

<https://doi.org/10.1038/s44264-024-00034-0>

Mineral-ecological cropping systems mitigate biodiversity-productivity trade-offs of the organic vs. conventional farming dichotomy



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Conventional agriculture significantly reduces biodiversity, while organic farming promotes it, but often yields half as much. Addressing this biodiversity-productivity trade-off is crucial for future agriculture. Mineral-ecological cropping systems (MECS) have been suggested as an alternative, blending organic and conventional methods by avoiding chemical-synthetic pesticides and using mineral fertilizers. In a German experiment with 168 parcels, we compared MECS, conventional, and organic systems in terms of ecological and economic performance. Arthropod diversity was measured through standardized species collections and DNA-metabarcoding. Productivity was assessed via yields and economic profits. MECS showed similar arthropod diversity to other farming systems, achieved 90% of conventional crop yields, and produced 1.8 times of the organic yield. Profits from MECS were on average 37% higher than the conventional system with a short wheat-maize-soy crop rotation. Further farm-level studies are needed, but MECS could be a reasonable alternative to both organic and conventional farming and can mitigate biodiversity-productivity trade-offs.

Biodiversity is dramatically declining, primarily due to the expansion and intensification of agriculture^{1,2}, while the food demand of a growing population³ is increasing. Political discourses, such as the European Commission's call to reduce pesticide use and risk by 50% by 2030, underline the need for a more biodiversity-friendly and productive agriculture of the future. Therefore, innovative cultivation systems are urgently needed.

Conventional agriculture relies on mineral fertilizers and chemical-synthetic pesticides for production, both of which can reduce insect diversity². In organic farming, neither chemical-synthetic pesticides nor mineral fertilizers are used⁴. In consequence, organic agriculture usually harbors higher levels of on-field biodiversity, but crop yields are 21% to 26% lower than in conventional farming⁵⁻⁷. Even more, organic cereal yields in Germany are only 51% of conventional cereal yields per unit area⁸. These yield gaps are often due to the lack of plant nutrition, which is not sufficiently covered by organic fertilization, lowering the quantity and quality (e.g. protein content) of organic produce⁹. Hence, yield gaps are a serious problem in organic agriculture. Thus, overall productivity

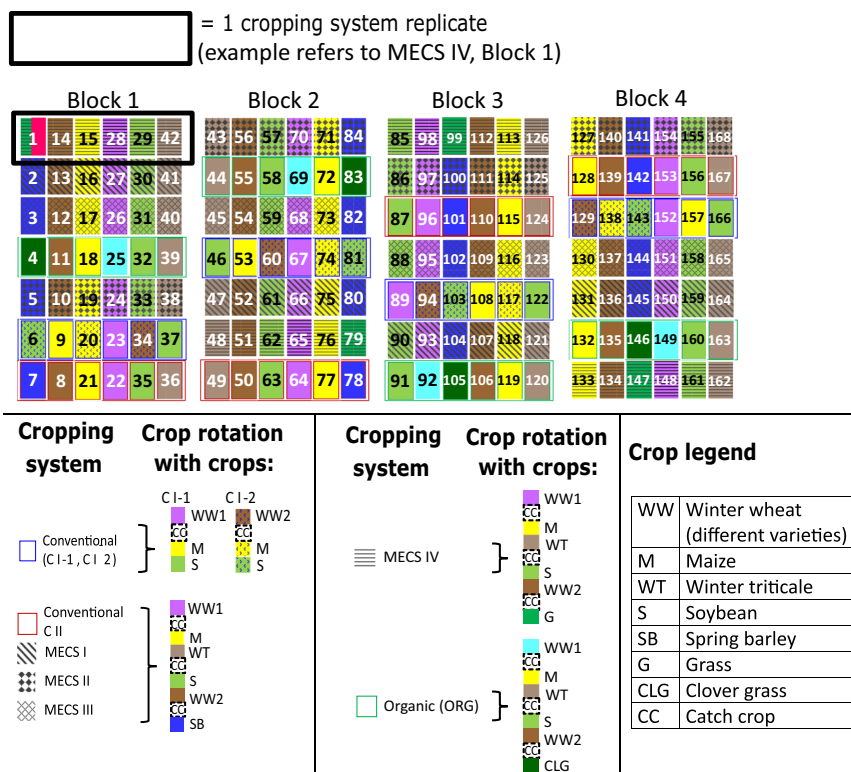
should be considered when choosing a cropping system¹⁰. Farmers also need to think of the profitability of different farming systems¹¹. For example, profits per hectare in organic farming are often double compared to conventional farming¹². As a consequence, we need agricultural systems that are both productive and profitable to encourage farmers' adoption of a new cropping system¹¹.

Recently, mineral-ecological cropping systems (MECS) have been proposed as a potential solution to the trade-off between productivity and biodiversity that characterizes conventional and organic cropping systems¹³. MECS follows an intermediate cultivation system that combines elements of conventional and organic farming. Similar to organic farming, no chemical-synthetic pesticides are used in MECS¹³. Instead, longer and improved crop rotations and new farming methods, such as equidistant seeding, are supposed to suppress weeds. It has been hypothesized that MECS, with their combination of biodiversity-friendly, pesticide-free cultivation methods with an optimal application of mineral fertilizers, should result in high biodiversity and yield¹³.

