial sample processing and refractometer measurement can be found in Supplementary Methods. The online system was designed not to allow more than two sampling pack requests per beekeeper for project resource reasons, however, it was noted that some beekeepers set up multiple online accounts using different email addresses to be able to request more sampling packs. This was identified by the spatial reference of the hives provided in their metadata.

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| **Figure 1:** Flowchart of the process that participating beekeepers and the honey samples go through, from creating an online account to sample collection and return to UK Centre for Ecology & Hydrology (UKCEH) for analysis. |

*Collection of associated sample meta-data from beekeepers*

Once a beekeeper has created an account and requested a sampling pack they are requested to answer 12 additional questions relating to the hive they collected the honey samples from (Table 1). It is not compulsory for the beekeeper to answer these questions, but it enables the scheme to explore associations between hive metadata and plant abundance and pesticide results from the corresponding honey sample.

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| **Optional question** | **Response options** |
| Beekeeper status | Amateur  Commercial |
| Which race of bee did you use in the selected hive? | Buckfast  Hybrid  *Apis mellifera* *carnica*  *Apis mellifera mellifera*  *Apis mellifera ligustica*  *Apis mellifera macedonica*  Other (please specify) |
| What is the hive type? | Commercial  Dadant  Flow hive  Langstroth  National Deep 14 x 12  National standard  Smith  Warre  WBC  Other |
| Number of hives kept at location over the last 12 months? | [number] |
| What is the estimated yield to date of honey from this hive for this year (lbs)? | [number] |
| If the above estimate of yield is based on multiple hives at the same locations (rather than the single hive you collected the sample from), how many hives is this? | [number] |
| Will you sell honey from this hive? | Yes  No |
| How would you rate the strength of this hive? | Good  Average  Weak |
| For 10 hive disorders (American foulbrood, European foulbrood, stonebrood, chalkbrood, nosema, chronic bee paralysis, deformed wing virus, cloudy wing virus, sacbrood virus, varroa) beekeepers were asked:  Have you had it?  Did you treat for it?  Have you still got it?  Unsure if you had it?  What treatments were used and when? | [box ticked for “yes”]  [box ticked for “yes”]  [box ticked for “yes”]  [box ticked for “yes”]  [text] |
| Did you give your bees additional feeding last year? | Yes  No |
| If you keep multiple hives at this site, over the past 12 months how many hives have you lost, if any? | [number] |
| If you keep multiple hives at this site, have you had any additional notable issues over the past 12 months? If yes, please give more information (e.g. failing queens, predation by wasps, poor winter survival etc.). | [text] |
| **Table 1:** Optional questions relating to honey yield and health of the hive sampled from for the scheme that participating beekeepers can access from their online account. | |

*Using eDNA barcoding to identify forage plants*

While honey is ostensibly nectar in origin it contains suspended pollen grains. The identification of such pollen grains from honey has a commercial use in terms of validating the origin of honey sold for human consumption, e.g. for monofloral honeys like Manuka or varieties from specific habitats such as heathland. However, the extension of this approach to all plant DNA suspended within honey provides an opportunity to quantify what plant species were foraged upon. Full details of the protocol for detecting plant taxa in NHMS honey samples are published in [39]. An initial small sample from the tube is extracted to test moisture content using a handheld refractometer (Supplementary Figure 4) with samples deviating from the expected 80% sugar being noted as being at risk from fermentation or microbial growth [40]. Then 15 g of honey is transferred into a 50 ml tube, which is filled to 50 ml with molecular grade water (Corning, USA) and heated at 56oC for one hour with regular vortexing. Wax is then filtered from the honey-water mixture using a Stomacher® bag (Seward, UK) and the filtrate passed through a sterile 1.2 µm membrane filter (Merck, Germany) using Nalgene reusable bottle top filter assembly. Vacuum suction is applied to the Nalgene filter to draw the honey-water filtrate through the membrane filter such that pollen grains and associated DNA are collected on the membrane filter. This membrane filter is folded into a cryogenic vial (Corning, UK) and stored at -80oC.

