DOI: 10.1002/2688-8319.12349

REGISTERED REPORT STAGE 1

Impacts of polycultural cropping on crop yields and biodiversity: A systematic map protocol

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Handling Editor: Kira Borden

Abstract

- 1. Agriculture is currently the largest driver of biodiversity-loss worldwide. There is a critical need to develop agricultural systems that protect and promote biodiversity, while also meeting local and global food needs. Ecological theory suggests that cultivating crops in diverse mixtures both maximises niche occupancy and generates additional niches, generating both higher yields *and* higher biodiversity than cultivation in monocultures. A large and growing body of agronomic research provides strong evidence for the potential productivity and biodiversity benefits of in-field crop-diversification strategies. This protocol sets out a methodology for a systematic map of evidence on yield- and biodiversity-outcomes in '*polycultures*'—systems of cultivation where multiple food crop species are grown together simultaneously at field-scale.
- 2. Systematic searches with a global scope will be conducted in Web of Science Core Collection, Scopus, and CAB Abstracts to yield a comprehensive sample of relevant published, peer-reviewed literature. The articles returned by searches will be subject to eligibility screening according to pre-defined inclusion criteria, at successive stages (title and abstract, and full text). Following this, we will extract data from eligible studies on study designs, survey and sampling protocols, experimental treatments and comparators, and outcomes measured.
- 3. A narrative synthesis, illustrated by tables, figures and maps, will describe the quantity and characteristics of the available evidence on the impacts of polycultural cropping on (i) crop yields, and (ii) agroecosystem biodiversity. We will also identify the research that examines these two outcomes in parallel. The synthesis will be accompanied by a published database containing bibliographic information as well as data (see '2') on study characteristics and outcomes.
- 4. *Practical implications*. The anticipated systematic map will provide a synthesis of current evidence regarding the potential yield- and biodiversity-impacts of polycultural cropping. We will identify key knowledge gaps, and 'clusters' of related evidence that could lend themselves to further quantitative synthesis via subsequent systematic reviews and/or meta-analyses. As such, the work will facilitate future appraisal of the potential of polyculture as a tool to bridge the currently

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Evidence

conflicting priorities of food production on the one hand and biodiversity conservation on the other.

KEYWORDS

agro-ecology, biodiversity, intercropping, land-sharing, land-sparing, mixed cropping, polyculture, yield

1 | **INTRODUCTION**

Global biodiversity-loss is occurring at a faster rate than at any previous time in human history, and agriculture-driven land use change is the principal driver of this trend (Benton et al., [2021](#page-8-0); Cardinale et al., [2012](#page-8-1)). At the same time, recent projections (reviewed in van Dijk et al., [2021](#page-10-0)) suggest that global food demand may increase by 35%–56% for the time period 2010–2050 (Alexandratos & Bruinsma, [2012](#page-8-2); van Dijk et al., [2021](#page-10-0)). These twin pressures present a critical challenge for humankind. How to ensure food security for the world's population, while simultaneously protecting and restoring the world's biodiversity?

Two contrasting models—termed '*land sparing*' and '*land sharing*' (Fischer et al., [2014](#page-8-3))—are commonly proposed as strategies for reconciling food production with conservation of biodiversity. In a *land sparing* approach, some land is set aside for wildlife, while productivity is maximised in high yielding, conventionally intensified agricultural areas. Conventional intensive monocultures are inhospitable environments for all but a small proportion of species (Geiger et al., [2010;](#page-8-4) Tilman, [1999](#page-10-1)), many of which acquire 'pest' or 'pathogen' status due to a combination of a superabundance of available food (Martinez et al., [2021](#page-9-0)), and the low predator populations associated with these landscapes. Crops bred to thrive in intensive monocultures typically depend upon high fertiliser and pesticide inputs, and application of these products has resulted in their near-ubiquitous pollution of soils, freshwaters, and oceans (Fowler et al., [2013](#page-8-5); Silva et al., [2019](#page-10-2)).

