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A novel framework to study the evolution of crop rotation diversity reveals changes towards regional crop type specialisation in Sweden

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ABSTRACT

Diversification of cropping systems can help decrease the negative environmental impacts of agriculture while increasing ecosystem service benefits to crop production. The crop diversification measure introduced by the 2013 CAP reform aimed to trigger the diversification of cropping systems. There is currently no framework to show how policies that aim to trigger diversification of cropping systems, affect crop rotation diversity at the field scale. In this study, we propose a framework to study the evolution of cropping system diversity, which comprises (1) building crop sequences for two periods using the Geo-spatial Application (GSA) database of the Integrated Administration and Control System (IACS), (2) calculating two indicators of diversity of crop sequences, (3) creating a typology of crop sequences, and (4) determining the significance of change and highlighting drivers of change by using mixed models. Our framework was tested on 1100,760 ha in Sweden, focusing on the periods 2005–2010 and 2011–2016, with four ways of categorizing crops (i.e., crop species, crop types, winter crops vs spring crops, botanical family) in five homogeneous production regions. Using different crop categorization is a way of expressing the robustness of the trends in diversity which account for various relationships among crops. We showed that the value of all diversity indicators in all regions decreased significantly between the two periods, except for the estimated agronomic quality of the crop sequence in the most productive regions where it increased. This general decrease could be explained by longer duration of rotational perennial leys and reduced cultivation of minor cereals, such as rye and oats in the later period. Overall, there was an 8 % increase in ley area, which was particularly evident in regions with less productive land, where the high proportion of ley often became permanent grassland. We found that the trend towards longer duration leys was strong in livestock farms, while regions with productive land favoured the inclusion of more annual cash crops in the rotation, especially oilseed rape, which contributed to the agronomic quality of the sequences. The framework could be widely adopted across Europe using the GSA database of the IACS to track diversification changes at a country and regional level and design appropriate policies to increase the diversity of crop rotations using the potential local drivers highlighted.

1. Introduction

Agriculture is responsible for many negative environmental impacts. Since 1850, agriculture has contributed 10–15 % of global greenhouse gases emissions (Smith et al., 2008, p. 20074), while the whole food system is currently estimated to contribute about 34 % (Crippa et al., 2021). Water bodies have been impacted in terms of quality due to nitrate and pesticides residues in many regions (Foley et al., 2011). Intensive agricultural systems are also threatening worldwide biodiversity (IPBES, 2016; Tilman et al., 2011). These impacts are the results of the expansion of agricultural land, the decline in landscape heterogeneity, the increased use of fertilizers and pesticides, and the conversion to systems with low crop diversity (Emmerson et al., 2016; Tscharntke et al., 2005).

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Diversification of cropping systems can help decrease the negative impacts of current agriculture, sustain production (Doré et al., 2011) and make food production more resilient to global changes (Bohan et al., 2022). Cropping systems can be diversified by intercropping and the use of subsidiary crops that are either under-sown in main crops or sown after the harvest of the main crops. However, the most important form of diversification is the introduction of more crops from different families and with different characteristics in the rotations (Hufnagel et al., 2020). Crop rotation has been defined in the literature as "the sequence of crops grown in succession on a particular field" (Wibberley, 1996). Crop rotational diversity can increase productivity of cropping systems (Smith et al., 2023), such as wheat-based systems (Agomoh et al., 2020), increase resilience to adverse growing conditions (Bowles et al., 2020), reduce the use of pesticides (Guinet et al., 2023) and increase the non-cropped biodiversity (Neyret et al., 2020), its associated ecosystem services (Peralta et al., 2018) and farmers' revenue (Tzemi and Lehtonen, 2022).

Policies have aimed to diversify farmers' crop rotations through various incentives. One example is the green payments from the first pillar of the EU Common Agricultural Policy (CAP) that require farmers with more than 30 ha of arable land to grow at least three crops with the most cultivated crop occupying less than 75 % of the cultivated land (introduced in 2013 CAP). Another example is the 'protein premium' of 100€.ha^{-1} provided to farmers growing grain legumes in 2020. The success of policies that aim to diversify agriculture have been questioned in the past due to the lack of an overview of changes in diversity with inaccurate data and knowledge at large scale (Roesch-McNally et al., 2018).

We have identified three types of methodologies that have aimed to identify crop and diversity change in agricultural land at large scale. The first type of study tracks patterns of crop sequence type providing a snapshot of the existing systems, but without specifically highlighting changes in time or diversity (Leenhardt et al., 2010; Mignolet et al., 2007; Mueller-Warrant et al., 2017; Xiao et al., 2014). In such studies at regional level, drivers of crop sequences have been identified by combining, for instance, expert interviews (e.g., with agronomists) with local statistical databases (Leenhardt et al., 2010; Murgue et al., 2016; Rizzo et al., 2019), but adopting this hybrid approach at national level would be too laborious. The second type of study focuses on spatial and possibly temporal crop diversity change at large scale, but without any emphasis on crop sequence (Aramburu Merlos and Hijmans, 2020; Conrad et al., 2017; Qiu et al., 2020; Schiller et al., 2024). In such studies, authors look at diversity for specific years and eventually at different spatial scales to identify diversity change and determinants from the farming system or land explaining the diversity but losing the general agronomic reasoning and temporal sequence of crops in the rotation. The temporal diversity of crops in the sequences is important as the magnitude of the pre-crop effects from legumes or oilseed rape observed in field experiments and farmers' fields depends on the choice of following crop (Angus et al., 2015; Peltonen-Sainio et al., 2019). Studies address the quality of crop rotations from different perspectives. These can be agricultural, rating the agronomic quality of crop rotations (Leteinturier et al., 2006; Vandevoorde and Baret, 2023) or use indicators from ecological studies such as the Shannon Index (Schaak et al., 2023). The third type of study is based on typologies of crop sequences, or cropping patterns, constructed to quantify the area change under each type of crop sequence as a proxy of cropping system change (Blickensdörfer et al., 2022; Janicke et al., 2022; Liu et al., 2022; Upcott et al., 2023). Peltonen-Sainio et al. (2017) found that Finnish farmers use a large range of crop rotation types, from monocultures (i.e., the same crop year after year) to diverse crop rotations, including several species and both annual and perennial crops. In a typification approach, Stein and Steinmann (2018) found a range of crop pattern diversity from monocultures to extremely diversified crop rotations. The typification approach alone makes it difficult to measure the change in diversity and the direction towards either specialisation or diversification of agricultural systems. These limitations are due to (i) the lack of available data on crop sequences at large scale over long time periods and (ii) the lack of diversity indicators that can be applied to crop sequences to show trends in diversity change.

