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Evolution of temporal diversification in crop sequences: a case study of Flanders

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ABSTRACT

Temporal crop diversification is increasingly promoted to enhance the sustainability and resilience of European agricultural systems, yet long-term field-level evidence on how crop sequences evolve remains limited. This study investigates changes in crop sequence typologies and complexity in Flanders between 2008 and 2023 using Geo-Spatial Application data, with particular attention to potato return times given this crop's growing economic importance and stringent phytosanitary requirements. Crop sequence typologies were identified for two eight-year periods, while complexity was assessed using the Rotational Complexity Index. Potato return times were analysed separately using a backward-looking approach. Flemish agriculture was dominated by a limited number of typologies, particularly permanent grassland, root crop sequences, and cereal-dominated systems. Although 38.5% of the agricultural area changed typology between the two periods, transitions occurred mainly among a restricted set of dominant systems. Changes in complexity were significant but small. Potato return times were mostly three or four years, with only modest shifts towards longer intervals, suggesting persistent agronomic and economic constraints. Overall, Flemish crop sequences are changing structurally, but without substantial increases in complexity. The proposed approach provides a transferable framework for monitoring temporal diversification and a basis for investigating the drivers of changes in crop sequence complexity.

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Crop rotation; crop sequences; crop diversification; IACS; GSA

1. Introduction

Diversifying the temporal order of crops cultivated on the same land is one of the oldest agronomic practices adopted by farmers (Barbieri et al., 2017). This practice has historically been associated with the concept of crop rotation (Farina et al., 2018), defined as the cyclical succession of different crops on a specific field (Leteinturier et al., 2006). Crop rotations are typically structured according to specific rules, including a defined return time—i.e. the number of years between successive occurrences of the same crop on the same field—and interactions between successive crops (Castellazzi et al., 2008). This practice delivers a range of well-documented agronomic benefits, including enhanced pest and weed control (Médiène et al., 2011; Selim, 2019), improved soil health and fertility (Basso et al., 2019; Rosa-Schleich et al., 2019), greater biodiversity (Beillouin et al., 2019; Tiemann et al., 2015), improved water storage and resilience to drought and heat stress (Beillouin et al., 2019; Bowles et al., 2020), and yield stabilisation or increases (Cernay et al., 2018; Rosa-Schleich et al., 2019). However, over the past century, agricultural intensification in Western countries—driven by genetic improvements, synthetic inputs such as fertilisers and pesticides, and increased mechanisation (Dornbush & Von Haden, 2017; Federico, 2005)—has led to greater crop specialisation and simplified rotations (Hijmans et al., 2016; Plourde et al., 2013). While this has enhanced productivity, it has also increased reliance on external inputs and contributed to biodiversity loss (e.g. Allan et al., 2015), soil and water pollution (e.g. Manevski et al., 2015; Zong et al., 2024), and the degradation

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of ecosystem services (e.g. Bommarco et al., 2013), raising concerns about the long-term sustainability of current agricultural systems (Bennett et al., 2012; Pretty & Bharucha, 2018).

Today, crop diversification is widely recognised as a pivotal strategy for mitigating the adverse effects of intensive agriculture (Isbell et al., 2011; Zhao et al., 2022). It serves as one of the fundamental principles underpinning various alternative farming approaches, including organic agriculture (Barbieri et al., 2017) and conservation agriculture (Palm et al., 2014). Moreover, it forms a central component of broader frameworks, such as ecological intensification (Bommarco et al., 2018) and sustainable intensification (Manevski et al., 2018; Pretty & Bharucha, 2018), which are designed to alleviate the environmental burden of agriculture while maintaining or enhancing productivity. European institutions have recognised the potential of crop diversification and its implications for European agriculture (European Commission, 2020, 2021; European Parliament, 2009), and in the recent past many attempts have been made to promote diversification among farmers, particularly within the framework of the Common Agricultural Policy (CAP) (2021; European Parliament, 2013). The current reform (2023–2027) places particular emphasis on temporal diversification, explicitly addressed under the Good Agricultural and Environmental Conditions (GAEC 7 - Crop Rotation)—the set of rules farmers have to observe in order to receive the direct payments; additionally, the reform allows Member States to promote practices that go beyond these minimum GAEC 7 requirements through voluntary instruments such as eco-schemes (European Parliament, 2021). However, these rules were softened after 2024 to adapt to changes in the geopolitical context; for example, spatial diversification can also be used to fulfil the CAP requirements.

When studying temporal diversification, it may be necessary to move beyond the concept of crop rotation (Steinmann & Dobers, 2013). The process of agricultural simplification has led farmers to prioritise economic factors over agronomic ones (Khoury et al., 2014), resulting in the decline of fixed rotations. These have been replaced either by more flexible rotations—progressively losing their cyclical aspect (Castellazzi et al., 2008; Dury et al., 2013)—or by simplified rotations with shorter cycles, typically spanning two or three years (Stein & Steinmann, 2018). Consequently, analysing longer timeframes may require evaluating thousands of permutations, with the risk of overlooking critical insights (Leteinturier et al., 2006; Vandevoorde & Baret, 2023). To address this challenge, this study adopts the concept of crop sequence, as defined by Leteinturier et al. (2006) as the 'order of appearance of the crops during a fixed period'. This approach offers greater flexibility, allowing for more freedom without the constraints linked to the concept of rotations.

Previous research has focused on predicting the most likely crop to be planted based on historical sequence records (Basso et al., 2019; Castellazzi et al., 2008; Dogliotti et al., 2004; Dury et al., 2012; Palka et al., 2026; Upcott et al., 2023), or on the reasons behind farmers' decisions to plant specific crops (Dury et al., 2012; Peltonen-Sainio et al., 2017; Socolar et al., 2021), which are often shaped by previous cropping decisions as well as current market conditions (Palka et al., 2026). Several studies have also evaluated the sequences implemented by farmers, assessing either their agronomic quality (Bockstaller & Girardin, 1996; Desmarez et al., 2026; Leteinturier et al., 2006; Vandevoorde & Baret, 2023) or their diversity (Chopin et al., 2026; Jänicke et al., 2022; Nowak et al., 2022; Reumaux et al., 2023; Schiller et al., 2024; Stein & Steinmann, 2018; Steinmann & Dobers, 2013; Vandevoorde & Baret, 2023), with the objective of representing the current state of agriculture in specific European countries. Such analyses have been made possible by the historical data provided by the Integrated Administration and Control System (IACS), an interconnected set of databases used to monitor subsidies associated with the CAP (Integrated Administration and Control System (IACS), n.d.).