Organic farming typifies the *land sharing* approach; the use of artificial inputs is prohibited or otherwise strictly limited, and although not universally the case (Tscharntke et al., [2021](#page-10-3)) organic farms tend to support greater on-farm biodiversity than conventional farms (Geiger et al., [2010;](#page-8-4) Tuck et al., [2014](#page-10-4)). Critically, though, organic cropping systems tend to suffer substantial yield-penalties compared to industrial cropping systems, and thus require a larger land-footprint to produce equivalent quantities of food. Meta-analytical studies of organic-conventional yield comparisons record different yieldgaps for different crop types; with rice, legumes and fruits showing the smallest differences, and cereals, root and tuber crops showing the largest (de Ponti et al., [2012](#page-8-6); Meemken & Qaim, [2018](#page-9-1); Ponisio et al., [2015;](#page-9-2) Seufert et al., [2012](#page-10-5)). Across all crop-types, mean yield gaps in organic farming are thought to average 19%–25% (Meemken & Qaim, [2018](#page-9-1)). Assuming constant food demand, widespread conversion from conventional intensive to organic farming (with the aim of better 'sharing' agricultural land with the rest of nature) would

BOX 1 What do we mean by *polyculture***?**

For the purpose of this research, we define polyculture as the simultaneous cultivation of multiple crop species and/ or genotypes, together at field-scale. This definition distinguishes polyculture from mixed mono-cropping (where crop diversity occurs between fields on a farm, rather than within fields), and from rotation cropping (where crop diversity occurs temporally between successive plantings or growing seasons). Crop species in a polyculture field may be fully mixed, with limited or no distinct arrangement, or may be arranged in neighbouring rows, or strips containing multiple rows. Critically, crop species are grown in closeenough proximity to allow biological interactions to occur between them (see Sections [1.1](#page-2-0) and [1.2](#page-2-1) below). Such interactions may occur at hyper-local spatial scales, for example, between the roots of neighbouring crop species, or over larger spatial scales, for example, via the impacts of component crop species on mobile invertebrate communities.

Our map will be focussed on *food-crop polycultures*—where the component crops in mixtures are harvested for food and/or feed (rather than for fibre, timber, or bioenergy). Food-crop polycultures are employed around the world; typically in small-scale, high-labour, knowledge-intensive subsistence farming where growers cultivate diverse crop mixtures to meet their own and/or local people's dietary needs (Brooker et al., [2015](#page-8-7)). In these contexts, polycultural cropping can promote stability of both yields and income in the face of environmental and market fluctuations (Falkowski et al., [2019;](#page-8-8) Martin-Guay et al., [2018](#page-9-4)), and sustained soil health and nutrient cycling over time, with minimal inputs (Brooker et al., [2015](#page-8-7)). Polycultural techniques remain rare in industrial agriculture, perhaps principally due to the perceived challenges of their implementation at scale.

necessitate further conversion of wild or marginal land in order to bolster yields to required levels (Meemken & Qaim, [2018](#page-9-1)). The resulting loss of undisturbed habitat would come at further detrimental cost to wildlife (Phalan et al., [2011](#page-9-3)).

The existing evidence presented above suggests that neither of these current approaches (*land sparing* or *land sharing*) is a sustainable option for meeting future food demand, in the context of widespread ecosystem degradation, biodiversity loss, and scarcity of available land.

This protocol and subsequent systematic map will examine a third way—'*polyculture*' (see Box [1](#page-1-0))—as an agronomic approach with the potential to avoid the trade-offs commonly associated with land sparing and/or land sharing, and to reconcile two critical priorities (that of food production and biodiversity conservation) which have historically been in conflict.

1.1 | **Crop-diversity—A basis for greater productivity?**

Ecological theory suggests that diversity within a natural ecosystem is an important determinant of its over-all productivity, stability, and nutrient cycling (Tilman et al., [2014](#page-10-6)). A landmark series of grassland experiments conducted over two decades showed that the primary productivity of a grassland ecosystem increased asymptotically with the number of co-occurring plant species and functional groups pre-sent in mixtures (Cardinale et al., [2007](#page-8-9); Hector et al., [1999;](#page-9-5) Tilman et al., [2014](#page-10-6)). Recent research has been devoted to exploring how this biodiversity-productivity relationship might be harnessed in agroecosystems. Can *diversified* agricultural cropping systems go some way toward resembling a natural ecosystem; providing increased and/or more stable aggregate yields when compared with monocul-tural systems (Beillouin et al., [2021](#page-8-10); Brooker et al., [2015;](#page-8-7) Martin-Guay et al., [2018](#page-9-4))?