In this paper, we propose a framework building on existing crop diversity studies to quantify changes in diversity of crop rotations, trace them back to crop sequence types and identify the drivers of change over time. The paper consists of a landscape agronomy approach to better understand spatio-temporal interactions among factors determining agricultural landscape change at large scale (Thenail et al., 2022) using Sweden as an example. To do so, our objectives were to (i) identify crop sequences at large scale using the Geo-spatial Application (GSA) of the of the Integrated Administration and Control System (IACS), which contains crops grown on individual fields as declared by farmers; (ii) evaluate the diversity change between the periods 2005–2010 and 2011–2016 using a broad range of indicators and crop categorization, (iii) link trends in the observed changes in diversity to the identified crop sequences and (iv) highlight possible biophysical and structural drivers of crop diversity change over time.

2. Material and methods

2.1. Study area

We focus on the agricultural landscape of Sweden, in which 2.6 million hectares are arable land and 450,000 ha are permanent grassland and semi-natural grassland (as opposed to temporal ley in crop sequences) (Statistics Sweden (SCB), 2017). In 2023, there were 56,171 agricultural enterprises, and the owners were, on average, 57 years old (Jordbruksverket, 2024). The average size of farms in Sweden at that time, was 40 ha, with 70 % being less than 30 ha and 12 % above 100 ha. Only 13,400 farmers worked full time on their farm. About 70 % of the arable land, all dairy cows and almost all pigs and cattle were managed by full time farmers. About 43 % of the farmers were dependent on income from outside their farm. (Jordbruksverket, 2024). As a result of the variation in biophysical and socio-economic conditions across the country, we separated the analysis of diversity by production region (called Skördeområden in Swedish) from Region 1 (Scania south of Sweden also referred to here as the 'most productive region') to Region 5 (forested regions in the south and north of Sweden also referred to here to as the 'least productive region'). This gradient represents a ranking from the best region in terms of fertility and productivity of land due to more suitable biophysical conditions to the least productive in the forest regions and the north of Sweden. Such regional delimitation is officially used by the Swedish Board of Agriculture ("Jordbruksverket") and has been used previously for comparing crop diversity and sequences between conventional and organic farming systems in Sweden (Reumaux et al., 2023) (Fig. 1).

2.2. Framework for analysing crop rotation diversity

The framework for analysing crop rotation diversity change over time contains several steps using the GSA database from the IACS which encompasses all physical blocks of land (i.e. stable and easily updated geographical unit of land with defined boundaries) in Sweden using fields declared by farmers. Our framework uses this data to build crop sequences and calculate a range of diversity indicators. A typology of crop sequences is created to identify the main changes in cropping systems, and crop sequences are analyzed on a yearly basis to identify changes in crop pairs. Finally, a regression model is developed to identify the drivers of diversity change (Fig. 2)

2.3. Crop data source and building of crop sequences

To assess crop rotations, we used the concept of crop sequences which has previously been proposed to cover both rotation with a fixed

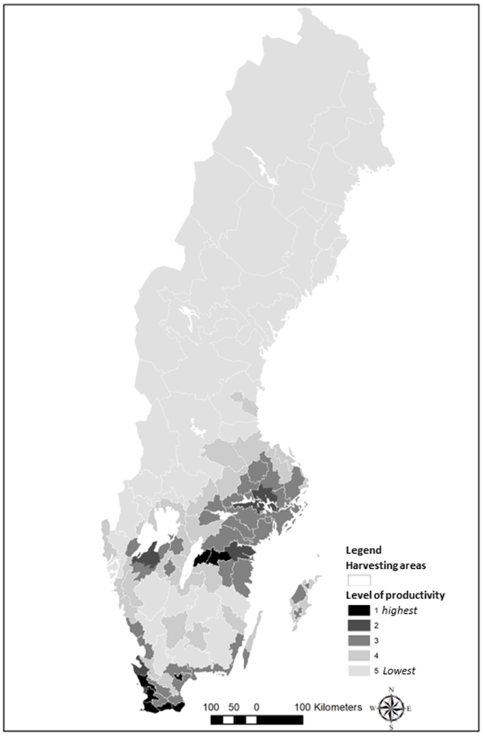

Fig. 1. Map depicting the different harvest areas in Sweden used as a reference system here.

sequence of crops over time and rotations with a flexible sequence (Bohan et al., 2011; Steinmann and Dobers, 2013). We analyzed crop sequences in Sweden over the period 2005–2016 using data from the GSA, which forms part of the IACS managed by the Swedish Board of Agriculture. This system provides annual records of crop declarations made by farmers at the field level. The period 2005–2016 was chosen to capture two 6-year crop sequences acknowledged as a sufficient period to describe crop sequences (Upcott et al., 2023). Additionally, a change in the structure of this geodatabase after 2016 made it difficult to build the crop sequences over a longer period.

The GSA contains data on the crops grown in blocks, each block being identified with a block ID (Kay and Milenov, 2008). A block encompasses one or several fields. A field is a management unit with a single crop. To identify crop sequences at field level, we first linked the blocks from year to year and then we linked the fields within each block from one year to another. Based on their ID, blocks in year i were in 93 % of the cases the same as the one in year i + 1. In the case where a block is split over time, one of the new blocks will retain the original ID while the others will get new IDs. We did not perform a spatial intersection of plots due to the high proportion of blocks remaining unchanged over time and because a change in the shape of the block will make it difficult to relate a large proportion of the area of the field inside a block from one year to another. This is because when blocks change over time (e.g., through splitting), it introduces additional uncertainty in tracking a field from one year to another, as the field may be part of multiple blocks or even be split itself. When following individual blocks, we can be confident that a field, even if its spatial configuration changes, remains within the same block from year to year. Hence, the number of blocks remained constant over the period for a complete crop sequence. After having linked blocks from year to year, we started linking the fields within the block from one year to the next. Within each block we discarded fields that were identical in size but labelled with different crops meaning that if 2 fields in year i have the same size, we could not identify them over time. After filtering out, we linked fields within the blocks considering the size of the field within the blocks, using six rules derived from Levavasseur et al. (2016) who proposed a method to build crop sequences in France where the structure of data is different (Kay and Milenov, 2008) (Supplementary Material B).

With the application of rules and control, we managed to include 41 % of the Swedish agricultural area which represents a total of 1,114,100 ha (530,447 fields) over 12 years. Depending on production region, crop sequences were described on between 32 % and 48 % of the agricultural area. For the most cultivated annual crops (>20,000 ha), the area shares for the crops in the sequences obtained for the year 2016 was similar to the crop shares of the total production area in official statistics. This means that the linking procedure did not contribute to over- or under- estimating the representativeness of crops at the national level. For pastures (grassland), the area was underestimated, but permanent grassland was largely excluded from the analysis. After this process, we filtered out fields continuously declared as environmental schemes or woody perennials (e.g. poplar, Christmas tree) during the whole study period. We finally obtained 491,000 fields with crop sequences from 2005 to 2016 representing 1,100,760 ha. More details about the validity of the reconstructed data are provided in Supplementary material B.