Nevertheless, previous analyses of crop sequences have faced several challenges. First, the frequent focus on a restricted timeframe, due to temporal data availability, makes it impossible to assess changes beyond a very brief time period. In fact, the literature suggests a minimum of seven consecutive years to effectively capture changes in cropping dynamics and adequately represent highly diversified sequences or those involving perennial crops (Leteinturier et al., 2006; Upcott et al., 2023; Vandevoorde & Baret, 2023). However, a limited number of studies have analysed crop sequences over long timeframes, examining periods between 10 and 26 years (Chopin et al., 2026; Desmarez et al., 2026; Jänicke et al., 2022; Palka et al., 2026; Reumaux et al., 2023; Whippo et al., 2026). Despite this extended temporal coverage, only Jänicke et al. (2022) and Desmarez et al. (2026) compared multiple time periods of at least seven years, and only the second study exceeded this minimum by considering time periods of 13 years. Moreover, these two studies

differ substantially in their analytical focus. Jänicke et al. (2022) concentrated primarily on diversity among crop types and functional groups, considering the effect of only the immediate preceding crop on the following one, while overlooking interactions between crops that persist for more than one year. Contrastingly, Desmarez et al. (2026) assessed the agronomic quality of crop sequences using an indicator adapted and validated for the Belgian region of Wallonia (Leteinturier et al., 2006; Vandevoorde & Baret, 2023), which cannot be used in other regions or countries without further adaptation through a process of expert consultation.

Second, with the exception of the case study by Vandevoorde and Baret (2023) on grassland regions, previous research has predominantly focused on all arable sequences, which are often dominated by maize or cereal monocultures, as observed in Bavaria and Lower Saxony (Jänicke et al., 2022; Stein & Steinmann, 2018). The dominance of these maize and cereal monoculture sequences risk obscuring the dynamics and changes of sequences involving other important crops, such as potato, which cannot be planted as frequently as maize or cereals due to high susceptibility of soilborne diseases (Li et al., 2023; Wright et al., 2017). Particularly, potato cultivation typically requires return times of at least three years and often longer depending on pedo-climatic conditions (Hills et al., 2020; Peters et al., 2003), whereas cereals are often grown in much shorter cycles or even in monoculture. Nonetheless, potatoes can be quite important in certain countries; for instance, in Flanders potatoes have gained considerable relevance, both in spatial coverage and economic importance (Agriculture Report 2024 (LARA), 2024). At the same, time potato cultivation requires substantial irrigation, nutrient inputs, and frequent use of crop protection products (Birch et al., 2012; Cooke et al., 2011; Hills et al., 2020; Pawelzik & Möller, 2014), thereby highlighting the need to examine in detail how potato is cultivated, particularly in those countries where it represents a key cash crop, such as Belgium. These dynamics extend beyond the Flemish context and call for a more crop-specific and transferable analytical approach.

This paper adopts an extended temporal scope to analyse changes in the typology and complexity of crop sequences over a 16-year period. Using IACS data from 2008 to 2023 for Flanders, it pursues three main objectives: (i) it identifies the main typologies of crop sequences implemented by Flemish farmers and examines how these have evolved over time; (ii) it evaluates changes in the complexity of these sequences; and (iii) it analyses the evolution of return times, with a particular focus on potatoes.

2. Materials and methods

Flanders is one of the three federal regions of Belgium, alongside Brussels Wallonia. It is divided into seven agricultural regions (Figure 1). The Dune region, located in the northwest, corresponds to the North Sea coastline. Further inland, and in the eastern limit of the north-central area near the mouth of the Scheldt River, there is the Polder region, which is characterised by land reclaimed from the sea and predominantly composed of clayey alluvial soils (Dumortier et al., 2006). The central part of Flanders is occupied by the Sandy region, which, like the Campine (Kempen) region in the northeast and east, is dominated by sandy soils. In contrast, the southern Sandy Loam region and Loam region are marked by a progressive increase in loamy soils, with the latter primarily located along the border with Wallonia, where the majority of the Loam region extends (Dondeyne et al., 2014; Dumortier et al., 2006). Additionally, the southeastern exclave, which borders Wallonia and the Netherlands, forms part of the Liège Grassland region.

Flanders lies in a temperate climatic zone influenced by the Atlantic Ocean and the North Sea (Dumortier et al., 2006). Annual precipitation ranges from approximately 700 mm to 850 mm, except in the southwestern exclave, where it averages between 1,000 mm and 1,100 mm (Sevenant et al., 2002). The region's topography is predominantly flat, with elevations ranging from 0 to 200 m above sea level. Altitude increases progressively farther inland, culminating in hilly terrain along the southern border with Wallonia. The highest point—at 288 m above sea level—is located in the southeastern exclave (Dumortier et al., 2006).

In 2023, the region's utilised agricultural area (UAA) covered 672,046 ha, with 371,896 ha (55%) dedicated to ley and forage crops, 224,470 (33%) allocated to other arable crops—especially cereals, potatoes, and sugar beets—and 29,891 ha (4%) used for vegetable production (Analysetabel recentste parceelsaangifte, 2024).