DNA is extracted from filters using a modified protocol [39] for the DNeasy® PowerPlant Pro Kit (Qiagen, Germany). Between 0.5-2 ng of extracted DNA is amplified using universal plant metabarcoding primers internal transcribed spacer 2 (ITS2) region in combination with dual-index barcodes [41], allowing the pooling of 384 honey samples into one sample for sequencing, and optimised for sequencing using Illumina MiSeq v3 chemistry (Illumina, USA) [42]. Prior to sequencing, each PCR amplicon is visualised by gel electrophoresis and any sample without a strong band in the region of 450-500 bp is not taken forward to sequencing. Following sequencing, sequences are de-multiplexed to originating samples and processed through the open access HONEYPI pipeline [43]. Data output from the HONEYPI pipeline consists of an identified list of taxa, and number of associated sequences found in each sample. Taxa identified as plants are phylotyped (grouped) to most resolved taxa, usually to species level. To ensure that curation of data is standardised within and between years quality control of the data is implemented. This involves checking numbers of reads in negative controls to ensure no contamination has occurred and checking there is similar sequencing depth between samples and across the dual-indexed primer plates, to ensure primers are performing equally. Sequenced samples are rarefied to a number of reads that ensures sufficient sequencing depth whilst maintaining sample numbers and excluding negative controls.

*Landcover habitat data associated with individual hives*

Local habitat data within a 2km radius of georeferenced sampled hives was extracted each year from satellite-derived land cover and cropping data products (Supplementary Table 1). The UKCEH Land Cover Maps (LCM) [14] detail 21 land cover classes for Great Britain and Northern Ireland including arable and horticulture, different classes of grassland, woodland, wetland, and upland systems, many of which are linked to UK Biodiversity Action Plan Broad Habitats [44]. We used the finest scale raster datasets available: 25m for all but LCM 2021, when the 10m dataset was released (Supplementary Table 1). Due to the timings of LCM publication versus data extraction, earlier data extractions used LCM 2015 while later extractions the previous year’s LCM (in practice this delay mirrors processing times for honey eDNA analysis; Supplementary Table 1). UKCEH Land Cover® *plus*: Crops (LC+ Crops) are vector datasets detailing annual crop classes per arable field parcel [45]. Crop classes include important flowering crops like oilseed rape, field beans and grass leys which provide nectar and pollen, as well as cereals. The number of crop classes increased from 11 to 16 between 2018 and 2022 by the diverging of existing classes to create new ones (Supplementary Table 1). Habitat data was extracted using ArcMap 10 [46] for hives sampled in 2018-2022, and RStudio [47] for hives sampled in 2023 to handle the finer-scale data.

*Dissemination of findings to participants*

Dissemination of results to participant beekeepers operated at three main levels. The first level of data dissemination is at the individual beekeeper level through information provided *via* their online user account. Beekeepers are sent the plant species detected in the honey sample they collected. These data are visible to beekeepers as a bar chart showing the 15 most abundant plant taxa in their honey samples, given as the scientific name and common name, and a list of all plant taxa detected in the sample (Supplementary Figure 5). In addition to this, information is provided on crops and habitats radius surrounding the hive to a 2km radius. These results are visible to beekeepers as two separate pie-charts: one detailing crops in the 2 km surrounding their hive and one detailing habitats (Supplementary Figure 6). Below the pie-charts are listed crops and habitats surrounding the hive that were detected in quantities too small to show on the pie-charts. The 1-4% of locations for which data were not uploaded were locations in Ireland or the Channel Islands, as these are not covered by the UKCEH Land Cover Maps.

The second level of data dissemination is targeted at members of the scheme and provide summary annual statistics through a newsletter. This is intended to maintain interest in the scheme and help create a community of members to maintain fidelity to the scheme over time. Over time the community has developed independently, with beekeeper forums expressing considerable interest and discussion when results are released.

The final level of dissemination to participants is though targeted stakeholder engagement talks provided to both local, regional and national beekeeper organisation.