2.3.1. *Crop categorization*

Due to the large number of unique crop codes (n = 94) recorded in the GSA, we aggregated crops into broader functional groups to avoid disproportionate influence from minor or infrequent crops. An aggregated categorization allows for mitigating the effects of diversification of crop species which are biologically and/or genetically very similar (e.g., wheat with triticale). Conversely, highly aggregated categorization will not bring much information and may hamper the understanding of the contribution of a single crop to diversity change. The effect of categorization was considered by running several analyses using alternative categorizations. Our first categorization reduced the codes from 94 to 18 groups, which we refer to as the "species" categorization. We also proposed three additional types of categorizations: i) agronomic categorization (e.g., value of break crops), ii) a family-based crop categorization, and iii) a season-based categorization (winter or spring sown crops or, additionally, perennial) (Supplementary Material C).

2.3.2. *Indicators of diversity*

To assess the change in diversity over the study period, we calculated two diversity indicators over two 6-year periods (2005–2010 and 2011–2016): i) the Simpson's Index of Diversity (SID) (Simpson, 1949) and ii) a score representing the agronomic value of crop sequences based on a sum of a score provided for each couple of preceding-following crops (Supplementary Material D).

The SID is a widely used ecological indicator reflecting the probability of the next observed plant or animal being a different species (Hurlbert, 1971) and is also used to reflect crop sequence diversity (Conrad et al., 2017). Generally, the SID indicates the richness and the evenness of species within a certain area (Magurran, 2004). In our case, the field area is fixed over years and only one crop category is cultivated every year. So only the number of times each type of crop occurs in the crop sequence varies and is taken into account. The abundance is the number of occurrences of a crop type in the sequence. Hence, the SID values can range from 0, which is a monoculture of an annual crop or continuous production of a perennial crop, to 1, which means that no cultivated crop is followed by a crop of the same species. The SID only accounts for the number of occurrences and not the temporal arrangement of crops in the sequence.

The agronomic value is the sum of the scores of previous crop effects (also called break crop, pre-crop, rotational or residual effect) for each couple of crops following each other during the entire sequence. The score ranges from 1 to 6, with 1 being the least beneficial and 6 the most beneficial, and was based on the combined effect of soil structure, disease, pest, weeds and nitrogen and was evaluated using the scores provided by Leteinturier et al. (2006) and adapted to the Swedish

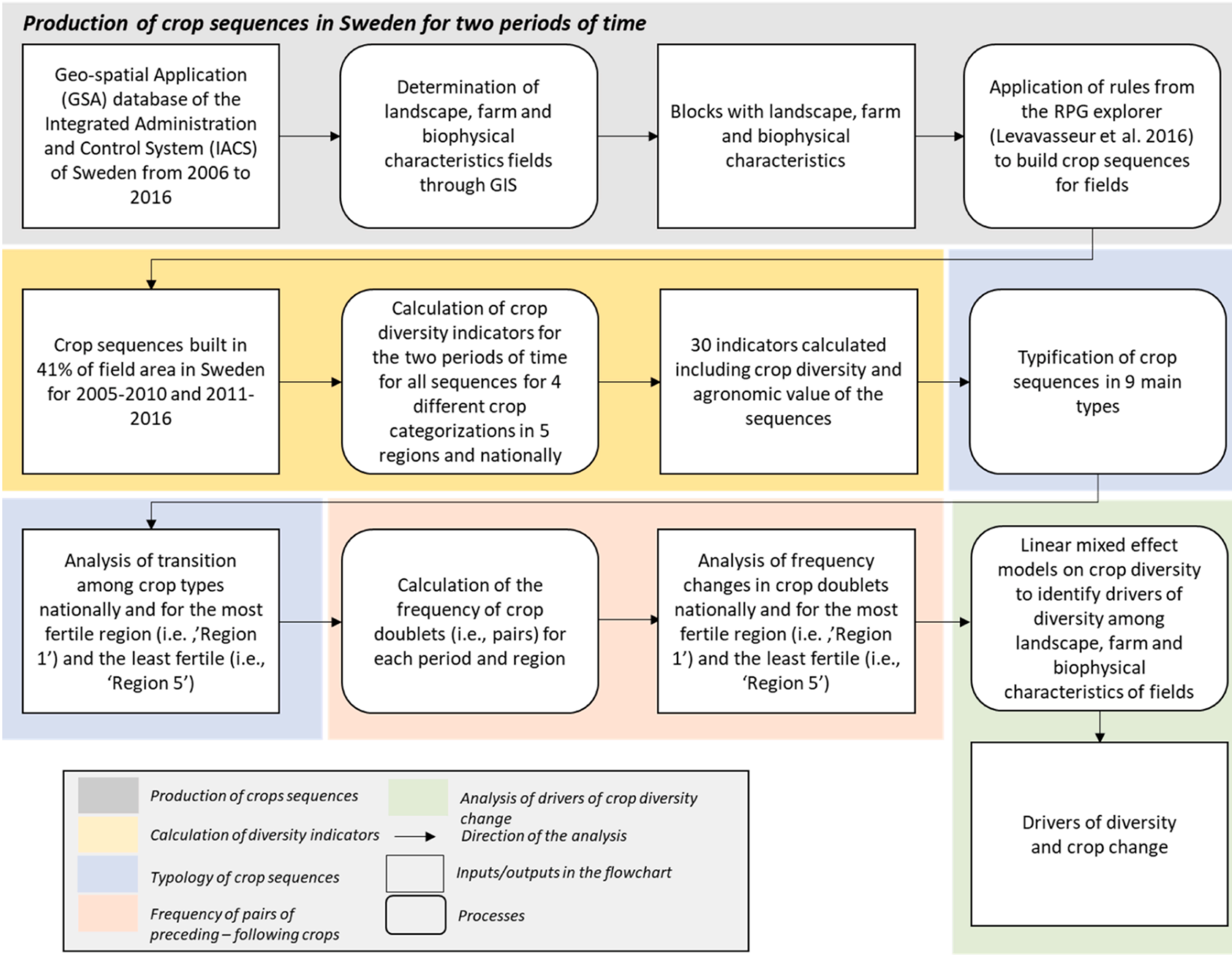

Fig. 2. Framework proposed to analyse crop sequence diversity using the GSA data of the IACS.

context (Supplementary material E). This indicator is used to capture the agronomic quality of crop sequences (Vandevoorde and Baret, 2023). The level and significance of diversification is evaluated by the magnitude of change in the indicators across the various categorizations and the statistical difference of these values between 2005 and 2010 and 2011–2016. This agronomic value was only calculated for the 'species' categorization as for other categorizations the pre-crop effect was considered too heterogenous among the categories.