Specialisation varies regionally. The western, central-western, and northeastern areas of Flanders are predominantly characterised by livestock farming, encompassing parts of the Polder, Sandy, and Sandy

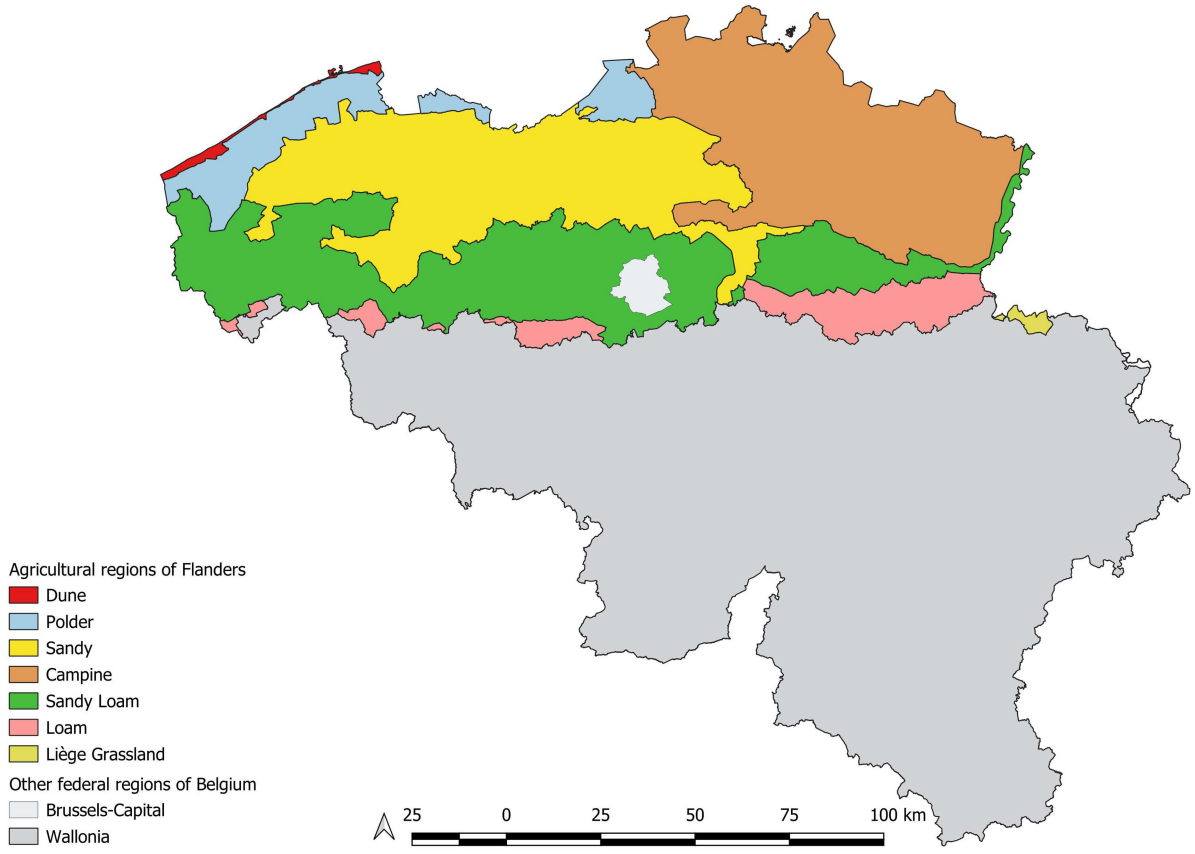


Figure 1. Agricultural regions of Flanders. Source: Landbouwstreken België (2023).

Loam regions, as well as the Campine. In contrast, the central, southern-central, and southwestern regions are primarily dedicated to arable crops, fruit, and vegetable cultivation, overlapping with parts of the Sandy and Sandy Loam regions, as well as the Loam region along the border with Wallonia (Agriculture Report 2024 (LARA), 2024).

In 2023, the area dedicated to potato cultivation reached 56,860 ha, accounting for 9% of the total utilised agricultural area (UAA) of 649,257 ha (Analysetabel recentste parceelsaangifte, 2024). In the same year, potato production represented 19% of the total crop output, with a value of €992.2 million out of €5,162.6 million (Economic accounts for agriculture, 2025). As highlighted in the Agriculture Report 2024 (LARA), 2024) , potatoes were also a major consumer of plant protection products in 2021, representing 33% of the total usage—0.96 million kg of active substance out of 2.9 million kg. Furthermore, potatoes accounted for 8% of the chemical nitrogen fertilisers applied, consuming 5 million kg of nitrogen out of 62.6 million kg.

Given the stringent constraints associated with this crop, particularly its phytosanitary requirements, Flanders has enforced a mandatory minimum period of at least two years before potatoes can be replanted in the same field, extended to three years for seed potato production, reflecting stricter phytosanitary requirements (Conditionaliteit – Gewasrotatie op bouwland (GLMC 7) 2024, 2024).

2.1. Data source and processing

Data were obtained from Open geodata: Landbouwgebruikspercelen (Agentschap Landbouw en Zeevisserij – Landbouwcijfers) (2024), covering the period 2008–2023. This dataset is part of the Geo-Spatial Application (GSA) system, one of the components of the IACS. It provides detailed information on the location, size, geometry, and main crop—defined as the crop recorded in May—of each field in Flanders for which CAP subsidies were asked. Using the unique identification code assigned to each field, it was possible to integrate data from multiple years, enabling the construction of sequences that represent the crop succession in each

field. This process was performed using QGIS (QGIS, 2023). By integrating data starting from 2023 and tracking backward to 2008, we were able to obtain a sequence of 16 years for each field present in 2023. Incomplete sequences were subsequently excluded, as missing data could indicate that subsidies were not asked for the same field every year or could be attributed to the splitting of larger fields. In total, 83,395 crop sequences were selected, occupying 117,064 ha (17% of the UAA). Alternative methodologies have been developed to derive crop sequences from GSA datasets while accounting for changes in field boundaries. One of the most widely used approaches is raster matching (e.g. Jänicke et al., 2022; Upcott et al., 2023), in which vector data are converted into raster grid cells that constitute the units of analysis. Compared with the method proposed in this study, rasterisation generally achieves high spatial coverage; however, it also results in a loss of spatial context because the original field boundaries are no longer retained (Pahmeyer et al., 2025). Consequently, it is less suitable for studies that aim to analyse crop sequences at the field level.