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Fig. 1 | Experimental setup: Overview of the cropping system replicates and their belonging crop rotations and crops on the experimental farm Heidfeldhof, Stuttgart, Germany. Each cell represents one of 168 numbered parcels organized in a randomized block experiment. Each parcel measured 9 m × 15 m with no space between parcels in one row, but between rows and blocks. Seven cropping systems (conventional I, conventional II, mineral-ecological cropping systems MECS I - IV and organic) comprise six crops each in their respective crop rotation and are replicated four times each (in each block). Each row in a block comprises one cropping system replicate (characterized by the pattern/box). Colors stand for the different crops. Supplementary Data 5 gives an overview of the parcel numbers referring to crop system, block, and crop as well as additional detailed information on applications of chemical-synthetic pesticides (CSP) and Nitrogen fertilizer.

Overview of the Experimental setup (168 parcels)



One of the most species-rich and functionally important taxonomic groups in agroecosystems are arthropods. Epigeic arthropods such as ground beetles, rove beetles and spiders are important antagonists of agricultural pests^{14,15}. Biological pest control is particularly needed in agricultural systems where chemical-synthetic pesticides are not used. Therefore, the promotion of epigeic arthropods in such systems is of particular ecological and economic importance and is frequently analyzed in comparisons of organic and conventional farming systems^{12,16,17}. Additionally, arthropod diversity correlates with other dimensions of field-level diversity, such as weeds or below-ground animal groups¹⁸.

All in all, systematic experimental comparisons of the ecological and economic performance of MECS compared to organic and conventional farming systems are still lacking. In this study, we compared the ecological and economic performance of conventional, organic, and MECS in a large-scale field experiment. In total, seven different cropping systems were studied: two conventional systems, four MECS and one organic system. Using a space-for-time-substitution approach, we studied the arthropod richness and diversity of all crop species of each cropping system in May - July 2022. Additionally, we assessed agricultural productivity in terms of yield and economic profitability expressed as gross margins, considering actual crop yields and multi-year average costs of all farming systems. We hypothesized that MECS show synergistic effects to overcome the trade-off between organic and conventional farming. Compared to conventionally managed cropping systems, we expected a higher arthropod richness. Also, MECS was expected to have a higher gross margin at the system level than the organic cropping system.

Results

Biodiversity and profit of cropping systems

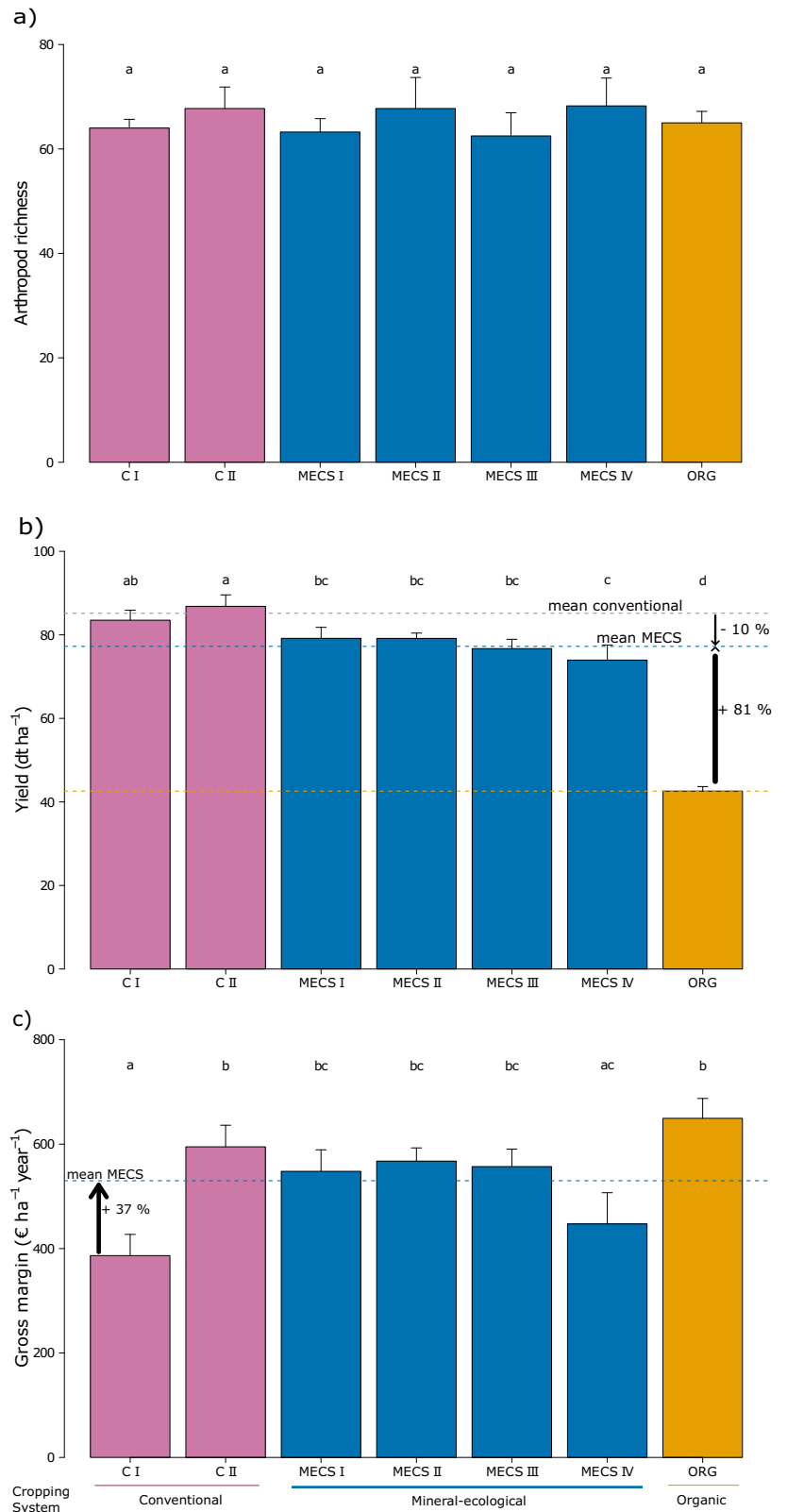
We assessed epigeic arthropod richness and diversity in each of the 168 parcels of the experiment using repeated sampling with pitfall traps, followed by DNA meta-barcoding of the specimen. In total, we identified 380