To sum up, we calculated the SID across four categorizations in five regions plus the national level, with six additional indicators based on agronomic quality, resulted in a total of 30 diversity indicators (4*6 = 24 SID indicators and 6 agronomic values) studied through the period of 2005–2010 and 2011–2016.

2.3.3. Crop sequence typification

We classified crop sequences to observe aggregated changes highlighting a change in diversity of crop sequences using a similar typology as Peltonen-Sainio et al. (2017). We described ten main crop sequence types in each of the two 6-year periods: 1) "Cereal monocultures" contains only spring or winter cereals for the 6-year period; 2) 'Monospecific cereal sequences' contains the same cereal crop species; 3) "Cereal sequences with one annual break crop" are sequences with 5 years of cereals (spring or winter cereal) with one year of break crop, e.g., ley, legume, oilseed crop or root crop, 4) "Cereal sequences with two or three annual break crops" are cereal sequences with 2–3 break crops (e.g., legumes, oilseed crop), but without root crops; 5) "Cereal sequences with perennial crops" includes at least two years of ley; 6) "Root crops"-sequences include more than 2 years of root or tuber crops (sugar beet or potatoes); 7) "Diverse sequences" include more than one year of ley as well as both spring and winter cereals and at least one other annual non-cereal crop; 8) "Fallow" are sequences with more than 3 years of fallow, 9) "Permanent pastures" contain ley or pasture for the 6-year period, and 10) "Other sequences" are sequences with mostly woody or vegetable production for more than three years. Transitions between sequence types can occur in both directions. To better understand the overall trend of these transitions, we calculated the net difference in area moving from one sequence type to another. This means that if changes occur in both directions from type A to type B and vice-versa, only the difference between the two is retained.

2.3.4. Pattern recognition of crop sequences

In addition to the diversity and crop sequence type study, we analyzed the temporal structure of crop sequences by extracting all the different pairs of preceding and following crops. This procedure of text extraction is similar to the one adopted in the Teruti-Miner tool which provides the area of the different crop pairs for a given region (Schott et al., 2012) with the form "preceding crop for year i – following crop for year i + 1", such as "winter wheat – winter barley". After extracting all crop pairs for each period studied, we compared the evolution of the share of each pair to identify trends in preceding-following crops that explain the change in sequence type and diversity. In this analysis, we made the distinction throughout the whole 12 years sequence between young leys (lasting 1–2 years) and old leys (>2 years) and zoomed in on Regions 1 and 5 that experience the most contrasting changes of pairs across time.

2.3.5. Biophysical and structural drivers of potential diversification

We selected potential drivers of diversity change in Sweden hypothesizing that they could have an effect on cropping system characteristics. We then collected data for each block and linked it to the corresponding fields. Such drivers included the monthly mean air temperature and rainfalls, the altitude, the slope, the soil texture (% clay, % silt and % sand) (Piikki and Söderström, 2017), the field area, farm area, livestock density was split between monogastric and ruminants (livestock unit ha^{-1}) using the livestock unit associated with each type of animal from FAO and the type of farm (crop farm/livestock farm/mixed) (Supplementary material G for further details).

2.4. Statistical analysis of the change in diversity over time

ll statistical analyses were performed with R 3.0.2 (R Core

All statistical analyses were performed with R 3.0.2 (R Core Team, 2020). Plots were constructed in R, using the package'ggplot2' (Wickham, 2016). We used the Wilcoxon Rank sum test, the non-parametric equivalent of paired *t*-test, for each production region and combined all the crop categorizations and indicators since our indicators are discrete variables. Results with such tests are similar to mixed models assuming the region as a random factor (Barr et al., 2013). In order to test the determinant factors in the diversity change between the period 2005–2010 and 2011–2016, we calculated the variation of the indicators between periods and then ran generalized linear models and mixed models with fixed and random factors. Fixed factors included the slope, altitude, livestock number, area of the field, area of the farm, the soil texture (% of silt, clay and sand) and farm type. Random factors included the farm number. We compared model fit among generalized mixed models and linear mixed models using the package 'lmerTest' (Kuznetsova et al., 2015). To avoid over parameterization and reach best fitting model, a comprehensive model including all explanatory variables was fitted and we ranked the best models using AIC criteria under linear conditions (glmulti function in R). We also tested the collinearity among variables of the selected model and removed variables that were considered redundant. Hence from this analysis, the proportion of sand and silt was removed.

3. Results

3.1. Temporal change in diversity indicators over time at national and regional level

At national level, the diversity of crop sequences and the agronomic value of the sequences decreased according to all combinations of indicators and categorizations of crops between the period 2005–2010 and 2011–2016 (see supplementary material G). At regional level, the calculation of the 26 out of 30 measures of diversity for the two periods showed a significant decrease in diversity ($p < 0.01$). The 4 indicators that do not follow this trend include the Simpson's Diversity index in Region 1 which does not experience any significant change between the two periods and the agronomic quality of sequences which actually increased in Region 1, 2 and 3 ($p < 0.01$; Fig. 3.).

For the "Simpson's Index of Diversity (SID)", there is an increasing gap between 2005 and 2010 and 2011–2016 in the value of indicators from Region 1 to Region 5. We observe a decrease of sequences with a SID of 0.8 in Region 1 and 2, accompanied by an increase of sequences with a value of 0.33. In Regions 3 and 4 we observe a decrease of sequences with a SID value of 0.73 and parallel increase of sequences with a value of 0.33 (Fig. 3.A) (see Supplementary Material H for examples of crop sequences). For the agronomic value of sequences, the trends are different. In Region 1, the number of sequences with a value of around 10 decreases, while the ones with a value of about 5 increases. In Regions 2 and 3, the number of sequences with values below 10 decreases, and the ones with a value above 10 increases, indicating improved agronomic quality. For Regions 4 and 5, the number of sequences above 10 decreases over time, and the number of sequences with a value below 10 increases, indicating reduced agronomic value (Fig. 3.B). For the first three indicators, these variations indicate a shift in crop sequences towards lower diversity and a decrease in the agronomic quality of crop sequences, particularly for the less productive regions.