'Niche complementarity' between crop species combined in polycultures may result in more comprehensive and efficient exploitation of available resources such as sunlight, water and nutrients (Brooker et al., [2015](#page-8-7); Li, Hoffland, Kuyper, Yu, Li, et al., [2020](#page-9-6); Li, Hoffland, Kuyper, Yu, Zhang, et al., [2020](#page-9-7); Ren et al., [2014;](#page-9-8) Yu et al., [2015](#page-10-7)). For example, crops with different rooting depths may access and utilise a larger portion of spatially stratified nutrient and/or water resources (Ding et al., [2021;](#page-8-11) Kremen & Miles, [2012](#page-9-9)), and crops that differ in the timing of their peak growth, maturity and senescence periods may maximise efficiency of light interception in the canopy across the season (Li, Hoffland, Kuyper, Yu, Li, et al., [2020](#page-9-6); Li, Hoffland, Kuyper, Yu, Zhang, et al., [2020](#page-9-7)). Co-occurring crop species may also directly or in-directly 'facilitate' one-another's growth (Brooker et al., [2015](#page-8-7); Ren et al., [2014](#page-9-8)), for example via provision of shade, shelter or structural support, provision of water and/or nutrients (Li et al., [2014](#page-9-10)), or via contributions to biological pest, pathogen or weed control (Letourneau et al., [2011;](#page-9-11) Mutyambai et al., [2019](#page-9-12); Ren et al., [2014](#page-9-8)). It should be noted, however, that competitive or other deleterious interactions may also occur in crop mixtures. Careful selection of appropriate species-partnerships, as well as design of complementary sowing and harvest times, planting densities and spatial arrangements are crucial for maximising positive, facilitative interactions between crop species in polyculture (Ren et al., [2014](#page-9-8)).

A large body of literature provides strong evidence for the potential yield-benefits of in-field crop diversification strategies (Beillouin

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et al., [2021;](#page-8-10) Himmelstein et al., [2017](#page-9-13); Iverson et al., [2014](#page-9-14); Li et al., [2022;](#page-9-15) Li, Hoffland, Kuyper, Yu, Li, et al., [2020](#page-9-6); Li, Hoffland, Kuyper, Yu, Zhang, et al., [2020](#page-9-7); Martin-Guay et al., [2018;](#page-9-4) Xu et al., [2020](#page-10-8); Yu et al., [2015](#page-10-7)). However, the vast majority of research undertaken to date has centred on 'intercropping' trials in grassland, forage, and arable systems, typically with a maximum of two crop species or varieties grown in combination. Research in higher-diversity polycultures, particularly in horticultural settings, remains sparse in the published literature.

1.2 | **Can polycultural cropping support more wild species?**

Increasing the diversity of crop-mixtures in agriculture is expected, in turn, to benefit non-crop biodiversity (Aguilera et al., [2020;](#page-8-12) Lichtenberg et al., [2017](#page-9-16); Rakotomalala et al., [2023;](#page-9-17) Tamburini et al., [2020;](#page-10-9) Tscharntke et al., [2021](#page-10-3)). In contrast to the large-scale patchworks of habitat provided by monocultural fields and the semi-natural features that may occur at their edges, polycultures create a much finer-scale mosaic of habitats *within* the cropped area. Diversified cropping systems can provide greater range—and continuity—of resources over space and time for communities of invertebrates (Brandmeier et al., [2021,](#page-8-13) [2023](#page-8-14); Guzman et al., [2019;](#page-8-15) Lichtenberg et al., [2017;](#page-9-16) Sciligo et al., [2022](#page-10-10)), amphibians (Collins & Fahrig, [2017](#page-8-16)), bats (Monck-Whipp et al., [2018;](#page-9-18) Syafiq et al., [2016](#page-10-11)), birds (Josefsson et al., [2017](#page-9-19); Katuwal et al., [2022](#page-9-20); Yahya et al., [2022](#page-10-12)), and soil microorganisms (Guzman et al., [2021;](#page-8-17) Lai et al., [2022;](#page-9-21) Stefan et al., [2021](#page-10-13)). In turn, increases in the abundance and/or the diversity of agriculturally 'beneficial' species (e.g. pollinators, predators, parasitoids) in polycultures are likely to impact positively on the health and productivity of the cropping system as a whole (Alarcón-Segura et al., [2022;](#page-8-18) Letourneau et al., [2011](#page-9-11); Pereira et al., [2015](#page-9-22)).