arthropod species (including taxonomically and genetically distinct species classified by bioinformatics; Supplementary Data 1 and 2). Each of the seven cropping systems comprised six crops in their respective crop rotation, with four replicates per system (details see Fig. 1 and Table 2 in Methods). All measurements per parcel (crop) were aggregated on the level of cropping system replicates. For example, arthropod richness was defined as the sum of all arthropod species of all six crop species in each cropping system replicate (see Supplementary Data 4). Thus, arthropod richness combines alpha diversity per crop species and species turnover (beta-diversity) across crop species within a system's crop rotation.

Arthropod richness at system level ranged from 54 (MECS III) to 84 species (MECS II) across the studied cropping systems (mean = 65 ± 7.5 SD) and did not differ significantly between systems (Likelihood ratio test: $X^2_6 = 2.092$; $P = 0.911$; Fig. 2a). The same was true for the Shannon diversity of arthropods (mean = 3.34 ± 0.20 SD; $F_{6,21} = 0.218$, $P = 0.967$). Neither arthropod richness nor Shannon diversity of arthropods were predicted by vegetation volume, use of chemical-synthetic pesticides, mineral fertilizer, and equidistant seeding (Table 1).

In addition to the biodiversity of the cropping systems, we assessed their agricultural productivity and profitability. Productivity was measured as crop yield per area, while profitability refers to the gross margins of the systems. Gross margins were calculated based on economic benefits from selling the agricultural produce after deducting variable costs for seeds, fertilizers, chemical and mechanic plant protection measures, other variable costs and interest costs (for details on gross margin calculations see Supplementary Data 3). Gross margins were then aggregated for all crops of each cropping system replicate (Supplementary Data 4). Prices were based on multi-year means from 2017-2021, while yields referred to the 2022 harvest in the experiment. Concerning the productivity, MECS (77.24 ± 5.12 dt ha⁻¹ yr⁻¹) achieved on average 90% of the conventional yield (85.17 ± 5.08 dt ha⁻¹ yr⁻¹), and produced 1.81 times the yield of the organic system over the entire crop rotation (42.59 ± 2.18 dt ha⁻¹ yr⁻¹; Fig. 2b and Supplementary Fig. 1). In terms of profitability, gross margins at system level

Fig. 2 | Average arthropod richness (a), yields (b), and gross margins (without subsidies) (c) of the seven cropping systems (mean + standard error). Different letters indicate statistically significant differences between systems ($P < 0.05$; Tukey-Test). **a** Arthropod richness does not differ between the cropping systems. **b** The dashed blue line indicates the mean of all MECS yields, which is 10% lower than the mean of all conventional yields (dashed pink line). Compared to organic yields, average MECS yields are 81% higher. **c** The dashed blue line indicates the mean of all MECS profits, which is 37% higher than the conventional system with a short crop rotation (C I).



ranged between 387 € (conventional I) and 650 € (organic) per hectare and year across systems (overall mean = 536 € ha⁻¹ year⁻¹ ± 111 € ha⁻¹ year⁻¹). Gross margins significantly differed between systems ($F_{6,21} = 4.746$, $P = 0.003$; Fig. 2c). While the conventional cropping system C I including soy achieved the lowest gross margins (mean = 387 € ha⁻¹ year⁻¹ ± 41 € ha⁻¹ year⁻¹), the organic system achieved the highest gross margins

(mean = 650 € ha⁻¹ year⁻¹ ± 38 € ha⁻¹ year⁻¹). The mean gross margins of MECS ranged between 447 € ha⁻¹ year⁻¹ (MECS IV) and 568 € ha⁻¹ year⁻¹ (MECS II). Overall, the mean gross margin of all MECS was intermediate between gross margins of organic and conventional cropping systems, being 37% higher than in the conventional cropping system with short crop rotation C I (all MECS: mean = 530 € ha⁻¹ year⁻¹ ± 23 € ha⁻¹ year⁻¹) (Fig. 2c).

Table 1 | Summary of effects of vegetation volume, usage of chemical-synthetic pesticides, mineral fertilizer, and equidistant seeding on arthropod biodiversity and economic profitability of cropping systems

	Chemical-synthetic pesticides (no/yes)	Mineral fertilizer (no/yes)	Equidistant seeding (no/yes)	Vegetation volume [m ³]
Biodiversity				
Arthropod richness	Not retained	Not retained	Not retained	Not retained
Shannon diversity of arthropods	Not retained	Not retained	Not retained	Not retained
Gross margins [€ ha⁻¹ year⁻¹]				
Gross margins	Not retained	-132.65 ($P = 0.024$)	Not retained	Not retained
Gross margins with subsidies	-160.05 ($P = 0.002$)	-238.75 ($P < 0.001$)	Not retained	Not retained

Shown are the results of the most parsimonious models after model identification using AICc (variables that were not retained in the best model are denoted with "not retained"). An overview of all compared models is available in the supplementary material (Supplementary Tables 1–4).