3.2. Patterns in diversity and crop sequence over time

At the national level, about 22 % of the field area experiences a change in crop sequence type, especially in Region 5, where 42 % of the area has experienced a transition, while other regions are more stable, with about 11–12 % of fields experiencing such change. We observed that at the national level, a major dynamic of change concerns the shift of 18 % of "Diversified sequences" towards "Permanent grassland" that last for the whole 6 years, which shows how the reduction in diversity mentioned previously translates into crop sequence change (Fig. 4). The number of "cereal rotations with perennial crops" has experienced two pathways of change, with 14 % becoming 'Permanent leys' and 13 %

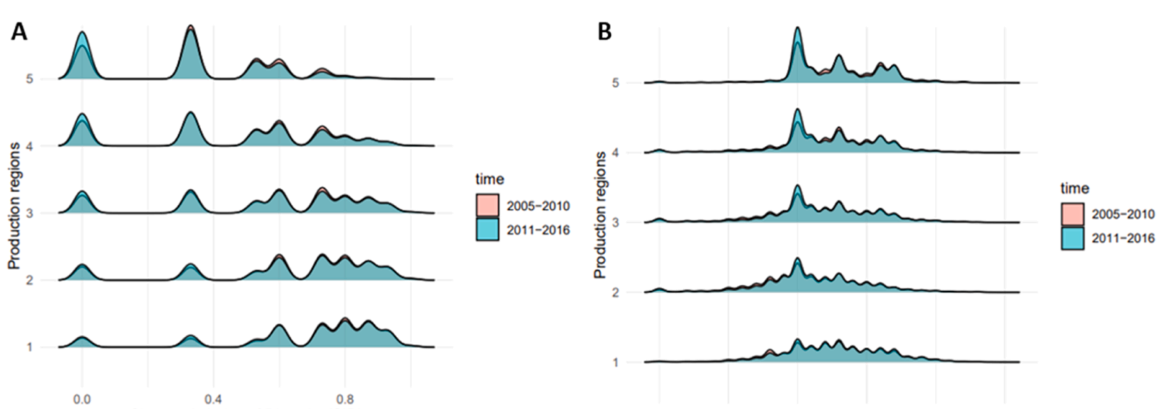

Fig. 3. Evolution of the two diversity indicators between 2005 and 2010 and 2011–2016 in Sweden for the crop categorization "Species" which shows the reduction in diversity across all regions with increasing severity from region 1–5. The higher the peak the higher the number of fields. For the agronomic transition, values range from 0 to 30, with higher values indicating higher agronomic benefits from the pre-crop effect (Supplementary material E).

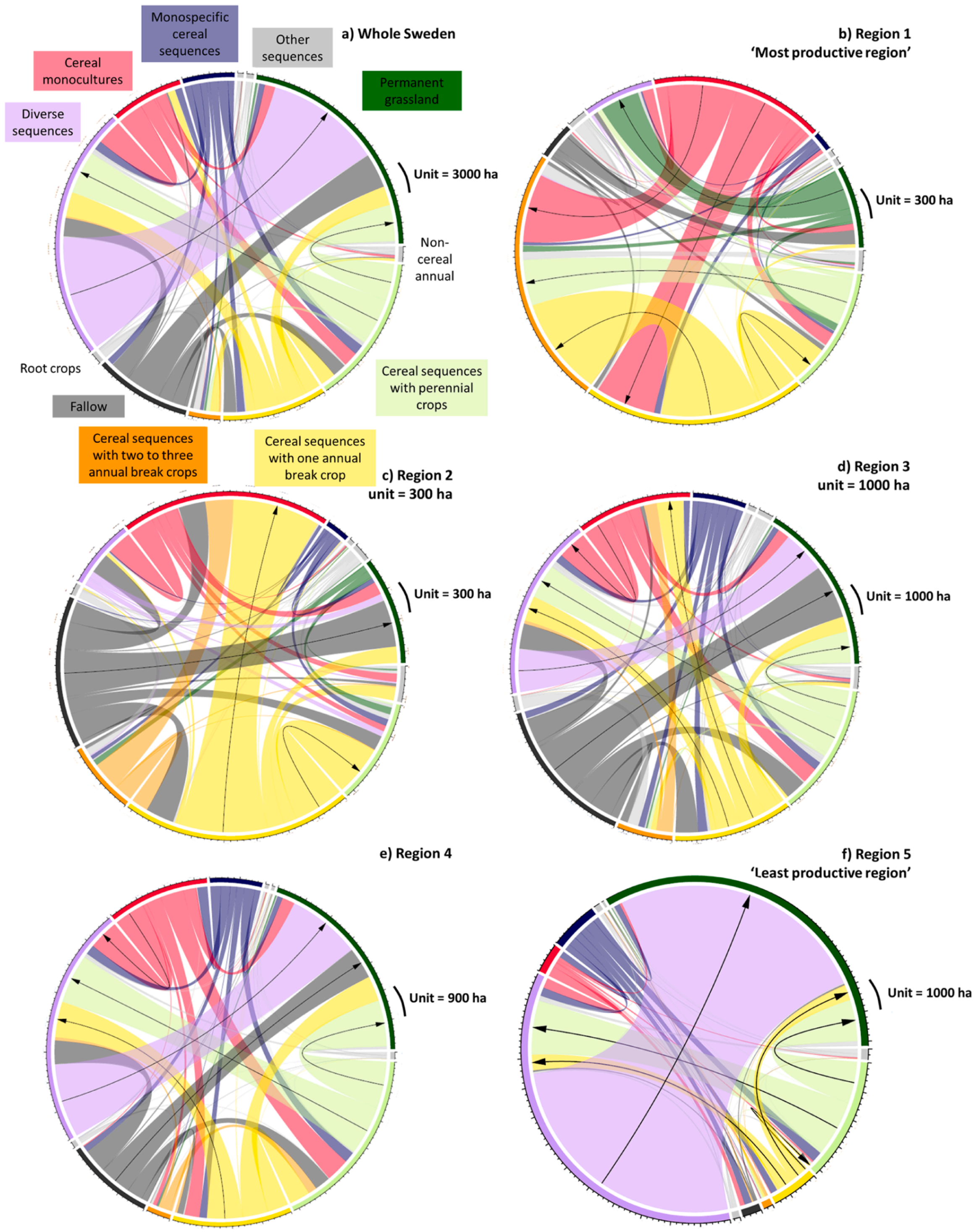

Fig. 4. Circular plot showing the transitions among crop sequence type between 2005 and 2010 and 2011–2016. Each crop sequence type is represented by a given colour. The ribbon shows transitions of fields from one type to another between the two periods. The width of the ribbon represents the area of fields in transition from one type to another. The more noticeable transitions of fields are highlighted with a black arrow.

becoming "Diversified rotations". When looking at the regional level, the trends in change across regions are different, as the transition from "Diversified sequences" and "Cereal sequences with perennial crops" to "Permanent grassland" is mostly happening in Region 4 and 5, with about 4000 and 12,000 ha, respectively, and to a lesser extent in Region 3, with about 3000 ha. Region 3 seems to experience a diversification process in parallel, as about 5000 ha previously under "Cereal sequences with one break crop", "Cereal sequences with 2–3 break crops", and 'Cereal sequences with perennial crops' have become 'Diversified sequences'. A similar process is occurring in Region 1, where about 3000 ha of land under 'Monocultures' and 'Cereal sequences with one break crop' have become more diversified towards 'Cereal sequences with one break crop' and 'Cereal with two to three break crops'. In Region 2, both processes of diversification and homogenization are happening simultaneously, with about 1000 ha shifting towards 'Monocultures' and 'Cereal sequences with perennial crops'.