However, the impacts of planned crop-diversity on associated wild biodiversity are complex and highly heterogeneous, since individual taxa (with their particular resource requirements, degrees of generalism or specialisation, degrees of mobility, and sensitivity to disturbance, etc.) will respond in different ways to crop diversification at different spatial and/or temporal scales. The influence of crop diversity at the field-scale is often shown to be modulated by the characteristics of the surrounding landscape (e.g. Hass et al., [2018;](#page-8-19) Magrach et al., [2023](#page-9-23); Tuck et al., [2014](#page-10-4)); including the type(s) of agriculture practiced in surrounding fields, and the relative presence or absence of semi-natural habitat features such as hedgerows, woodlands, grasslands and/or water bodies (Martínez-Núñez et al., [2022](#page-9-24)). The identity of the component crops included in polycultures (and their respective functional traits, which determine their value for different wild taxa) can also be highly significant in influencing the responses of other species (Beyer et al., [2021](#page-8-20); Guzman et al., [2019,](#page-8-15) [2021](#page-8-17); Hass et al., [2018](#page-8-19); Martínez-Núñez et al., [2022](#page-9-24)).

As with the existing research on crop diversity and yield, the majority of research on this topic has been focussed on intercropping trials incorporating a relatively small number of crop species. Further

work in higher-diversity polycultures (e.g. in horticultural market gardens (Guzman et al., [2019](#page-8-15), [2021](#page-8-17)) and agroforests (Falkowski et al., [2019](#page-8-8); Lovell et al., [2018](#page-9-25); Pumarino et al., [2015](#page-9-26)))—which might more closely resemble natural ecosystems in that they incorporate a greater multiplicity of crop functional traits and inter-species interactions—would be highly valuable in assessing the potential of polyculture to enhance agroecosystem biodiversity.

2 | **OBJECTIVE OF THE SYSTEMATIC MAP**

Several previous reviews and meta-analyses have investigated the impacts of on-farm diversification strategies (including—but not limited to polyculture) on crop yield (e.g. Himmelstein et al., [2017](#page-9-13); Iverson et al., [2014;](#page-9-14) Li, Hoffland, Kuyper, Yu, Li, et al., [2020;](#page-9-6) Li, Hoffland, Kuyper, Yu, Zhang, et al., [2020;](#page-9-7) Martin-Guay et al., [2018](#page-9-4); Xu et al., [2020;](#page-10-8) Yu et al., [2015](#page-10-7)), and on associated biodiversity (e.g. Iverson et al., [2014](#page-9-14); Letourneau et al., [2011](#page-9-11); Lichtenberg et al., [2017](#page-9-16); Pumarino et al., [2015;](#page-9-26) Rakotomalala et al., [2023](#page-9-17)). Based on our review of these publications and their bibliographies, we estimate that the literature on crop-diversity, crop-yield and associated biodiversity has been comprehensively synthesised up to and including the year 2013. Our report will begin with a narrative synthesis of key findings from these and other reviews relevant to our research topic. In addition, we will focus our own systematic search and screening process on the 10-year period from January 2014 to the present day (see Section [3](#page-3-0)). Our systematic map—with a global scope—will identify and draw together the available evidence base concerning the impacts of polycultural cropping on (i) crop yield and (ii) associated biodiversity. The map will also identify knowledge clusters and gaps, and make recommendations for future research directions.

The aim of this protocol is to devise a method for systematically identifying, collating, and coding relevant published, peer-reviewed journal articles for inclusion in the map. The following research questions have been formulated:

• RQ1: '*What evidence is available regarding the impacts of polycultural cropping techniques on crop yields?*'

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• RQ2: '*What evidence is available regarding the impacts of polycultural cropping techniques on field-scale agroecosystem biodiversity?*'

The research questions have been developed according to the population, intervention, comparator, and outcome elements [PICO (Foo et al., [2021](#page-8-21))] described in Tables [1](#page-3-1) and [2](#page-3-2).

We will also identify and describe the available research which examines the two outcomes of interest (crop yields and biodiversity) in parallel (see Section [3](#page-3-0)).

3 | **MATERIALS AND METHODS**

The mapping exercise will be conducted according to the guidelines and standards set out by the Collaboration for Environmental Evidence (CEE, [2018](#page-8-22)) and will conform to the Reporting Standards for Systematic Evidence Syntheses in environmental research (ROSES—Haddaway et al., [2017](#page-8-23)).