In accordance with UK General Data Protection Regulation(GDPR) regulations, the personal details provided by participants in creating their account and requesting a sampling pack are stored within an Indicia database hosted at UKCEH and can only be accessed by members of NHMS staff with password-protected administrative rights to the website. When metadata is downloaded from the website for data analysis the file is saved on a network drive that only members of NHMS staff have access to. Assignment of a unique eight-digit code to each sample ensures that participant personal data is not visible to those processing the samples. The NHMS newsletter is sent from a password-protected account and all participants are automatically blind carbon copied on emails, so that their identity and email address are not shared with other participants. There is an option at the bottom of the newsletter allowing participants to unsubscribe from the mailing list and participants may contact UKCEH’s Data Protection Officer at any time to request their data is removed from NHMS records.

**Results**

*Participation in the scheme*

In the scheme’s launch year, 2018, 251 beekeepers requested a sampling pack (Supplementary Table 2) with this rapidly increasing to 780 sampling pack requests in 2019 and increasing again from 1,414 through to 1,864 between 2020 and 2022. As of 2023 the scheme significantly reduced the number of sampling packs provided to beekeepers for reasons of eDNA barcoding costs with the aim of reducing processed samples to 384. As a result, there were 1,026 pack requests in 2023 and 767 in 2024. The majority of samples have been sent in from the South of England (Figure 2). Despite attempts to recruit more beekeepers from the North of England and Scotland, the East of England, South East of England, London and South West of England typically composed on average between 55-62% of samples (Supplementary Table 3). Attempts were made from 2023 onwards to increase the proportion of samples collected from other regions, resulting in a reduction to 49% of 2023 samples being collected from the East of England, South East of England, London and South West of England and 45% of 2024 samples (Supplementary Table 3). Although samples from 2018 were predominantly from July and August reflecting the late start date of the scheme, from 2019 onwards samples were provided from April, with numbers gradually increasing until August whereafter they dropped off thereafter (Figure 3). Not all sampling packs led to the return of samples, with for example in the scheme’s first year 188 of the 251 sent out being returned. The return rate was, however, remarkably consistent between years at between 70% to 79% (Supplementary Table 2).

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| **Figure 2:** Red dots indicate the location of hives that honey samples were collected from in 2018, the year the scheme started, and hive locations sampled from in 2022, which was the year in which the greatest number of samples was collected. |

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| **Figure 3:** Number of honey samples collected per month from 2018-24. |

*Meta-data provided by beekeepers*

The percentage of beekeepers who responded to each of the twelve optional questions in the online questionnaire once they had requested a sampling pack is shown in Supplementary Figure 7. The lowest response rates (<10%) occurred in 2018 and 2019 for beekeeper status, race of bee, hive type, intention to sell honey and whether additional feed was given to the sampled hive, and in 2018 for the number of hives kept at the location sampled. Despite there being the lowest response rates to certain optional questions in 2018, there were also the highest response rates to other questions in this year: >68% of beekeepers sharing their estimated honey yield for the year, the strength of the sampled hive, diseases observed in/treatment given to the sampled hive and the number of hives lost at sampled location for 2018. The optional question with the lowest response rates across 2018-24 was for the number of hives harvested at the location sampled (24-44%). Overall, between 34% and 56% beekeepers responded to the optional questions across the five years.

Across all years, the percentage of beekeepers who provided notes about notable issues in the past 12 months in hives kept at the location sampled (e.g. failing queens, predation by wasps, poor winter survival) ranged from 33% to 48% resulting in 2,970 comments. Upon inspection, some comments purely stated “no”, “none” or “N/A” – after removal of these comments there were 2,243 comments detailing problems with hives. The most reported issues were failed or failing queen(s), predation by wasps and drone-laying, followed by varroa infestation and disease, including chalkbrood, sacbrood, nosema, European foulbrood (EFB) and chronic bee paralysis virus (CBPV). The top 100 words used in these comments are shown in Supplementary Figure 8.