3.3. Structural change in sequences at national and regional level

At the national level, major trends emerge in the pairs of preceding and following crops especially the decrease of fallow land (fallow after fallow) which then represents 4.1 % of the 881,359 ha in the period 2011–2016 (Table 1), a 30 % increase in old leys (30 % of the land) and a 20 % reduction in young leys (7.8 % of the land). The area cultivated with oats after oats (2.3 % of the land) and spring barley after spring

Table 1
Proportion of the different pairs (i.e. couple of preceding and following crops in the sequence in 2011–2016 for the whole Sweden (upper table), region 1 (middle table) and region 5 (lower table). The colours are percentages of variation of the pair of preceding and following crop from the first period to the second. The column on the left represents the preceding crop and the crop on the upper line is the following crop.

2011-2016	Beans	Fallow	Young ley	Old ley	Mixtures	Oats	Others	Peas	Potatoes	Rye	Spring barley	Sugar beet	Spring rape	Spring wheat	Tritical	Winter barley	WOSR	Winter wheat
National level- Beans						0.1					0.1			0.1				0.1
Fallow		4.1	0.6		0.1	0.4	0.2				0.3			0.1			0.1	0.4
Young ley		0.3	7.8	7.1	0.1	0.2	0.1				0.2			0.1			0.1	0.2
Old ley		0.6		29.1	1.0	1.5	0.4				2.0			0.3	0.2		0.2	0.5
Mixtures		0.1	1.5		0.4	0.1					0.1							
Oats		0.4	1.9		0.1	2.3	0.1	0.1		0.1	1.6		0.1	0.4	0.1			0.9
Others		0.2	0.5				2.6				0.2							0.1
Peas											0.1							0.3
Potatoes									0.2		0.1							0.1
Rye						0.1				0.1	0.1						0.1	
Spring barley		0.5	2.9		0.2	1.6	0.1	0.2	0.1	0.1	3.8	0.10	0.2	0.5	0.2	0.1	0.4	1.2
Sugar beet											0.2							
Spring rape						0.1					0.2			0.2				0.3
Spring wheat		0.1	0.4		0.1	0.5					0.6		0.1	0.4				0.2
Tritical			0.1			0.2					0.3				0.2			0.1
Winter barley																	0.1	
WOSR										0.10	0.1				0.1			1.0
Winter wheat	0.2	0.3	0.2		0.1	1.1	0.1	0.2	0.1	0.1	1.9	0.2	0.2	0.2	0.1	0.1	0.3	1.9
Region 1- Beans						0.1					0.1			0.2				0.6
Fallow		1.8	0.2			0.1	0.1				0.1						0.4	0.6
Young ley		0.2	3.2	2.6			0.1				0.1			0.1			0.2	0.4
Old ley		0.3		8.5	0.2	0.2	0.1				0.5			0.1	0.1		0.4	0.9
Mixtures			0.3		0.1													0.1
Oats		0.1	0.7			0.3				0.1	0.3			0.1				1.2
Others		0.4	0.4				4.7		0.1		0.3	0.1		0.2				0.9
Peas																	0.3	1.3
Potatoes									0.1		0.3							0.2
Rye		0.1	0.1			0.1	0.1	0.1	0.1	0.7	0.3	0.1			0.1		0.4	0.1
Spring barley	0.2	0.4	1.2		0.1	0.5	0.5	0.6	0.2	0.4	3.1	0.5	0.2	0.2	0.2	0.2	3.7	3.8
Sugar beet						0.1	0.1	0.1	0.1		3.3			0.3				0.5
Spring rape														0.1				0.6
Spring wheat	0.1	0.1	0.2			0.2	0.1	0.1			0.3			0.2			0.1	0.5
Tritical	0.1		0.1			0.2					0.3				0.3		0.1	0.1
Winter barley																0.1	0.6	0.1
WOSR		0.1	0.1							0.4	0.1			0.1	0.2	0.1	0.1	7.2
Winter wheat	0.7	0.8	0.5		0.1	1.4	0.7	1.0	0.2	0.4	6.1	3.3	0.3	0.4	0.4	0.4	2.5	9.4
Region 5-Beans																		
Fallow		2.2	0.5		0.1	0.2					0.3							
Young ley		0.2	10.3	10.1	0.1	0.2	0.1				0.3							
Old ley		0.8		46.1	1.9	1.9	0.5		0.1		3.6			0.3	0.2			0.1
Mixtures			2.5		0.5	0.1					0.1							
Oats		0.2	2.0		0.1	1.4					0.7			0.1				
Others			0.5				0.6											
Peas																		
Potatoes			0.1						0.2		0.1							
Rye																		
Spring barley		0.3	4.3		0.2	0.5					3.5		0.1	0.2				0.1
Sugar beet																		
Spring rape											0.1							
Spring wheat			0.3			0.1					0.1			0.1				
Tritical						0.1					0.1							
Winter barley																		
WOSR																		
Winter wheat						0.1					0.1							

-100%	-75%	-50%	-25%	0	25%	100%	200%

*WOSR = Winter oilseed rape

barley (3.8 % of the land) decreased by 20 % and 10 %, respectively.

The agronomic value of rotations in the most productive region (Region 1) increased due to an increase of winter wheat after winter oilseed rape by 30 %, which represents 7.8 % of the area of region 1 (81,155 ha in 2011–2016), a decrease of fallow land (fallow after fallow) by half (1.8 % of the land) and to a minor extent a decrease of winter wheat following spring barley by 10 % (3.8 % of the land). Conversely, the area of some pairs of low agronomic value increased, particularly winter wheat after winter wheat by 20 % (9.4 % of the land) and spring barley after winter wheat by 10 % (6.1 % of the land). The duration of leys also increased significantly as shown by the 70 % increase of the pair old ley – old ley (8.5 % of the land). In Region 5, no significant increase of agronomically beneficial pairs of preceding following crops was identified. On the contrary, the duration of leys increased significantly as shown by the 20 % increase in the number of pairs old ley – old ley, which in the period 2011–2016, constituted 46 % of the area in the region. Mechanically, in parallel to this increase in old ley duration, the young ley – old ley pair decreased by 20 % to occupy 10.1 % of the area. The spring barley – spring barley pair decreased by 20 % (3.5 % of the area), while the old ley – spring barley pair increased by 10 % (3.5 % of the area) (Table 1).