The dataset was refined through a three-step screening process. First, fields were selected based on the crops present in their crop sequences, retaining those associated with arable, mixed, or horticultural production. Fields linked to non-relevant land uses (e.g. buildings, fruit trees, timber production, ornamental flowers, and greenhouses) were excluded. A complete list of included and excluded crop and land-use categories is provided in the Supplementary Material. As highlighted by previous authors (Jänicke et al., 2022; Leteinturier et al., 2006; Vandevoorde & Baret, 2023), the reporting of temporary and permanent grassland has evolved over time, with this distinction no longer recorded after 2020. To ensure consistency across the entire study period, all grassland observations were aggregated into a single category ('grassland). This step resulted in the selection of 76,119 fields, occupying 108,487 ha (16% of the UAA).

Second, the distinct 328 crops identified in the original dataset were classified into 18 crop sub-groups and 10 broader groups (Table 1). This classification was based on a framework provided by the Flemish Ministry of Agriculture and Fisheries (Vruchtafwisseling met vlinderbloemige 2024, 2024) and further refined by considering both agronomic importance and botanical families (see Supplementary Material for the extended list of included and excluded crops and land uses).

Third, only the fields with sequences containing at least one observation of potatoes between 2008 and 2023 were selected. However, for a subset of these fields, it was not possible to reconstruct a complete crop sequence for the full study period, leading to their exclusion form the analysis. This led to the inclusion of 28,760 fields (46,903 ha; 7% of the UAA). These were used for the analysis of the return time of potatoes.

2.2. Typification of crop sequences

To identify the typologies of crop sequences implemented in Flanders, we used the classification developed by Peltonen-Sainio et al. (2017) and expanded by Chopin et al. (2026), adapting it to the context of the

Table 1. Crop sub-groups and groups (based on Vruchtafwisseling met vlinderbloemige 2024 (2024)).

Crop sub-group	Notes	Sub-group code	Group code
Winter cereals	Includes wheat, barley, oat, rye and triticale	WC	C
Spring cereals	Includes wheat, barley, oat, spelt, millet and sorghum	SC	C
Maize	Includes grain maize and silo maize	M	C
Grain legumes	Includes dry peas, dry beans, dry broad and field beans, lentils, lupins, chickpeas and soy	L	L
Grassland	Includes temporary and permanent grassland	G	G
Leguminous grass	Includes alfalfa and clover	LG	G
Potatoes	Includes early and non-early potatoes	P	P
Sugar beet		Sb	Sb
Fodder beet		Fb	Sb
Herbs	Includes asparagus, radish, eggplants, basil, chives, cauliflower, kale, broccoli,	V	V
Vegetables	cabbages, pumpkins, lettuce, celeriac, parsley, pepper, leek, rhubarb, Brussels sprout, medicinal herbs	V	V
Vegetables (legumes)	Includes green paean, green beans, green broad and field beans	VL	V
Root, bulb, and tuber vegetables	Includes carrots, onions, shallots, turnip, parsnip, rutabaga, salsify beetroot, angelica root, witloof and chicory root	RV	V
Hemp		He	He
Flax	Include oil and fibre flax	Fl	Fl
Winter oilseed rape	Includes other Brassicaceae	WOSR	R
Summer oilseed rape	Includes other Brassicaceae	SOSR	R
Undeveloped land/fallow		Fa	Fa

study region and a length of eight years. We identified 12 typologies of crop sequences: (i) 'Monospecific cereal sequences', in which the same cereal species was repeated for all eight years; (ii) 'Cereal monocultures', in which only winter cereals, spring cereals, or maize were grown across all eight years; (iii) 'Cereal sequences with one annual break crop', which contained cereals for seven years and one year of any non-cereal crop; (iv) 'Cereal sequences with two or three annual break crops', in which there were five or six years of cereals and two or three years of break crops, such as oilseed crops, legumes, or vegetables (maximum two years), with a maximum of one year of root crops tolerated; (v) 'Cereal sequences with perennial crops', which contained at least two years of grassland (including alfalfa and clover) with the remaining years exclusively under cereals; (vi) 'Root crop sequences' which included at least two years of root crops (e.g. potato, sugar beet); (vii) 'Horticultural sequences' in which there were three or more years of vegetable crops; (viii) 'Diverse sequences', which included at least one year of cereals, at least one year of grassland, and at least one other annual non-cereal crop; (ix) 'Grassland sequences', in which at least one year of grassland was present alongside at least one non-cereal annual crop, with no cereal years; (x) 'Permanent grassland', with all eight years under grassland; (xi) 'Fallow' which included at least four years of fallow; and (xii) 'Other', for sequences not meeting any of the above criteria. To avoid ambiguity and ensure mutually exclusive classification, priority was given to 'Monospecific cereal sequences' over 'Cereal monocultures'—the former could be seen as a sub-group of the latter—and to 'Root crop sequences', 'Horticultural sequences', and 'Fallow', which could otherwise have been misclassified as 'Diverse sequences'. To identify changes in the distribution of crop sequence typologies over time, each sequence was divided into two eight-year sub-sequences: the first spanning from 2008 to 2015, and the second covering 2016 to 2023. The classification was then applied independently to each sub-sequence, allowing individual fields to shift between typologies across the two periods.