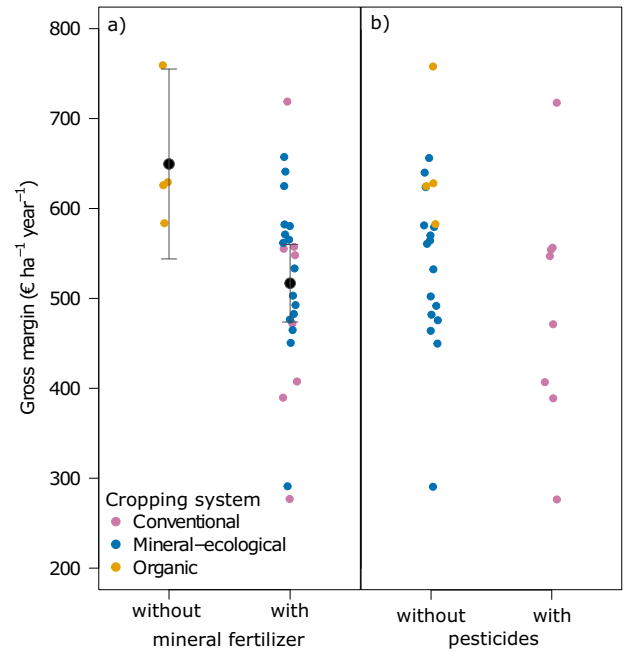


Fig. 3 | Influence of (a) mineral fertilizer and (b) chemical-synthetic pesticide use on gross margins (€ ha⁻¹ year⁻¹) of cropping systems. Colored dots represent the different cropping systems, including conventional, mineral-ecological, and organic cropping systems. Black dots and bars indicate mean values ± confidence intervals when the difference between factors is significant. **a** Conventional cropping systems with mineral fertilizer use show significantly lower profits than cropping systems without mineral fertilizer use. **b** For (not) using chemical-synthetic pesticides, there is no significant difference.

Both biodiversity variables and gross margins were tested for effects of vegetation volume, the use of chemical-synthetic pesticides, mineral fertilizers and equidistant seeding (Table 1). Gross margins were lowered in systems where mineral fertilizers were used (estimate = -132.65, $P = 0.024$), while the use of chemical-synthetic pesticides was not retained in the best model (Fig. 3). When subsidies were considered for gross margins, the use of chemical-synthetic pesticides and mineral fertilizers reduced gross margins. Contrarily, the biodiversity indices arthropod richness and Shannon diversity were not influenced by any of the variables (Table 1).

Biodiversity-profit trade-offs and synergies of cropping systems

We used generalized linear models to investigate the relationship between biodiversity, meaning arthropod richness and Shannon diversity, and gross margins. Comparing all studied cropping systems, we found no general trade-off between gross margins and arthropod richness (estimate on log-scale = -6.108×10^{-5} , $X^2_1 = 0.082$; $P = 0.775$) or Shannon diversity (estimate = -3.753×10^{-5} ; $F_{1,26} = 0.011$, $P = 0.916$). However, we found great variability in the combined biodiversity-profit performance of the seven studied cropping systems. Here, the mineral-ecological cropping systems (MECS), particularly MECS II, provided the best ecological-economic combination with high arthropod richness and profit (Fig. 4).

Observations of all systems were highly scattered, leading to representations of all conventional and mineral-ecological cropping systems in every quadrant of Fig. 4. Across all cropping systems, data points in the win-win- and lose-lose-situations of Fig. 4 were most prominent, showing each 32% of all observations. All mineral-ecological cropping systems, as well as C II and the organic system were present in win-win-situations. C I performed worst in that it did not result in any win-win outcome.

Discussion

In this study, we investigated the potential of novel mineral-ecological cropping systems (MECS) that combine the use of mineral fertilizers with

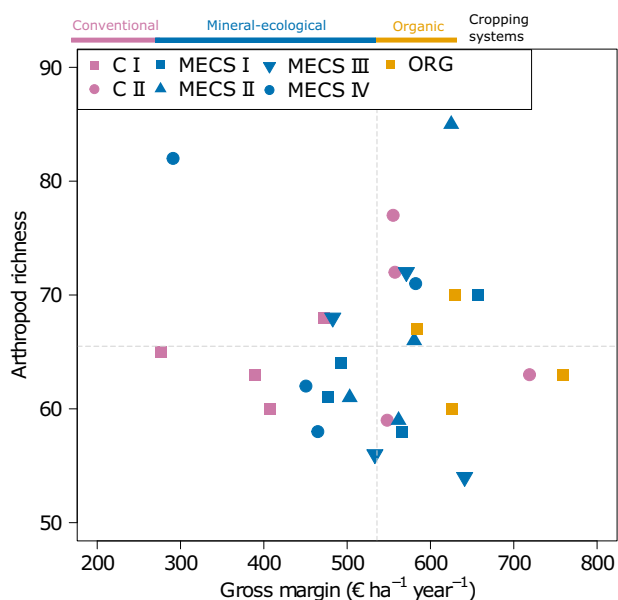


Fig. 4 | Biodiversity-profit relationships of the studies cropping systems. Shown are arthropod richness and gross margins for each replicate of the seven cropping systems (conventional: C I and C II; mineral-ecological: MECS I – IV; organic: org). The dotted lines indicate mean profit and species richness, respectively. Win-win-situations are displayed in the upper right quadrant where both arthropod richness and gross margins are highest. Win-lose-situations (upper left quadrant) represent high arthropod richness, but low gross margins, lose-win-situations (lower right quadrant) stand for the opposite case, and lose-lose-situations (lower left quadrant) for both low arthropod richness and gross margins.