3.1 | **Searching for articles**

An initial exploratory survey of the literature was conducted using the *Web of Science Core Collection* database, in order to inform the identification of appropriate search terms for incorporation into strings. The search terms relate to PICO elements 2 and 4 (Intervention and Outcome, see Tables [1](#page-3-1) and [2](#page-3-2)). Search terms *within* the two PICO categories will be combined in sets using the Boolean operators 'OR' and 'AND'. The two sets will then be combined using the Boolean operator 'AND' (see Boxes [2](#page-4-0) and [3](#page-4-1)). The operator 'NOT' excludes records featuring specific terms that are irrelevant to the research questions. An asterisk (*) is a 'wildcard' that represents any group of characters; as such its use in search terms enables inclusion of multiple word endings. Quotation marks enclose exact phrases. Examples of full search strings (in Web of Science Core Collection format) are provided in Boxes [2](#page-4-0) and [3](#page-4-1). A full list of search strings (customised to adhere to the accepted for-mats of the other databases to be searched) is provided in File [S1](#page-10-14).

TABLE 1 Components of RQ1: '*What are the impacts of polycultural cropping techniques on crop yield?*'.

TABLE 2 Components of RQ2: '*What are the impacts of polycultural cropping techniques on field-scale agroecosystem biodiversity?*'.

BOX 2 Search strings for RQ1 (here presented in Web of Science Core Collection format)

Set 1; Intervention terms:

(Separate searches are carried out in TI (title), AB (abstract) and AK (author keywords) fields, and all three are combined using OR)

TI = (polycult* OR polycrop* OR intercrop* OR inter-crop* OR multicrop* OR multi-crop* OR "mixed crop*" OR agroforest* OR "market garden*" OR "companion crop*" OR allotment^{*}) OR AB=(polycult^{*} OR polycrop^{*} OR intercrop^{*} OR inter-crop* OR multicrop* OR multi-crop* OR "mixed crop*" OR agroforest* OR "market garden*" OR "companion crop*" OR allotment*) OR AK=(polycult* OR polycrop* OR intercrop* OR inter-crop* OR multicrop* OR multi-crop* OR "mixed crop*" OR agroforest* OR "market garden*" OR "companion crop*" OR allotment*).

Set 2; Outcome terms:

(Separate searches are carried out in TI (title), AB (abstract) and AK (author keywords) fields, and all three are combined using OR)

TI = (((((yield* OR productivity OR "LER" OR "land equivalent ratio" OR "overyielding" OR "land use efficiency") NOT (fish* OR pond* OR aqua* OR biofuel* OR bioenergy* OR livestock OR forage*))))) OR AB = (((((yield* OR productivity OR "LER" OR "land equivalent ratio" OR "overyielding" OR "land use efficiency") NOT (fish* OR pond* OR aqua* OR biofuel* OR bioenergy* OR livestock OR forage*))))) OR AK = (((((yield* OR productivity OR "LER" OR "land equivalent ratio" OR "overyielding" OR "land use efficiency") NOT (fish* OR pond* OR aqua* OR biofuel* OR bioenergy* OR livestock OR forage*))))).

The two sets (Intervention terms and Outcome terms) are then combined using AND.

We will refine search-returns for RQ1 by applying a number Web of Science categories (Agronomy; Environmental Sciences; Ecology; Agriculture Multidisciplinary; Plant Sciences; Food Science Technology; and Horticulture). We will also refine both searches by document type (articles and reviews), by language (English) and by publication period (from January 2014 to present).

3.1.1 | Publication databases

Searches will be conducted using three widely-used bibliographic databases; Web of Science Core Collection, Scopus and CAB Abstracts (see customised search strings in File [S1](#page-10-14)).

BOX 3 Search strings for RQ2 (here presented in Web of Science Core Collection format)

Set 1; Intervention terms:

(Separate searches are carried out in TI (title), AB (abstract), and AK (author keywords) fields, and all three are combined using OR)

TI = (polycult* OR polycrop* OR intercrop* OR inter-crop* OR multicrop* OR multi-crop* OR "mixed crop*" OR agroforest* OR "market garden*" OR "companion crop*" OR allotment^{*}) OR AB=(polycult^{*} OR polycrop^{*} OR intercrop^{*} OR inter-crop* OR multicrop* OR multi-crop* OR "mixed crop*" OR agroforest* OR "market garden*" OR "companion crop*" OR allotment*) OR AK=(polycult* OR polycrop* OR intercrop* OR inter-crop* OR multicrop* OR multi-crop* OR "mixed crop*" OR agroforest* OR "market garden*" OR "companion crop*" OR allotment*).