*Honey DNA analysis*

In 2018, 2019 and 2021, pollen data was produced for 95-98% of the returned honey samples (Supplementary Table 2). The 2-5% of returned samples for which plant DNA data was not produced in these years were samples that did not produce a strong band upon visualisation by gel electrophoresis, which means the DNA extraction and/or PCR amplification step of the Honey DNA analysis pipeline was unsuccessful for this sample. In 2020 and 2021, honey DNA data was produced for 70-74% of the returned samples. This reflects the number of samples that can be included in a sequencing run (*n =* 384). In 2018 all returned samples fitted into one sequencing run and in 2019 all returned samples fitted into two sequencing runs; however in 2020 the decision was made to continue with two sequencing runs, which fitted 775 of the 1113 (70%) returned samples. In 2021, due to the increase again in returned sample numbers, three sequencing runs were financed and were able to fit the majority of the returned samples, whereas in 2022 the three sequencing runs fitted 74% of the returned samples. At the time of writing, honey DNA data was being generated for 2023 and 2024 samples.

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| **Figure 4:** stylised plots showing distributions of five plant genera (*Brassica, Trifolium, Impatiens, Rubus* and *Myosotis*) detected *via* plant DNA in honey collected from four UK geographical bands. “Scotland” is comprised of Scotland alone. “North” is comprised of NUTS regions for North West England, North East England, Yorkshire and the Humber, Isle of Man and Northern Ireland. “Midlands” is comprised of Wales, West Midlands, East Midlands and East of England. “South” is comprised of South East England, South West England and London. |

Figure 4 is a stylised representation of typical plant DNA data that is generated from a year of honey samples to clearly show data trends across sample months and between geographies. A detailed breakdown of the top 40 plant genera detected in samples can be found in Supplementary Figure 9. Figure 4 shows data for samples collected between May and September, when most samples are collected, and shows the distribution of five dominant plant genera across four geographical bands of the UK: Scotland, North, Midlands and South. The five dominant plant genera are *Brassica* (yellow; predominantly oil seed rape but also cruciferous vegetables), *Trifolium* (purple; *Trifolium repens* or white clover), Impatiens (pink; *Impatiens glandulifera* or Himalayan balsam), *Rubus* (pale blue; brambles) and *Myosotis* (*Myosotis sylvatica* or woodland forget-me-not). Other plant genera are shown in grey for the purpose of Figure 4. When plant DNA data is visualised overall for the UK the trends are dominated by data from the southern regions, as this is where the majority of samples were collected, whereas if geographical bands are structured by longitude different trends emerge. All geographical bands see dominance of *Brassica* in May and June samples when oil seed rape flowers and a rise of *Rubus* in July to September when most bramble species flower; however *Rubus* is much more dominant in the South and Midlands than in the North or Scotland. By contrast, *Impatiens* – which represents the invasive species Himalayan balsam – is much more dominant in the North than in other geographical bands. It is interesting to note that most plant genera detected from DNA in honey in the North, Midlands and South are represented by the five genera shown in Figure 4, whereas Scotland has a much greater diversity of forage that is shown in grey as “other species”.

*Landscape context of sampled hives*

Figure 5 shows an example distribution of crops and landcovers in the 2km surrounding the hives that samples were collected from. A full breakdown of crop and landcover percentages is given in Supplementary Table 3 for each year from 2018 to 2022. At the time of writing, habitat data was in the process of being generated for 2023 and 2024 samples.