the avoidance of synthetic chemical pesticides to overcome the trade-off between biodiversity and agricultural productivity that currently characterizes conventional and organic farming. MECS substantially reduced the yield gap observed between conventional and organic agriculture while achieving similar gross margins as organic agriculture. The diversity of epigeic arthropods of MECS, organic and conventional farming systems was alike. Consequently, MECS can provide synergies between biodiversity and profit at the cropping system level.

With a growing world population, it is important to maintain or even increase yields as a key factor for food security³. As highlighted by other studies^{5–7}, we found that organic yields were only half the amount of conventional yields. This large yield gap between conventional and organic agriculture could mean that a global, large-scale conversion to organic farming could jeopardize food security unless significantly more land is devoted to food production⁷. New sustainable, diversified cropping systems, such as MECS, might help to reduce this yield gap¹⁹ and increase yield stability while requiring less land than organic farming^{20,21}. We found that MECS can reduce this yield gap, as predicted by Zimmermann et al.¹³. While MECS (77.24 ± 5.12 dt ha⁻¹ yr⁻¹) could achieve 90% of the conventional yield (85.17 ± 5.08 dt ha⁻¹ yr⁻¹), it achieved 1.81 times the yield of the organic system (42.59 ± 2.18 dt ha⁻¹ yr⁻¹). In this regard, MECS can mitigate the biodiversity-yield trade-off existing between organic and conventional farming.

While maintaining high yields is important, the choice of farming system is also strongly influenced by the potential economic profit¹¹. In our case study, we found that MECS can be at least as profitable as conventional farming (mean profit of MECS being 37% higher than conventional system I; Fig. 2c). This is in line with studies showing that diversified farming practices allow at least similar profits as in conventionally intensified agriculture^{20,22}. It is important to note that only selected cropping systems with specific crop rotations were included in the analysis. For example, we did not consider root crops such as sugar beet, where yield losses in pesticide-free cropping systems can be comparatively high²³. Further

analysis, including other crop types and locations over a longer period of time, is therefore needed to gain further insight into the robustness of our results. The inclusion of potential subsidies available to farmers for pesticide-free crop production strengthens the economic advantage of MECS over conventional agriculture. Depending on the crop type, MECS can be subsidized with up to 150 € ha⁻¹ yr⁻¹ in Germany (e.g., for pesticide-free crop production under the new Eco-schemes framework of the Common Agricultural Policy 2023–2027 of the European Union).

In terms of agricultural profitability, MECS showed benefits compared to conventional agriculture and similar profits to organic production. Regarding biodiversity, we could not observe clearly pronounced differences, although diversified agricultural systems like MECS and organic farming in general should enhance species diversity^{20,24}. The biodiversity effects of MECS may have been limited due to the relatively limited size of our experimental parcels and the mobility of epigeic arthropods^{25,26}. However, other studies with similarly-sized experimental crop parcels found strong effects of crop identity on arthropod diversity²⁷. Possibly, differences in species diversity between systems may not become apparent for several years. Thus, our experiment, which had been running for only three years at the time of our study, might not show effects on biodiversity yet. In addition, the fact that our cropping experiment had been established on a conventionally managed farm may have limited the available species pool for colonizing the parcels, including those that were managed organically or as MECS. Finally, by using pitfall traps, we only focused on epigeic arthropods as an indicator of biodiversity.

Follow-up studies on the biodiversity potential of MECS on the farm scale will shed light on the broader biodiversity potential of MECS at the field and farm level and the possible role of the landscape context. Non-crop arable plants, for example, have already been studied for mineral-ecological cropping systems²⁸. However, future studies should include additional taxa (e.g. non-crop arable plants, soil biota) and also other functional groups of arthropods (e.g., pollinators). In such farm-scale studies, we would expect more positive biodiversity outcomes for diversified farming such as MECS than in conventional agriculture^{29,30}. On top of that, MECS can indirectly save biodiversity, compared to organic farming, as less land needs to be converted for agriculture and thus could be saved in other habitats³¹. Additionally, MECS can significantly reduce the yield gap between conventional and organic agriculture while achieving similar gross margins as in organic agriculture. Thus, MECS are ecologically and economically promising farming systems that could mitigate the trade-offs between biodiversity and productivity that exist in the current dichotomy between organic and conventional agriculture and represent a valuable alternative to both farming systems.

Methods

Experimental design

The large-scale cropping experiment with 168 parcels was established in 2019 on the experimental farm Heidfeldhof of the University of Hohenheim, Stuttgart, Germany (48.71432 N, 9.19149 E; Fig. 5). Each parcel measured 9 m x 15 m. Seven different cropping systems with six crops each were installed randomly and replicated four times. Two conventional cropping systems were compared to one organic and four different types of mineral ecological cropping systems (MECS). Thus, we used a sample size of $N = 28$ cropping system replicates for our analyses (Fig. 1).