Set 2; Outcome terms:

(Separate searches are carried out in TI (title), AB (abstract) and AK (author keywords) fields, and all three are combined using OR)

TI = ((((divers* OR biodivers* OR richness OR abundance OR assemblage) AND (beneficial* OR "natural enem*" OR predator* OR parasitoid* OR pollinat* OR insect* OR arthropod* OR invertebrate* OR bird* OR bat* OR amphibian* OR mammal*) NOT (fish* OR pond* OR aqua* OR biofuel* OR livestock)))) OR AB = ((((divers* OR biodivers* OR richness OR abundance OR assemblage) AND (beneficial* OR "natural enem*" OR predator* OR parasitoid* OR pollinat* OR insect* OR arthropod* OR invertebrate* OR bird* OR bat* OR amphibian* OR mammal*) NOT (fish* OR pond* OR aqua* OR biofuel* OR livestock)))) OR AK = ((((divers* OR biodivers* OR richness OR abundance OR assemblage) AND (beneficial* OR "natural enem*" OR predator* OR parasitoid* OR pollinat* OR insect* OR arthropod* OR invertebrate* OR bird* OR bat* OR amphibian* OR mammal*) NOT (fish* OR pond* OR aqua* OR biofuel* OR livestock)))).

The two sets (Intervention Terms, and Outcome Terms) are then combined using AND.

3.1.2 | Supplemental searches

Forward searches for citing papers

In addition, we will conduct forward-searches for articles citing the relevant review articles identified during our searches. This will enable us to check for additional recent papers not identified by the search strategy detailed above.

Grey literature and books

Search and screening of book chapters and grey literature at the global scale would be beyond the scope of this systematic map. As such, the map will be limited to published, peer-reviewed journal articles only.

3.1.3 | Assessing the comprehensiveness of the search strategy

The comprehensiveness of the proposed search strategy has been assessed using two test-lists of 10 relevant 'benchmark' articles (10 articles each for RQ1 and RQ2). The test lists were compiled by the reviewing team, informed by their prior knowledge of the topic and by reviewing the bibliographies of relevant review articles. The test lists are provided with this protocol as a supplementary file (File [S2](#page-10-15)). Where articles from the test lists were not captured in initial 'trial' searches, the reasons for their exclusion were identified and the search strings (and associated category-based filters) were refined accordingly. Both test lists were captured fully when finalised searches from all bibliographic databases were combined.

3.2 | **Article screening and eligibility criteria**

3.2.1 | Article screening pilot

As part of the development of this protocol, the reviewing team carried out a preliminary searching and screening pilot (see Table [3](#page-5-0)). First, all records retrieved via the three database searches (6307 in total for RQ1, and 1273 for RQ2) were downloaded to two Microsoft Excel spreadsheets. A random subset of 100 articles was extracted from the spreadsheets (50 each for RQ1 and RQ2). Each of the extracted records was then screened against a set of pre-determined inclusion/exclusion criteria, by two independent members of the reviewing team. Pilot screening was carried out in two successive stages: first on the basis of the title and abstract, and then on the basis of the full text for all articles retained at title/abstract stage. Screening decisions (at both stages) were compared between reviewers, and reasons for any discrepancies were discussed against the inclusion/ exclusion criteria. Where necessary, these criteria were refined for clarity and specificity.

Notably, none of the 100 randomly selected articles accessed during the pilot screening phase met the inclusion criteria for both RQ1 and RQ2 simultaneously. We expect that the volume of articles

addressing both outcomes in parallel will be relatively small. The finalised screening criteria are summarised in Table [4.](#page-6-0)

3.2.2 | Finalised searching and screening protocol

Upon publication of this protocol, the agreed searching and screening process will begin. All records retrieved by searches in the three bibliographic databases will be exported to the web-based collaboration platform Covidence (Covidence Systematic Review Software, [2018](#page-8-24)), where any duplicates will be automatically identified and merged. Each record will then be assessed for inclusion at successive stages, using the pre-defined eligibility criteria (summarised in Table [4](#page-6-0), and appended in File [S3](#page-10-16)).