2.3. Complexity analysis

We evaluate the complexity of crop sequences using the Rotational Complexity Index (RCI), developed by Socolar et al. (2021) based on the work of Bowles et al. (2020) and Tiemann et al. (2015). The RCI, which has thus far been applied exclusively in an American context, provides a measure of the complexity of a given sequence; higher values generally indicate more diverse and complex sequences, which are often associated with improved pest and disease regulation, enhanced soil health, and a reduced reliance on external inputs. The RCI is obtained by breaking the concept into two primary components: the number of crops present in the sequence (n) and the species turnover (T), which represents the changes in crops that occur on a specific field over time. This is further divided into three subcomponents. First, the year-to-year turnover (T_1), which captures changes in crops between consecutive years and can be interpreted as a binary indicator at each time step (i.e. whether the crop in year y_n differs from that in y_{n+1}). For example, a sequence such as ABABABAB results in frequent changes between years ($T_1 = 7$), whereas a sequence such as AAAAAAAA would result in no change ($T_1 = 0$). Second, the two-year turnover (T_2), which reflects the changes in crops over a two-year interval (i.e. between y_n and y_{n+2}). This component captures recurring patterns that are not captured by T_1 alone. For instance, in an alternating sequence such as ABABABA, T_1 would be very high, while T_2 would be equal to zero, indicating short return intervals for the crops in the sequence. In contrast, a sequence such as ABCABCAB would result in high values for both T_1 and T_2, reflecting greater temporal diversity. Third, the pseudo-turnover (T_p), which is designed to account for the presence of perennial crops, such as clover, lucerne, or grassland, which may remain in the field for multiple consecutive years. Without this adjustment, such sequences would be treated similarly to monocultures—the repeated cultivation of the same crop over consecutive years—despite their distinct agronomic characteristics. T_p therefore adjusts the turnover measure by accounting for consecutive occurrences of perennial crops, ensuring that their contribution is not underestimated. The RCI is computed as follows:

$$RCI = \sqrt{n\frac{T_1 + T_2 + T_p}{2}} \tag{1}$$

To analyse the changes in complexity of the selected sequences, each one was divided into two eight-year sub-sequences: the first spanning from 2008 to 2015, and the second covering 2016 to 2023 (see Table 2 for

Table 2. Examples of n, T_1, T_2, T_p, RCI for four hypothetical eight-year crop sequences. A, B, and C represent annual crops, while *P* represents perennial crops (adapted from Socolar et al. (2021)). T_p is computed by counting the number of *P* after the first one.

Sequence	n	T_1	T_2	T_p	RCI
AAAAAAAA	1	0	0	0	0.00
ABABABAB	2	7	0	0	2.65
ABCABCAB	3	7	6	0	4.42
APPPPAAA	2	2	3	3	2.83

examples). After calculating the RCI for each sub-sequence, the unique ID assigned to each original sequence allowed for a direct comparison of the metrics over time. The analysis was conducted in R (R: A Language & Environment for Statistical Computing, 2024) using the package '*dplyr*' (Wickham et al., 2023).

Socolar et al. (2021) justified the use of the term 'rotational' on the grounds that they employed crop sequences as a proxy for crop rotation. However, this interpretation is open to debate, particularly as the RCI does not account for the cyclical components that characterise crop rotations. Nevertheless, this metric remains a valuable tool for studying the complexity of crop sequences.

2.4. Return time analysis

To analyse the return time of potatoes, we calculated the number of years between successive occurrences of potatoes within each of the 28,760 sequences over the period 2008–2023. For each field and year in which potatoes were observed, the return time was defined as the number of years since the previous occurrence of potatoes on the same field. A backward-looking approach was adopted, whereby for each year with potato cultivation, previous occurrences were identified by tracing the sequence back in time. This procedure was applied consistently across all years in the dataset.

Consistently with the rest of the study, the maximum return time considered was six years. This is because a return time of length l requires $l + 1$ consecutive years of observations. Extending the analysis to longer return times would have reduced the number of usable observations at the beginning of the time series, as earlier data would be required. For example, in the sequence PMMMMMP, the return time between the two occurrences of *P* is six years, corresponding to the number of years between the first and second occurrence. More generally, a return time of l indicates that a crop reappears after l years without that crop being cultivated. As a consequence of the backward-looking approach, the first six years of the dataset (2008–2013) cannot be used to estimate longer return times, as earlier observations are not available.

2.5. Statistical analyses

To determine whether there was a significant difference in RCI values between the two periods under analysis, we used the Wilcoxon signed rank test (also known as Wilcoxon matched pairs signed rank). This non-parametric test is the standard method for comparing two related groups without assuming normality in their distributions (Scheff, 2016), making it particularly appropriate for this analysis, as the normality assumption was not satisfied. For the same reason, to account for differences in agricultural regions within the same period, a Kruskal-Wallis test was conducted. In the case of a significant difference (p-value < 0.05), a post-hoc Dunn's test with Bonferroni's correction was applied (Scheff, 2016). Both analyses were performed in R (R: A Language & Environment for Statistical Computing, 2024); using the package '*dunn.test*' specifically for the second (Dinno, 2026).

To analyse the dynamics of return times, since we had a series of observations over time, we employed a modified version of the Mann-Kendall test, as proposed by Hamed and Rao (1998). The original test is a widely used non-parametric method designed to detect monotonic trends in time series, whether upward or downward (Kendall, 1975; Mann, 1945). The modified version adjusts for the presence of serial correlation in the data, without losing power relative to the original test when the data are independent. The analysis was conducted in R using the package '*modifiedmk*' (Patakamuri, 2021).

3. Results

3.1. Crop sequence typologies

In total, 76,119 fields with complete sequences data and no excluded crops were identified, covering 108,486.8 ha. The majority of this area was located in the Sandy Loam (33,166 ha), Sandy (32,966 ha), and Campine (22,939 ha) region, while smaller shares were found in the Polder (9,448 ha), Loam (9,347 ha), and Liège Grassland (507 ha) regions. A small number of fields were attributed to the Dune region (63 fields, covering 100 ha) or were not assigned to any agricultural region (12 fields, totalling 13.4 ha). In the first case this can be explained by the location of these fields at regional boundaries, where more than half of their area fell within neighbouring regions; while in the second this was due to their location falling for more than a half either in Wallonia or Brussels. Given their negligible extent, these fields were excluded from the regional analysis but retained in the analysis at the level of Flanders.