The MECS used mineral fertilizers but no chemical-synthetic plant protection products (for more detailed information see Supplementary Data 5). Furthermore, MECS can be characterized by a diverse crop rotation, resistant crop varieties, equidistant seeding, bioeffectors, spatially targeted ammonium fertilizer, weed harrowing and the use of biocontrol agents¹³. In the experiment, MECS' crop rotations were designed as follows: winter wheat – catch crop – maize – winter triticale – catch crop – soy – winter wheat – catch crop – spring barley. Four different types of MECS were tested with the same basic crop rotation, but other differing features (Table 2). Only MECS IV replaced grass for spring barley in the crop rotation.



Fig. 5 | Aerial view of the cropping systems experiment. Photo by University of Hohenheim/NOcsPS project.

In addition, two conventional cropping systems with either short (winter wheat – catch crop - maize - soy) or long crop rotation (see MECS) were established. Finally, one organic cropping system, following standards of the European Union for organic agriculture was established (crop rotation: see MECS, but with clover grass instead of spring barley).

Biodiversity assessment of cropping systems - Field work

Ground-dwelling arthropods were sampled with pitfall traps in all 168 plots of the experiment. The traps were set up in the morning and left in the field for 48 h. They were then collected in the morning. The pitfall traps were placed in a tube that stabilized the soil. Each tube contained a 250 ml bottle, 1/3 of which was filled with a 36% salt solution. A funnel (10 cm diameter) led into this bottle and was covered with a 2 cm mesh to prevent non-arthropods (e.g. small mammals) from falling in (Supplementary Fig. 2). Trapping was repeated three times on the following days, covering changes across the spring and summer phenology of crops and arthropods: 2–4 May, 20–22 June, and 18–20 July 2022. Weather conditions were favorable in all trapping periods (Supplementary Table 5).

At each trapping event, we measured the vegetation height (m) with a yard stick at three different locations in each parcel. Additionally, two people independently estimated the soil cover per m² at one spot in each parcel. Vegetation height and the estimates of soil cover were averaged. We then multiplied both variables to estimate the vegetation volume (m³) per parcel as a proxy of vegetation biomass³². The vegetation biomass included both crops and weeds as they together make up the structure that is relevant for arthropods as refuge area³³.

Biodiversity assessment of cropping systems - Metabarcoding

Species identification of arthropod samples was performed using DNA metabarcoding following the protocol published by Hausmann et al.³⁴. Each sample was dried in a 60°C oven for at least eight hours and subsequently homogenized in a FastPrep96 machine (MP Biomedicals) using sterile steel beads in order to generate a homogeneous mixture of arthropods. Prior to DNA extraction, 1 mg of each homogenate was weighed into sample vials and processed using adapted volumes of lysis buffer with the DNeasy Tissue Kit (Qiagen, Hilden, Germany) following the manufacturer's instructions. For amplification of the mitochondrial 5'-CO1 Illumina-ready primers derived from the primer pair by Leray et al.³⁵. (dgHCO 5' – GGWACWGGWT-GAACWGTWTAYCCYCC – 3' mlCOIntF 5' – TAAACTTCAGGGT-GACCAAARAAYCA – 3') using forward and reverse HTS primers, equipped with complementary sites for the Illumina sequencing tails. In a

Table 2 | Overview of the main characteristics of the seven cropping systems used in the experiment

The seven cropping systems	
Conventional (C): Chemical-synthetic pesticides and mineral fertilizer application	
C I	Short crop rotation
C II	Longer crop rotation
Mineral ecological cropping systems (MECS): no chemical synthetic pesticides, but mineral fertilizer application	
MECS I	Normal seeding with optimized mineral standard fertilization
MECS II	Equidistant seeding with optimized mineral standard fertilization
MECS III	Equidistant seeding with positioned, optimized mineral fertilization using CULTAN technology with stabilized ammonia fertilizer, leaf fertilization, bioeffectors & Zn, Mn, Si
MECS IV	Normal seeding with optimized mineral standard fertilization, but with grass (perennial ryegrass) instead of spring barley
Organic (ORG): no chemical-synthetic pesticides, no mineral fertilizer application, according to EU organic standards	

Additional detailed information on applications of chemical-synthetic pesticides (CSP) and Nitrogen fertilizer can be found in Supplementary Data 5.

subsequent PCR reaction, index primers with unique i5 and i7 inline tags and sequencing tails were used for the amplification of indexed amplicons. Afterwards, equimolar amplicon pools were created and size selected using preparative gel electrophoresis. The pooled DNA was purified using MagSi-NGSprep Plus beads (Steinbrenner Laborsysteme GmbH, Wiesnbach, Germany). A bioanalyzer (High Sensitivity DNA Kit, Agilent Technologies) was used for a final check of the base pair distribution and concentration of the amplicons before the creation of the final library. High-throughput sequencing (HTS) was performed on an Illumina MiSeq using v2 (2*300 base pairs, 600 cycles, maximum of 20mio reads) chemistry (Illumina).