An initial 'consistency check' will be performed on a subset of the total records to be screened; approximately 5% for each of the two research questions. Inter-reviewer agreement (between two independent members of the review team) will be evaluated by calculation of a Cohen's kappa coefficient (*k*> 0.6 considered as 'consistent'; Séchaud et al., [2022](#page-10-17)). In the case of inconsistent agreement, the reasons for discrepancies will be discussed, and the criteria further clarified and/or refined. Successive rounds of consistency checks will take place until consistent agreement is achieved. Following this, the remaining records will be assessed for inclusion by a single reviewer. All articles retained at the title/ abstract stage will subsequently be screened on the basis of the full text. Inter-reviewer consistency checks will be performed (as above) on successive subsets of approximately 5% of total full-text records. Once consistent levels of agreement are achieved, the remaining full-text records will be assessed for inclusion by a single reviewer.

Where a reviewer is uncertain about whether-or-not to include a publication at the first screening stage, they will tend toward inclusion to the second stage. Where there is further doubt (during full text screening) a final decision on inclusion will be taken via discussion between members of the review team as a whole. Reviewers will not screen studies that they have themselves authored. A list of articles excluded at the full-text screening stage (and the specific reasons for their exclusion) will be provided as a supplementary file with the published systematic map.

Articles that meet the inclusion criteria for both RQ1 and RQ2 at the full-text screening stage (e.g. those which examine both outcomes in parallel) will undergo data extraction for each of the two research questions separately (see Section [3.4](#page-6-1)). In addition, they will be collated in a bibliographical database of all such articles and discussed in the narrative synthesis.

TABLE 3 Pilot screening summary: Numbers of articles screened, retained at each stage, and the estimated number of papers to be included in the final map.

TABLE 4 Criteria for inclusion in systematic map.

3.3 | **Study validity assessment**

We do not plan to undertake a formal critical appraisal of internal study validity, since the focus of the systematic evidence map is simply to draw together the current knowledge base on a complex and relatively broad research topic.

3.4 | **Data coding**

We will extract meta-data from all included studies using pre-piloted data coding templates (working templates appended; see Files [S4](#page-10-18) and [S5](#page-10-19)). The coding templates were developed through piloting the process of data extraction from articles included in our 'test list' of relevant benchmark articles. The data to be coded will include: bibliographic information, details of study characteristics and

design, details of the populations, interventions, and comparators studied, and the types of outcomes reported. Data coding will take place via population of three inter-linked tables (approach adapted from Séchaud et al., [2022](#page-10-17)). The first table—'*References*'—will contain bibliographic information for all articles included. The second table—'*Study Characteristics*'—will record information on study locations, durations and designs, and scales. The final table—'*Evidence Points*' will record information on the populations, interventions and comparators, and outcomes studied, and any additional variables included in factorial experiments. Where multiple independent measures of crop yield and/or biodiversity are reported from a single study, these will be coded in additional separate rows. Studies meeting the inclusion criteria for both RQ1 and RQ2 (i.e. studies that address both outcome variables in parallel) will be coded separately for the two RQs, via the two data coding templates. They will also be collated in a separate bibliographical database.

The data extraction and coding process is designed to provide a useful and structured resource, with sufficiently detailed information to be of use in future work (James et al., [2016](#page-9-27)). It is expected that the data extraction sheet and coding options will be furtherdeveloped in a partly iterative process, expanding the range of options as they are encountered during the extraction phase of the study (following Haddaway et al., [2014](#page-8-25)). The final data extraction sheet (along with detailed coding instructions) will be provided as a supplementary file along with the final report.

To ensure that data extraction is being conducted in a repeatable and consistent manner, all reviewers will extract data from an initial subset of 40 of the articles retained at full-text screening (20 for each research question). The extracted data will be compared, and cases of disagreement or inconsistency will be discussed to improve the repeatability of the extraction process; for example by clarifying the definition of a variable, re-formulating the categories of a variable where there are checklists, or adding additional variables where appropriate. Successive rounds of 'dual reviewer' data extraction (40 papers per round) will continue until it is considered that consistent agreement has been achieved, after which the data extraction process will be continued with a single reviewer extracting data from each included record. Where necessary, data will be extracted from figures using the digital tool 'Data Thief' ([https://www.datathief.](https://www.datathief.org/) [org/](https://www.datathief.org/)).