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| **Figure 5:** example breakdowns of habitat data for 2 km surrounding sampled hives averaged by year. The top pie-chart shows crop data, where “Other” is a designated crop category and “Winter Beans” and “Spring Beans” are combined due to low values. The bottom pie-chart shows landcover data, with “Heather”, “Littoral Sediment”, “Heather Grassland”, “Calcareous Grassland”, “Saltmarsh”, “Saltwater”, “Supralittoral Sediment”, “Fen Marsh Swamp”, “Supralittoral Rock”, “Littoral Rock” and “Bog” combined into “Other” due to low values. |

*Recruitment and retention of participant beekeepers*

Key to recruitment of the scheme in the early years was ongoing interaction between the scheme researchers and the beekeeping community, including e-mail updates, newsletters and presentations for beekeeping societies. Subscription to the NHMS newsletter is used as an indicator of interest in the scheme. As of June 2025, the NHMS newsletter had a total 4,950 individuals on its mailing list who had created an account on the website from 2018-2025, of which 4,649 (94%) were still subscribed. This means that 301 (6%) individuals opted to unsubscribe from receiving the newsletter at some point after creating an account. Mailchimp communication software has recorded an average open rate of newsletters as 61.5% thus, at current subscription numbers, approximately 4,370 individuals will open a newsletter. Frequently reported complaints by beekeepers linked to the scheme relate to delays in the provision of honey DNA derived foraging data. These delays originated both from the COVID epidemic shutting or laboratories as well as due to personnel changes critical to sample processing.

**Discussion**

In this paper we describe the establishment and running of the National Honey Monitoring Scheme (NHMS) over the first five years following its inception. With over 3,500 beekeepers involved and 5,789 honey samples collected between 2018 to 2024 the scheme has been a citizen science success story and shown rapid growth in beekeeper participation. At present we believe this to be one of the largest citizen science projects involving eDNA in operation worldwide. We have shown the viability of using honey bees as “environmental monitors” that through their large foraging ranges integrate information on resource utilisation of wild, crop and ornamental garden plants at landscape scales. The information on resource utilisation has produced a valuable data set for understanding long term consequences of changing management of the UK countryside and its likely impact on pollinators though forage availability. This data has the potential to be combined with other spatially explicit data sets, including those on landcover data, crop types, pesticide use, or climate. for the 2 km radius surrounding each hive and metadata provided by beekeepers regarding hive health and honey yield produces a large and multi-faceted dataset that will provide valuable insights into honey bee health and foraging behaviours under different environmental pressures.

***Why the scheme has been successful***

There are multiple reasons for the scheme’s success. Firstly, it was setup in consultation with the BBKA, BFA and beekeepers such that those who would be participating in the scheme were involved in its design. This is crucial when designing and implementing any citizen science project to ensure it is accessible and of interest to those you wish to participate but was particularly important for this scheme because collecting honey samples from a hive of ~50,000 bees presents challenges that may not be evident to a non-beekeeping researcher. Secondly, the team running the scheme invested substantial time and energy into advertising it through presentations at beekeeping conferences, articles in beekeeping magazines and talks to beekeeping associations. Coupled with word-of-mouth between beekeepers, this engagement resulted in news of the scheme spreading rapidly through the beekeeping community. Thirdly, and this cannot be understated, is the motivation of the beekeepers themselves to take part in the scheme. Many individuals take up beekeeping because of an interest in pollinators and the environment and are therefore enthused to contribute to a citizen science initiative researching both. Likely the greatest motivation for beekeepers is finding out, free-of-charge, what their bees have been foraging on when they receive the results from plant DNA analysis of their honey sample. This is information a beekeeper cannot easily find out unless they, or someone they know, is experienced in melissopalynology or they pay a company that offers honey analysis as a service. The low number (4%) of beekeepers who have unsubscribed from receiving the newsletter indicates that interest in the scheme is being maintained, even though only a percentage of these subscribers are submitting samples each year, such that receiving honey DNA analysis data cannot be the only motivator for being involved in the scheme.