Paired ends were merged using the -fastq_mergepairs utility of the USEARCH suite v11.0.667_i86linux324 with parameters: -fastq_maxdiffs 99, -fastq_pctid 75, fastq_trunctail 0. Adapter sequences were removed using CUTADAPT K5 (standard parameters). Sequences not containing the appropriate adapter sequences were filtered out using the -discard-untrimmed parameter. The remaining preprocessing steps (quality filtering, dereplication, chimera filtering, and clustering) were conducted with the VSEARCH suite v2.9.16. Quality filtering was carried out with the VSEARCH -fastq_filter utility (parameters: -fastq_maxee 1, -minlen 300). Sequences were dereplicated using -derep_fulllength (parameters: -sizeout, -relabel Uniq), first at the sample level (output: all.derep.uc) and then at the combined dataset level, after all sample files were merged into a large FASTA file (all.fasta), which was also filtered for singletons (sequences appearing only once in the entire dataset and considered as noise; parameters: -minuniquesize 2, -sizein, -sizeout, -fasta_width 0; result file: all.derep.fasta). To conserve computational resources, a pre-clustering step (at 98% identity) using the -cluster_size VSEARCH utility with the Centroids algorithm was performed before chimera filtering (parameters: -id 0.98, -strand plus, -sizein, -sizeout, -fasta_width 0, -centroids; input: all.derep.fasta; outputs: all.preclustered.uc, all.preclustered.fasta). Chimeric sequences were then identified and removed from the resultant file using the VSEARCH -uchime_denovo utility (parameters: -sizein, -sizeout, -fasta_width 0, -nonchimeras; input: all.preclustered.fasta; output: all.denovo.nonchimeras.fasta). The remaining sequences were then clustered into OTUs with 97% identity using -cluster_size (parameters not specified). To create the OTU table, a custom Perl script was used to extract all non-chimeric non-singleton sequences from the dereplicated dataset (inputs: all.derep.fasta, all.preclustered.uc, all.denovo.nonchimeras.fasta; output: all.nonchimeras.derep.fasta), and then all non-chimeric non-singletons from each sample (inputs: all.fasta, all.derep.uc, all.nonchimeras.derep.fasta; output: all.nonchimeras.fasta). The Perl script's task was to recover all

quality- and chimera-filtered sequences from the individual samples, including singletons and sequences removed during the dereplication rounds. The resulting file (all.nonchimeras.fasta) was then used to assign reads to OTUs and create the OTU table (parameters: `-cluster size all-nonchimeras.fasta, -id 0.97, -strand plus, -sizein, -sizeout, -fasta_width 0, -uc, -relabel OTU, -centroids otus.fasta, -otutabout otu_table.txt`). To reduce the risk of false positives, a cleanup step was conducted, excluding read counts in the OTU table that were $< 0.01\%$ of the total number of reads in a sample. OTUs were blasted (parameters: Program: Megablast; maximum hits: 1; scoring (match mismatch): 1-2; gap cost (open extend): linear; max E-value: 10; word size: 28; max target seqs 100) against (1) a custom database downloaded from GenBank (a local copy of the NCBI nucleotide database downloaded from <ftp://ftp.ncbi.nlm.nih.gov/blast/db/>), and (2) a custom database created from data downloaded from BOLD (www.boldsystems.org), including taxonomy and BIN information, using Geneious (v.10.2.5 - Biomatters, Auckland, New Zealand) and following the methods described in Morinière et al.³⁶. The resulting csv files contained the OTU ID, BOLD Process ID, BIN, the Hit-%-ID value (percent overlap similarity (identical base pairs) of an OTU query sequence (with its closest counterpart in the database), the Grade-%-ID value (combination of query coverage, E-value, and identity values for each hit with weights of 0.25 and 0.5, respectively, identifying the longest and strongest identity hits), the length of the top BLAST hit sequence, and the information on phylum, class, order, family, genus, and species for each discovered OTU, which were exported from Geneious and combined with the OTU table generated by the bioinformatics preprocessing pipeline. In addition to BLAST, as an extra control measure, the OTUs were classified into taxa using the naive Bayesian classifier of the Ribosomal Database Project (RDP), trained on a curated COI dataset of arthropods and chordates (plus outgroups; see Porter & Hajibabaei³⁷). To further reduce the risk of false positives, the combined result table was then filtered, excluding read counts in the OTU table that were $< 0.01\%$ of the total number of reads in a sample. Additionally, OTUs based on negative control samples were removed, i.e., if the total number of reads in the negative controls exceeded 20% of the total number of reads in the OTU. The OTUs were also annotated with taxonomic information from NCBI (downloaded from <https://ftp.ncbi.nlm.nih.gov/pub/taxonomy/>), followed by the creation of a taxonomic consensus between BOLD, NCBI, and RDP. Interactive Krona diagrams were created using KronaTools v1.3 from the taxonomic information. The bioinformatics can be reviewed in detail again in the supplementary part of Uhler et al.³⁸.

Biodiversity assessment of cropping systems - Arthropod richness and diversity

The data that we retrieved after metabarcoding and bioinformatics was then processed as follows: non-arthropod entries, entries with identification accuracy $< 95\%$, and those with less than 300 base pairs were disregarded from the analysis. Additionally, entries with the same Barcode Index Numbers (BINs) were aggregated. This procedure reduced the number of BINs from 561 in the raw data to 380 in the cleaned data. In this study, we use the term “species” equivalent to unique BINs from the metabarcoding method. An overview of the resulting 380 species and their corresponding information on class, order, family, genus and species (if applicable) is available in Supplementary Data 2. For each of these species, we also have the information on the number of reads present per cropping system replicate ($N = 28$) (Supplementary Data 1). This table was then used to calculate arthropod richness and diversity, representing together the biodiversity of a system (see Supplementary Data 4). Arthropod richness represents the number of species present per cropping system replicate (number of reads > 0). Arthropod diversity refers to the Shannon diversity index. For this purpose, we calculated the proportion of reads per species and cropping system replicate to the total sum of reads per species.