3.4. Drivers of change in crop sequences in Sweden

All factors except monogastric animal density and the amount of rainfall significantly impacted the diversity in the sequences, specifically the increase of perennials, particularly old leys, in the sequence between the two periods (Table 2). We can see that it is mostly large crop farms with large fields that tend to diversify. Conversely, livestock and mixed farm orientation triggered a decrease in diversity, with the area and duration of leys increasing on farms and the cereal area reducing in parallel. The diversity process occurred in fields that had higher clay content, which offers better levels of fertility and thus broadens the portfolio of crops that can be grown, along with the temperature and the altitude. Crop rotations were more likely to become diversified in fields with higher rather than lower average annual temperatures. Sloping land has also been increasingly converted into old leys. We also ran a mixed model to explain the agronomic value of crop rotations (Supplementary Material I), which showed similar effects for most variables, except for 'Monogastric density at the local level', 'Clay content of the field', and the 'Mixed farm type', which exhibited opposite significant trends. Typically, farms with monogastric animals and mixed farms tend to include a lower proportion of ley crops and more diverse crops for animals, which significantly contribute to increasing the agronomic value of crop rotations. As fields with clay soils are generally more fertile, they can be cultivated with a larger portfolio of crops.

Table 2
Results of the mixed effect model on the diversification process which is represented by the difference between the SID value with the crop categorization "Species" between 2011 and 2016 and 2005–2010.

Factors	Value	Std.Error	t-value	p-value
(Intercept)	-0.146266	0.01143175	-12.7946	< 0.01
Area of the farm (ha)	0.000072	0.00000909	7.9282	< 0.01
Area of the field (ha)	0.000612	0.00019275	3.1759	< 0.01
Ruminants density at local level (LSU/ha)	0.033490	0.00670835	4.9922	< 0.01
Monogastric density at local level (LSU/ha)	−0.002953	0.00294193	−1.0036	0.316
Clay content of the field (%)	0.000458	0.00009799	4.6732	< 0.01
Altitude (m)	0.000095	0.00001831	5.1911	< 0.01
Temperature (℃)	0.018622	0.00111530	16.6966	< 0.01
Rainfalls (mm/yr)	−0.000138	0.00010733	−1.29020	0.197
Slope (%)	−0.003480	0.00047574	−7.3139	< 0.01
Farm type - Livestock	−0.173137	0.00329151	−52.6010	< 0.01
Farm type - Mixed	−0.024924	0.00303236	−8.2193	< 0.01

4. Discussion

We combined three types of crop rotation studies namely an approach based on crop diversity indicators, a crop sequence analysis and a typification approach to establish relationships between crop diversity changes and underlying drivers. This combination highlights i) the variation in functional and structural diversity of crop sequences and their agronomic quality, ii) the change in crop rotation types associated with this variation, and the changes in structure of preceding and following crops, and iii) the identification of underlying farm level drivers that can explain changes. The framework enabled us to use national or regional statistics to identify changes in crop sequences. Crop sequences are one of the most important components influencing the intensity and diversity of cropping systems. The framework also allowed us to use a statistical approach to understand how changes in support for some crops can potentially reverse temporal trends in crop choice and sequence.

4.1. Benefits of identifying crop rotation change rather than crop-based change

Our analysis showed that a decrease in the cultivation of some cereals created a transition in crop rotation types from diversified and ley-based cereal rotations towards continuous leys or pastures in most agricultural areas in Sweden during the study period. Crop statistics and land use studies supported by these statistics allow crop change to be quantified, as in a previous study in the south of Sweden, where a decrease in cereals and an increase in leys was reported between 2002 and 2010 (Trubins, 2013). However, such land use change studies do not allow analysis of how crop sequences change over time in the way we have been able to observe them in our study area. From statistics, the increased proportion of ley could be perceived as a positive trend in crop rotations as introducing one year of ley in cereal based cropping system is positive in terms of environmental impacts (Prade et al., 2017) and more grassland is generally positive for biodiversity (Prangel et al., 2024). Additionally, introducing rotational perennial ley in cereal-based cropping systems positively contributes to several ecosystem services, including carbon sequestration, soil structure and, more generally, soil health (Martin et al., 2020). However, longer leys or conversion to permanent grassland could indicate agricultural extensification or land abandonment, the latter defined as arable land where management does not occur for a minimum of 4 years (Prishchepov et al., 2021). This is aligned with the mapping of land abandonment risk at European level that shows that the least productive regions in Sweden are at risk of land abandonment (Perpiña Castillo et al., 2021).

4.2. The need for several diversity indicators and regional assessment

Our study shows the value of using several diversity indicators to study diversification of crop rotations across several crop categorizations and across scales as this can give a more nuanced perspective on the reality of diversification or homogenization of agriculture, as compared to previous studies (Nilsson et al., 2022; Schaak et al., 2023; Stein and Steinmann, 2018; Vandevoorde and Baret, 2023). For example, in the most productive region (Region 1) we observed that functional diversity of crop rotation decreased but our agronomic indicator increased: rotations are less diverse but agronomically better. A previous study in Sweden highlighted a decrease in crop diversity from 2013 to 2019 with associated identified drivers of change but without assessing the specific change in crop rotations that triggered this decrease in diversity (Sjulgård et al., 2022). The cereal area in Sweden has decreased over the period 1995–2012 since EU accession, but this decrease has mostly affected regions where yield productivity is lower, while in the most productive regions, the area of winter wheat has increased along with winter oilseed rape, which has increased this agronomically positive pair of crops, helping to maintain and increase the agronomic quality of crop rotations (Jordbrusverket, 2014). Indeed, winter oilseed rape and sugar beet as preceding crops to winter wheat have been shown to lead to a significantly higher yield of about 1.00 and 0.43 t.ha^{-1}, respectively, compared to wheat after wheat (Groeneveld et al., 2024). Angus et al. (2015) reported a similar level of yield increase in a global meta-analysis including a large number of experiments performed in Sweden.

Besides the use of different indicators of crop diversity, we observed that when testing our diversity indicators against several crop categorizations, the significance of changes in diversity could vary. For example, when using the botanical "family" categorization, changes in diversity were only significant at the national level ($p < 0.05$). This suggests that changes in botanical diversity (i.e., diversity based on plant families) were detectable only at the national level, whereas changes in diversity based on crop use (i.e., the variety of different crop types grown in fields)were consistently detectable across all spatial levels. In general, the way agronomists categorize crops can vary from one study to another depending on the classification criteria adopted (i.e., seasonality, crop use and genetic proximity) and this can create variations in the number of categories and the crops included in them. While studying changes in diversity in Sweden, Sjulgård et al., (2022) and Schaak et al., (2023) used 13 and 10 crop categories respectively and our study used 10 crops and 18 crops for our agronomic and species categorization, respectively. Strong rationale should be provided for the categorization of crops to avoid under-estimation or over-estimation of diversity change. Alternatively, studies can also produce some sensitivity analysis to ensure that trends observed are not an artefact of uninformed choices in categorizing crops.