***Trends in participation in the scheme***

The increase in participation in the scheme between 2019 (777 sampling pack requests) and 2020 (1,414 sampling pack requests) may have been influenced by the COVID-19 pandemic when lockdown measures resulted in individuals spending more time at home and therefore having greater capacity to register and take part in the scheme. It is not possible to know whether the scheme would have experienced the same participation rates in the absence of these measures, but the continued growth of the scheme in post-lockdown years suggest that the scheme would have proved successful with or without the pandemic. The majority of honey samples are sent in from southern regions of the UK. It is likely that the distribution of the honey samples we receive reflects the distribution of honey bee hives in the UK, but this cannot be verified as there is no publicly available map of all registered honey bee hives in the UK. As the scheme asks beekeepers to provide honey samples, it may also be that beekeepers with greater honey yields are more likely to spare honey for testing and that beekeepers in the south of the UK experience greater yields than those in the north due to more favourable weather conditions for honey bee foraging. It is also possible that, because the scheme is run from the UKCEH site based in Wallingford in Oxfordshire, the team has had greater engagement with beekeepers and beekeeping associations based in the south of England. While this may apply to in-person events, the NHMS team have made concerted efforts to engage with beekeeping associations further afield via recorded presentations available on the website, online presentations and articles in nationwide beekeeping magazines in order to recruit beekeepers from the North of England, Wales, Northern Ireland and Scotland.

***Biases within the data***

As a voluntary participation scheme the NHMS has inherent sampling biases associated with who wishes to participate, and when they decide to do so. There are clear geographical biases, as described already, with sample representation being overwhelmingly from the South of England. In part this simply reflects the greater number of beekeepers linked to the higher populations of people in the south of the UK. However, this has not been the only driver of this bias: an early failure to interact sufficiently with regional country-specific beekeeping societies may have hindered participation in these regions. Over the longer-term, significant effort has been made to increase participation in these areas, e.g. Scotland and Wales.

Samples provided to the scheme show strong temporal patterns with the peaks occurring in May/June and August corresponding to honey harvests in Southern England, where the majority of samples have been collected from. It is generally accepted in the beekeeping calendar that honey bees utilise a first nectar flow from mid-April to end of May and a second nectar flow from mid-June to early August and will complete the concentrating and capping of honey in the weeks following these nectar flows. As a result of these distinct nectar flows we would expect to see a marked transition in floral resources being foraged throughout the year.

It speaks to the motivation of participating beekeepers that up to 46% of samples (in 2020) were a result of multiple submissions throughout the year. Perhaps unexpected was that beekeepers would setup multiple accounts using different email addresses to get around the limit of two sampling pack requests per year per account. While a possible drawback of this to the scheme is a cluster of sample collections from small geographical areas of the UK, it also opens the possibility of investigating how forage patterns change between seasons from the same hive or apiary or across subsequent years.

***Provision of additional metadata***

It is encouraging, and valuable to the scheme, that ~50% beekeepers who requested a sampling pack each year opted to complete the optional questions in the online questionnaire that they were directed to after requesting a sample pack. Beekeepers are encouraged, if they train with a beekeeping association, to keep meticulous records of their hives during hive checks - recording the behaviour of their bees, weather conditions, signs of disease and honey yield – so many will have these data to-hand already and have proved willing to share them with the scheme. It is important to note that answering these questions is not required to submit a honey sample for plant DNA analysis and thus further indicates an interest in the scientific outcomes of the scheme. This provision of metadata has resulted in an unexpected bonus for the scheme in that there is a comprehensive dataset of hive observations, coupled with landcover data, for hive locations that did not necessarily return honey samples or whose honey samples were not included for DNA analysis. Even without the plant sequence data, these data and observations can be used to look for associations between land-use, honey yield and observed bee disease. It is important to note that the quality of these data may vary with beekeeper experience, particularly in relation to identification of diseases, which can be hard to identify in some cases. Even so this information remains highly complementary to the data on resource utilisation.

A benefit of using a citizen science approach to sample collection is the geographical coverage that can be achieved by many individuals collecting samples simultaneously, instead of one researcher or research group attempting to collect samples from all over the UK at the same or different time points. With this comes a significant reduction in finances spent on staff time and resources. As of March 2023, it was calculated that the collection, processing and honey DNA sequencing of a single honey sample cost ~£250 – the majority of which was staff time spent on sampling pack preparation and sample processing. If staff were required to travel and collect the samples too, the per sample cost to the scheme would have been considerably higher.