Once the coding process has been completed, a random sample of the total pool of included articles will be separately coded (for quality assurance), by a reviewer who is independent of the project team (James et al., [2016](#page-9-27)).

3.5 | **Data synthesis and presentation**

We will provide a narrative synthesis of the evidence drawn together through the systematic mapping process. Descriptive texts (structured to answer the two primary research questions) will be illustrated by tables, figures, and maps in order to make the synthesis as visual and navigable as possible. In addition to the narrative synthesis, we will provide a searchable bibliographic database and data extraction tables as supplementary files. These resources will enable other researchers to navigate to primary articles included within the map, or to explore particular research themes in greater detail according to their interests. We will identify key knowledge gaps (areas that are under-represented in the current evidencebase), and 'clusters' of related evidence that could lend themselves to further quantitative synthesis via subsequent systematic reviews and/or meta-analyses (James et al., [2016](#page-9-27)).

4 | **DISCUSSION**

The goal of this project is to produce a systematic map of published, peer-reviewed literature examining the impacts of polycultural cropping on (i) crop yield and (ii) field-scale agroecosystem

biodiversity, in parallel. While we acknowledge that additional valuable information could be gleaned from grey literature sources, we will restrict our searches to peer-reviewed journal articles since we expect these to contain the most robust data. Although no geographical limitations will be placed on literature searches, inclusion will be limited to documents published in the English language due to the language-limitations of the reviewing team. Because of these limitations, the map cannot be said to be a truly 'comprehensive' synthesis at a global scale. We do anticipate, however, that it will include the majority of the literature which has been published to date on the topic.

The proposed map will provide a synthesis of current evidence regarding yield- and biodiversity outcomes in polyculture. We will identify key knowledge gaps, and 'clusters' of related evidence that could lend themselves to further quantitative synthesis via subsequent systematic reviews and/or meta-analyses. As such, the work will facilitate ongoing assessment of the potential of polyculture as a tool for sustainable for future food production—an agronomic approach with the potential to move beyond the classical dichotomy of land sparing versus land sharing—and to reconcile two critical priorities which have historically been in conflict.

AUTHOR CONTRIBUTIONS

The study was conceived by Alfred Gathorne-Hardy, Barbara M. Smith and Daisy A. Martinez. This manuscript was prepared by Daisy A. Martinez, and Alfred Gathorne-Hardy and Barbara M. Smith edited successive drafts. All authors read and approved the final manuscript.

ACKNOWLEDGEMENTS

The authors thank the reviewers for their valuable feedback and suggestions that have considerably improved the manuscript. They also thank Fiona Brown, the Academic Support Librarian in Veterinary Medicine, Roslin Institute and Biological Sciences, and College Lead for Library Academic Support (CSE) at University of Edinburgh, for her guidance and support with developing the search strategy.

FUNDING INFORMATION

Daisy Martinez is funded by the Edinburgh Doctoral College Scholarship.

CONFLICT OF INTEREST STATEMENT

The authors declare no conflict of interest.

PEER REVIEW

The peer review history for this article is available at [https://www.](https://www.webofscience.com/api/gateway/wos/peer-review/10.1002/2688-8319.12349) [webofscience.com/api/gateway/wos/peer-review/10.1002/2688-](https://www.webofscience.com/api/gateway/wos/peer-review/10.1002/2688-8319.12349) [8319.12349](https://www.webofscience.com/api/gateway/wos/peer-review/10.1002/2688-8319.12349).

DATA AVAILABILITY STATEMENT

We will not be archiving any data associated with this protocol, since the protocol does not include data. Once the anticipated systematic

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

File S1: Search strings, customised for each of the three databases to the searched.

File S2: 'Test-lists' of relevant benchmark articles.

File S3: Detailed screening criteria.

File S4: Data extraction template (Research Question 1).

File S5: Data extraction template (Research Question 2).

File S6: ROSES form for the systematic map protocol.

How to cite this article: Martinez, D. A., Gathorne-Hardy, A., & Smith, B. M. (2024). Impacts of polycultural cropping on crop yields and biodiversity: A systematic map protocol. *Ecological Solutions and Evidence*, *5*, e12349. [https://doi.](https://doi.org/10.1002/2688-8319.12349) [org/10.1002/2688-8319.12349](https://doi.org/10.1002/2688-8319.12349)