4.3. Overview of change in diversity as a first step for policies to reverse potential decreases

This framework can help identify whether policies aimed at diversifying agriculture have been successful, which is important because it has been reported that policymakers lack an overview of changes in diversity due to inaccurate data and knowledge (Roesch-McNally et al., 2018). As we tested the change in diversity, before and during/after the 2013 European Union CAP greening reform, it seems that this reform did not have readily quantifiable effects on increasing crop rotation diversity in Sweden as whole. However, since the obligation to diversify crop choice only apply to farms larger than 30 ha and that many farms in the study are smaller than 30 ha, impacts of the reform could be hidden. In France, where farms are, on average, larger this effect was found (Diop and Védrine, 2025; Sauquet, 2023). On livestock farms, it is likely that the opportunity to produce silage from leys has to some extent allowed home produced silage to replace the use of increasingly costly concentrate (Spörndly and Nilsdotter-Linde, 2011). However, the change is even more likely to be the result of specialisation that has been a general trend in agriculture through recent decades (de Roest et al., 2018) combined with extensification through converting leys to low input permanent grass in more marginal areas, as evidenced by the increasing proportion of old leys in the less productive regions. To obtain EU subsidies on mixed crop-livestock farms, farmers were likely faced with the choice of maintaining annual crops or leaving their land under perennial grassland, which could then be harvested for fodder to use on farm or sell. During the period, barley areas decreased due to lower demand for feed grain, driven by a declining number of pigs and cows. Oats also decreased, probably because of lower profitability compared to other crops, and growers increasingly preferred higher-yielding winter wheat. (Eklöf, 2014). Lower crop diversity on livestock farms, compared to crop farms, has also been shown recently in other areas, like central Germany (Janicke et al., 2022). In that region, farmers chose to produce more cereals, but this option was likely not considered feasible in Sweden where cereal yields are lower, particularly in areas with much livestock. This specialisation on fewer crops could also be because farmers are working part-time on their farm and rely on off- farm income, so they have fewer resources to allocate to diversification. Additionally, skills and equipment are needed to diversify which are more often found on large farms (Meynard et al., 2018; Rissing and Burchfield, 2024). A previous study supported this also for Sweden, where authors showed that large and medium sized farms can benefit economically from a stronger emphasis on diversification (Nilsson et al., 2022).

The significantly increased areas of permanent, possibly unmanaged, grasslands would probably require increased financial compensation to incentivize active management of this land again (Wallander et al., 2019; Stenkese, 2017). Higher levels of incentives for other crops (e.g., legumes) to increase profitability coupled with increased support in terms of advice, availability of improved varieties, market structures and security, consumption incentives, among other factors, would allow for increased diversification in such farms (Leclère et al., 2024; Meynard et al., 2018, 2017).

Finally, our analysis indicates that warmer temperature lead to higher crop rotational diversity. As the average start of the growing season in Northern Europe has advanced more than 9 days since the 1970s, this has favoured the cultivation of winter cereals in larger areas, such as winter wheat in Regions 1 and 4 and winter barley in Regions 1 and 3 (Eckersten et al., 2008). Warmer temperatures may offer more opportunities for growing a wider range of crop species, but climate change will also be challenging for maintaining the resilience of farming systems in Sweden (Juhola et al., 2017).

4.4. Limitations of the approach

Limitations of the approach are inherent to the type of data used and the type of drivers considered here. Firstly, the IACS database provides great insight into real agriculture, but not all farmers report their crops, which may contribute to omitting systems of interest and missing a portion of the arable land in the country/region targeted. We described the crop sequences on 41 % of the declared area. This proportion of area can seem low, but is relatively large compared to other studies using the LPIS data, such as Stein and Steinmann (2018), who linked 34 % of fields in Saxony for a period of 7 years (Germany). Additionally, information regarding cover crops and crop variety is missing, which means that the study of diversity is restricted to main crops at species level. In the present study, we have divided the ley crop into two crops, young and old leys, which is based on the assumption that leys change species composition and traits as they get older, but this division is quite arbitrary since the term ley covers a wide diversity of species mixtures, species associations, and management types, such as the frequency of cutting. The crop sequences considered here are fixed, so we may undermine the diversity of long rotations (Castellazzi et al., 2008) which are difficult to identify without a clear starting crop thus we cannot assess if crops are rotated in a fixed order or if farmers are continuously adapting their rotations (Xiao et al., 2014). Secondly, not all drivers can be integrated into the framework developed. Even though we were able to identify temperature, slope, and livestock type and density as drivers of diversity, other socioeconomic aspects could not be captured. For instance, constraints on diversification include genetic progress, approval of phytosanitary products, market incentives, or advice on some minor crops (Voisin et al., 2014). This can only be highlighted qualitatively, but it remains difficult to see the weight that these drivers carry compared to more spatially located ones.

5. Conclusion

In the framework developed in this paper, we were able to highlight a significant decrease in the diversity of crop sequences in Sweden over the period 2005–2016 across two indicators of diversity and different crop categorizations. However, this national-scale change hides different directions of change in diversity at the regional level. Overall, diversification has occurred in productive areas where crop sequences have become of higher value agronomically, especially with more winter wheat after winter oilseed rape. On the other hand, a process of homogenization of production is occurring in large parts of the land in less productive regions with the replacement of diversified crop rotations by permanent grasslands. In productive regions, located in the south, the larger farm size and relatively warmer temperatures compared to other regions have allowed them to retain a larger crop portfolio than smaller farms in the mixed and forested landscapes in the southern highlands and towards the north. In those regions, smaller farms with likely fewer resources and more constraining climates have less propensity to diversify their cropping systems. This decrease in diversity, particularly observed in less productive regions, calls for more ambitious policies and financial support for farmers to adopt more crops and improve the management of their pastures, which would contribute to preventing potential risks of land abandonment in regions of lower agronomic potential. The framework can be widely adopted in European countries with the established Land Parcel Identification System to monitor changes in crop rotation diversity, which is one of the most important indicators of agricultural intensification and sustainability.

CRediT authorship contribution statement

Ingrid Öborn: Writing – review & editing, Supervision, Project administration, Funding acquisition. **Christine Watson:** Writing – review & editing, Supervision, Conceptualization. **Pierre Chopin:** Writing – review & editing, Writing – original draft, Methodology, Formal analysis, Data curation, Conceptualization. **Hermouet Suzanne:** Formal analysis, Methodology, Writing – review & editing. **Göran Bergkvist:** Writing – review & editing, Supervision, Conceptualization.

Declaration of Competing Interest

Authors have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.eja.2025.127848.

Data availability

The authors do not have permission to share data.

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