***Opportunities for exploiting the honey archive***

There is growing interest in the use of honey bees for environmental monitoring [48-50] and the scheme has been an important proof-of-concept for this approach. The scheme has accumulated over 5,500 honey samples in its archive since 2018 and these samples are likely to contain a wealth of eDNA. This eDNA may, for example, allow detection of honey bee pathogens and parasites within the hive [51], plant pathogens present in the area surrounding the hive [52], or even provide an early warning of Asian Hornets in the vicinity of the hive via detection of airborne eDNA [53]. The data already accumulated by the scheme has the potential to address numerous pressing environmental questions including the impacts of land use or climate change on the availability of critical forage resources. The scope of this dataset to answer these questions across time (2018-2024) and geographical space (the whole of the UK) is currently unparalleled.

In addition, the archive of honey samples provides additional resources for understanding environmental pressures on honey bees with this having direct relevant for wild pollinators and in particular wild bees. It is obviously simplistic to assume resource utilisation by honeybees reflect that of wild bees, however there will be species specific differences between all species resulting from either preference or competitive exclusion [54-56]. However, honeybees are relatively short tongue generalists and so likely have significant cross over in flowering resources utilisation with many wild species, a fact that may lead to competition in some cases [54-56]. Currently, collaborations have been initiated with wider partners in the research community to understand exposure to pharmaceuticals in honey resulting from bioaccumulation in pharmaceutical residues originating from the sue of sewage biosolids used as a soil conditioner on arable fields, to identify commercial honey adulteration by sugar solutions, and to determine the asymptomatic prevalence of important bee diseases such as Nosema, Foulbrood and Chalkbrood. From 2019 onwards, pesticide residues have been assessed from honey samples to support the UK Government indicator of ‘Exposure and adverse effects of chemicals on wildlife in the environment’ to inform its 25 Year Environment Plan [57]. This is intended to understand long term changes in risk of pesticide exposure from agricultural, domestic and urban amenity use of pesticides and currently uses gas and liquid chromatography–mass spectrometry to quantify, as of 2024, 135 herbicides, fungicides and insecticides [58]. Plant DNA sequencing in honey can also be used to track the emergence and spread of invasive plant species within the UK; with the invasive Himalayan Balsam (*Impatiens glandulifera*) being an example of such a species frequently detected within honey samples. Such assessments may also provide insights into how invasive species are integrating into pollinator trophic interactions with wider plant communities [59]. Additionally, the application of alternative molecular techniques to the archived DNA (such as quantitative PCR and metagenomics) has the potential to expand beyond forage distribution to address important questions on how pollinators interact with other multi-kingdom members of the landscape, like fungi, viruses, arthropods and microbes [51, 60, 61].

**Conclusions**

Environmental monitoring is critical to understand long term changes in environmental quality and provides an opportunity to implement reactive mitigation measures at large scale to address the identified risks. As such, long term monitoring is critical to supporting regional and national policy decisions and can help provide an evidence base for conservation-based non-governmental organisations. However, the cost of such monitoring is often highly prohibitive and in many cases this means that significant limitations are placed on its temporal or spatial replication, or monitoring is inferred though indirect approaches such as earth observation satellite imagery. Here we have shown how citizen scientist beekeepers can inform this process by providing information of multi-trophic patterns in biodiversity and resource utilisation from plant species occurrence to resource utilisation by honey bees. Given the huge economic value of pollinators in supporting crop and wild plant pollination as well as the socio-economic role of beekeeping specifically this information has multifaceted value. Importantly, we have found beekeepers to be highly engaged and scientifically-minded citizen scientists who have contributed valuable metadata and geographically widespread samples to the scheme, in a cost-effective manner, which is crucial for our understanding of how environmental change impacts pollinator health and success. Currently the scheme costs ~£150 to barcode plant DNA within the honey, while additional analyses such as pesticide residues may quadruple this figure and do not account for general scheme running costs. Such running costs place at risk the long-term viability of this scheme, however, it is the continued duration of these national scale data sources that justifies their value allowing trends over time to be assessed and related to larger scale drivers of change such as climate.

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