At the Flemish scale (see Table A1 in the Appendix), during the period 2008-2015, more than a half of the agricultural area was occupied by 'Permanent grassland' (32,559 ha, 30.01%) and 'Root crop sequences' (28,559 ha, 26.32%). When combined with 'Cereal sequences with one annual break crop' (12,201 ha, 11.25%) and 'Monospecific cereal sequences' (11,631 ha, 10.72%), these typologies accounted for over three-quarters of the total agricultural area. In the subsequent period, 2016-2023, 'Root crop sequences' became the dominant typology (33,965 ha, 31.31%), followed by 'Permanent grassland' (31,638 ha, 29.16%) and 'Cereal sequences with one annual break crop' (11,414 ha, 10.52%). This is the result of a change in crop sequence typologies that has affected 38.5% of the agricultural area (see Figure 2 and Figure A1 in the Appendix). The most notable transitions occurred from cereal-based typologies, particularly 'Cereal sequences with one annual break crop', 'Monospecific cereal sequences', and 'Cereal sequences with two or three annual break crops', towards 'Root crop sequences'. At the same time, reverse transitions were observed from 'Root crop sequences', which along with 'Monospecific cereal sequences' and 'Cereal monocultures' shifted towards 'Cereal sequences with one annual break crop'. This indicate that, while an important share of the area underwent change, these transitions were structured around a limited number of dominant typologies. Interestingly, in both periods, more than 99% of the area covered by 'Monospecific cereal sequences' was maize monoculture, while in 'Cereal monocultures' the area with sequences dominated by maize was 89% in 2008-2015 and 91% in 2016-2023, suggesting a dominance of this crop over other cereals.

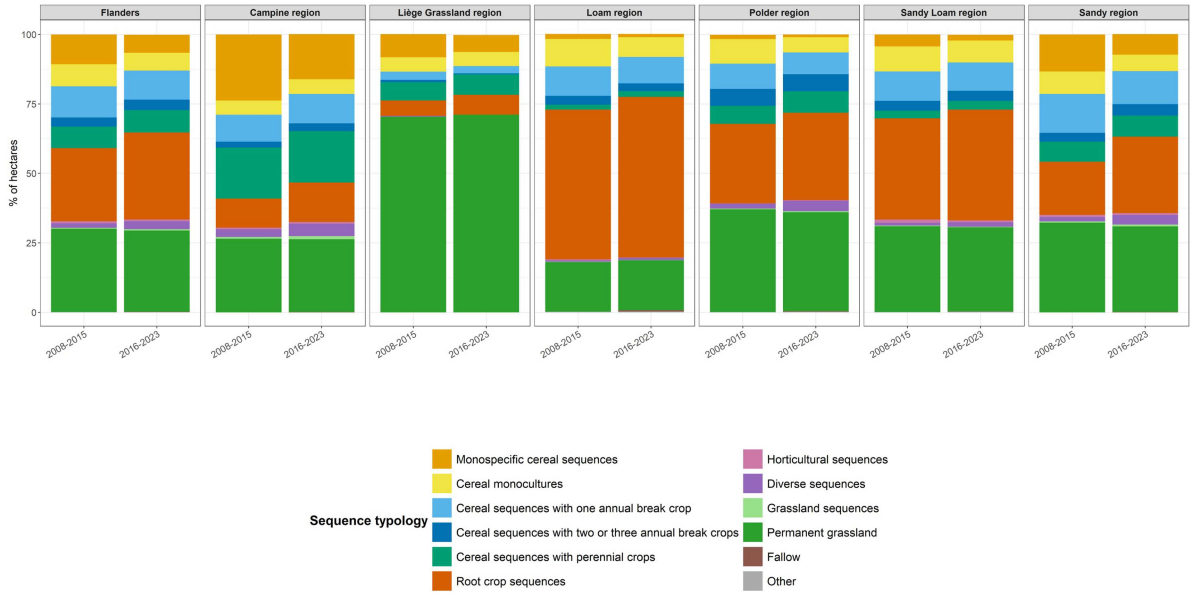


Figure 2. Distribution of crop sequence typologies in Flanders, as well as in the Loam, Sandy, Polder, Campine, Sandy Loam, and Liège Grassland regions. Flanders also include fields located in the Dune region and with no agricultural region assigned.

Distinct dynamics emerge when examining changes within individual agricultural regions (Figure 2 and Table A1). The Liège Grassland region exhibited a high degree of stability, with only 16.4% of the area undergoing a change in typology, followed by the Loam region (27%). In contrast, approximately one-third of the area transitioned in the Sandy Loam (32.3%) and Polder (32.6%) regions, while higher levels of change was observed in the Sandy (44.3%) and Campine (46.6%) regions. Although no single dominant transition pattern was identified at the regional level, several consistent patterns can be observed. In the Sandy, Loam, Polder, and Sandy Loam regions, changes were characterised by simpler cereal sequences—'Monospecific cereal sequences' and 'Cereal monocultures'—moving towards 'Root crop sequences' or more diversified 'Cereal sequences with one annual break crop'. Interestingly, in all four regions an important share of the area was affected by a bidirectional change between 'Root crop sequences' and 'Cereal sequences with one annual break crop', highlighting the lack of a clear directional trend. Conversely, in the Campine region the major changes were from simple cereal sequences towards grassland dominated typologies—'Permanent grassland' and 'Cereal sequences with perennial crops'; similar transitions were also registered in the Sandy region, although there transitions towards 'Root crop sequences' remained dominant. Taken together, both Flemish-level and regional analyses indicate that 'Root crop sequences' and 'Cereal sequences with one annual break crop' play a central and interconnected role in the transition landscape in Flanders, acting as both origin and destination of the most common typology changes (see from Table A2 to Table A7 in the Appendix for an overview).

3.2. Complexity of crop sequences in Flanders

At the Flemish scale, RCI values ranged from 0 to 6.75 in both periods. The median value increased from 2.00 in 2008–2015 to 2.45 in 2016–2023 (Table 3). Between the two periods, 28,048 fields (41,262.9 ha, 38% of the area) experienced an increase in crop sequence complexity, while 18,515 fields (26,145.4 ha, 24.1%) experienced a decrease. The remaining 29,556 fields (41,078.4 ha, 37.9%) showed no change in complexity. The Wilcoxon signed rank test confirmed a statistically significant difference between the two periods ($V = 388{,}043{,}337$, $p < 0.001$), suggesting an overall trend towards greater crop sequence complexity. However, the negligible effect size ($r = 0.03$) indicates that the magnitude of change was very small, likely attributable to the large sample size ($n = 76{,}119$), which increases statistical power to the point where even small differences become statistically significant.