Productivity and economic profitability

Productivity was based on actual crop yield per hectare (Supplementary Data 3). As a measure of profitability, we used gross margins, which enables the

evaluation of the production efficiency of different crops in a system³⁹. Here, we use the terms profit, gross margins and profitability interchangeably. Gross margins (€ ha^{-1}) were calculated as the difference of benefit and variable costs: $\text{gross margin} = \text{economic benefit} - \text{variable costs}$. In the main text, gross margins / economics profits always refer to gross margins calculated from multi-year averaged prices without subsidies, if not indicated differently. After calculating gross margins on parcel level (Supplementary Data 3, they were aggregated for each cropping system replicate for statistical analysis – see Supplementary Data 4). For aggregation, crop rotations CI-1 and CI-2 (Fig. 1) were fused together, to also receive a crop rotation lasting 6 years and assure comparability of the systems among each other.

The calculation of the gross margins was based on the actual measures carried out by the trial technicians in the individual plots and the natural yields of the respective plots. However, no price information from the trial farm is used for the calculation of direct costs. These may be distorted, for example, because the experimental farm uses much smaller amounts of certain fertilizers than a working farm would. All calculations were based on multi-year price averages (2017–2021), assuming a farm of 100 hectares. However, input and yield quantities were based on actual data from the trial farm in 2022.

Economic benefits included benefits from yield and, when considered, subsidies. For MECS, conventional prices for the products were assumed. All prices for the produced crops were taken from LfL (Bayerische Landesanstalt für Landwirtschaft) calculation data⁴⁰. Subsidies were assumed based on the first pillar of the Common Agricultural Policy, including direct payments for all cropping systems and the voluntary eco-scheme 6 for MECS. Additionally, subsidies from the second pillar were assumed for MECS and the organic system, including measures from a Baden-Württemberg specific program (FAKT measures D2, E3, E12⁴¹).

Economic variable costs referred to costs for seeds, fertilizers, chemical and mechanic plant protection measures, other variable costs and interest costs. The use of organic seed was assumed for the MECS systems. For fertilizer costs, price rates of the LfL Bayern for basic nutrients were assumed. Repair costs and fuel consumption according to the KTBL process calculator were used⁴². A diesel price of 1.22 €/l was assumed. The selection of mechanization variants was based on the actual equipment available at the trial site. Complete self-mechanization was assumed; at the same time, no personnel costs were assumed. For chemical-synthetic pesticides, the mean values of the prices of various online stores and price lists of various agricultural dealers for 2022 were used and then adjusted for the period of 2017–2021 using the German producer price inflation for pesticides. The calculations included an assumed interest rate of 5%.

Statistical Analysis

To investigate the biodiversity-profit trade-offs and synergies of the cropping systems, we performed several analyses using R4.3.2⁴³. Statistical analyses were based on the aggregated data in Supplementary Data 4 ($N = 28$). First, we used a generalized linear model (glm) with Poisson distribution to model arthropod richness as a function of gross margins. Model assumptions were checked and approved for all (generalized) linear models used. A possible significant relationship between these variables was analyzed using a Chi-squared test. Additionally, gross margins were also used for a linear model (lm) with Shannon diversity as response variable.

Second, we modeled arthropod richness (glm), as well as Shannon diversity and gross margins (without and with subsidies) (lm) with the possible predictors vegetation volume, equidistant seeding, usage of chemical-synthetic pesticides and mineral N fertilizer. We used multi-model inference to assess all models with all possible combinations of predictor variables and to finally identify the most parsimonious combination of predictors for each response variable. Based on Akaike's information criterion corrected for small sample-sizes (AICc), all of these models were ranked using the MuMIn package in R⁴⁴. From all models that were in the delta AICc range of < 2 , we took that model as best model that had the lowest degrees of freedom combined with the lowest delta AICc value. The summaries of the best models were then checked for estimates and significance of the variables included.

Reporting summary

Further information on research design is available in the Nature Research Reporting Summary linked to this article.

Data availability

All data to reproduce the analyses are included as supplementary data.

Received: 25 March 2024; Accepted: 27 October 2024;

Published online: 18 December 2024

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Acknowledgements

Our special thanks go to Yasha Auer and several students who helped in collecting the biodiversity data. We thank the project coordinators of the NOcsPS project and the technical staff of the trial farm Heidfeldhof at the University of Hohenheim for conducting the study experiment. We thank the editor and the anonymous reviewers for their comments that helped to improve the manuscript. This research was funded by Bundesministerium für Bildung und Forschung (BMBF), grant number 031B0731A. Publishing fees were supported by Funding Programme Open Access Publishing of University of Hohenheim.

Author contributions

I.G., E.B., M.K.K. conceived the idea. M.K.K., F.W., C.S. and T.K. collected data. M.K.K. with contribution by I.G., F.W., C.S. and J.M. analyzed the data. M.K.K. wrote the manuscript with input from all authors.

Funding

Open Access funding enabled and organized by Projekt DEAL.

Competing interests

The authors declare no competing interests.

Additional information

Supplementary information The online version contains supplementary material available at <https://doi.org/10.1038/s44264-024-00034-0>.

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