At the agricultural region level (Figure 3), a statistically significant increase in RCI between the two periods was observed in five regions ($p < 0.001$ in all cases). However, effect sizes were consistently negligible to small ($r > 0.1$ to $r = 0.12$), suggesting that the magnitude of change was limited across all regions. The Polder and Loam regions showed the largest effect sizes ($r = 0.12$ and $r = 0.11$, respectively), with median increasing from 2.65 to 2.83 in the Polder region and from 3.24 to 3.67 in the Loam region. In contrast, the Sandy, Sandy Loam, and Campine regions showed negligible effect sizes ($r < 0.1$), with modest or no change in median RCI. The Liège Grassland region was the only one where no significant change was

Table 3. Differences in Rotational Complexity Index (RCI) values between the period 2008–2015 and the period 2016–2023, for all fields in Flanders, as well as the fields in the Loam, Sandy, Polder, Campine, Sandy Loam, and Liège Grassland regions. For each group, the median and the interquartile range (IQR; 1st quartile—3rd quartile) were reported. Flanders also include fields located in the Dune region and with no agricultural region assigned.

		RCI		
Agricultural region	N. plots	2008–2015	2016–2023	Effect size
Loam region	5,937	3.24 (1.87–4.06)[a]	3.67 (1.87–4.47)[e]*	0.11
Sandy region	25,546	1.87 (1.87–3.00)[b]	2.00 (1.87–3.46)[f]*	<0.1
Polder region	4,652	2.65 (1.87–3.87)[c]	2.83 (1.87–4.00)[g]*	0.12
Campine region	14,159	1.87 (0.00–2.65)[d]	1.87 (1.73–2.83)[h]*	<0.1
Sandy Loam region	25,532	2.65 (1.87–3.87)[c]	2.83 (1.87–4.06)[g]*	<0.1
Liège Grassland region	218	1.87 (1.87–2.00)[b,d]	1.87 (1.87–2.00)[h]	<0.1
Flanders	76,119	2.00 (1.87–3.46)	2.45 (1.87–3.67)*	<0.1

Different letters (a, b, c, d, e, f, g, h) within the same study period denote a significant difference using the Kruskal-Wallis test followed by a post hoc Dunn's test at a significance level of 0.05 with Bonferroni's correction.

*Denotes a significant variation (p-value < 0.001), obtained from a Wilcoxon signed rank test performed for all value comparisons between the periods 2008–2015 and 2016–2023.

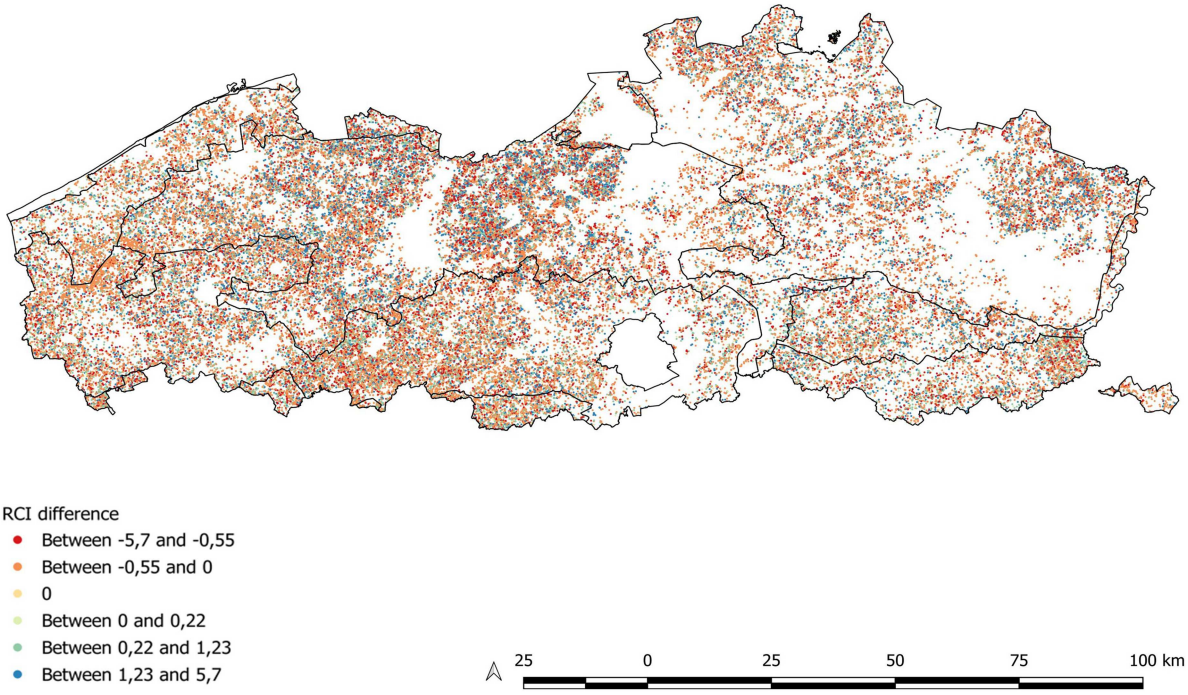


Figure 3. Spatial representation of the differences in Rotational Complexity Index (RCI) values between the period 2008–2015 and 2016–2023.

detected ($p > 0.5$), though caution is needed due to its small sample size ($n = 218$ fields). In general, this confirms what observed in the general analysis of Flanders.

Beyond temporal changes, significant differences in RCI were also found among agricultural regions within each period. The Kruskal-Wallis test confirmed highly significant differences in RCI distribution across regions in both 2008-2015 ($\chi^2 = 7{,}624.585$, $df = 5$, $p < 0.001$) and 2016–2023 ($\chi^2 = 6{,}416.113$, $df = 5$, $p < 0.001$). Dunn's post-hoc test with Bonferroni correction revealed that most pairwise regional comparisons were statistically significant in both periods, with two exceptions: (i) the Polder and Sandy Loam regions were not significantly different from each other in either period ($p = 1.00$ in 2008–2015, $p = 0.08$ in 2016–2023), which is consistent with their similar median RCI values (2.65 in 2008–2015; 2.83 in 2016–2023); and (ii) the Liège Grassland region was not significantly different from the Campine ($p = 0.40$) and the Sandy ($p = 0.63$) regions in 2008-2015, nor from the Campine region ($p = 1.00$) in 2016-2023, reflecting the similarly low RCI median values shared by these regions (1.87 in both periods). The Loam region consistently showed the highest median RCI (3.24 in 2008–2015; 3.67 in 2016–2023). Overall, this reflects fundamental differences among the Flemish agricultural regions (Figure 4).

3.3. Return time evolution

At the Flemish scale, the 4-year return time was the most common throughout the entire period, followed by the 3-year return time, together accounting for approximately 70% of all potato returns in both fields and hectares (Figure 5(A-D)). The 5-year return time was the third most frequent, while 1-year, 2-year and 6-year return times remained consistently marginal. The Mann-Kendall test revealed significant increasing trends for the 3-year, 4-year and 5-year return times in both fields and area ($p < 0.001$, $p < 0.001$, and $p < 0.01$ for fields; $p < 0.001$, $p < 0.001$, and $p < 0.01$ for hectares, respectively), while no significant trends were detected for 1-year, 2-year and 6-year return times ($p > 0.05$ for all). In absolute terms, the number of fields with a 4-year return time increased from 1,051 in 2014 to 1,381 in 2023 (+31%), while 3-year and 5-year return times rose from 994 to 1,186 (+19%) and from 438 to 661 (+51%), respectively. Consistent patterns were observed in hectares. However, when examining the relative share of each return time (Figure 5 (B) and (D)), the picture is more nuanced—the proportions remained broadly stable over time,

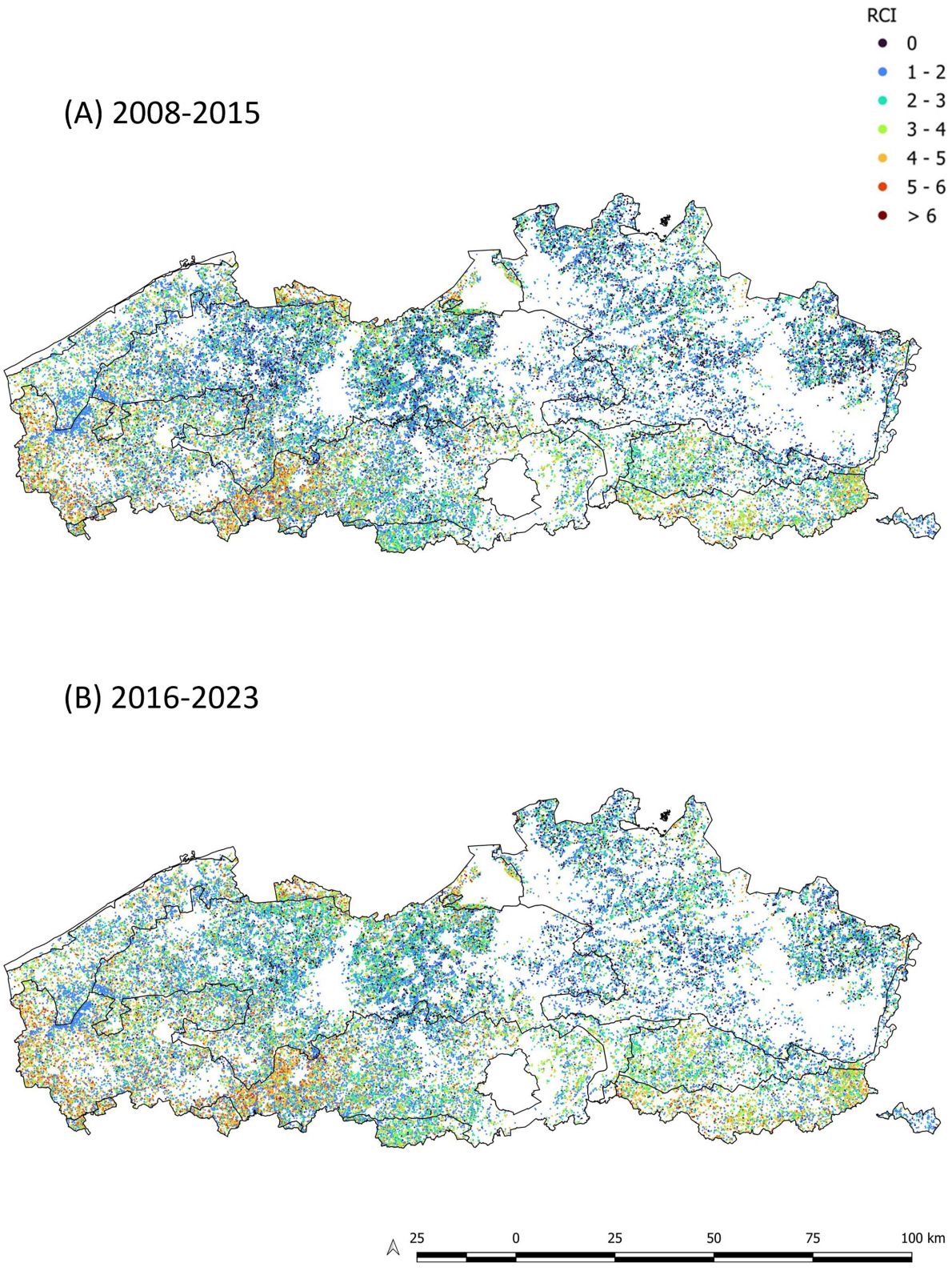


Figure 4. Spatial representation of the Rotational Complexity Index (RCI) for the period (A) 2008–2015 and (B) 2016–2023 in Flanders, Belgium.

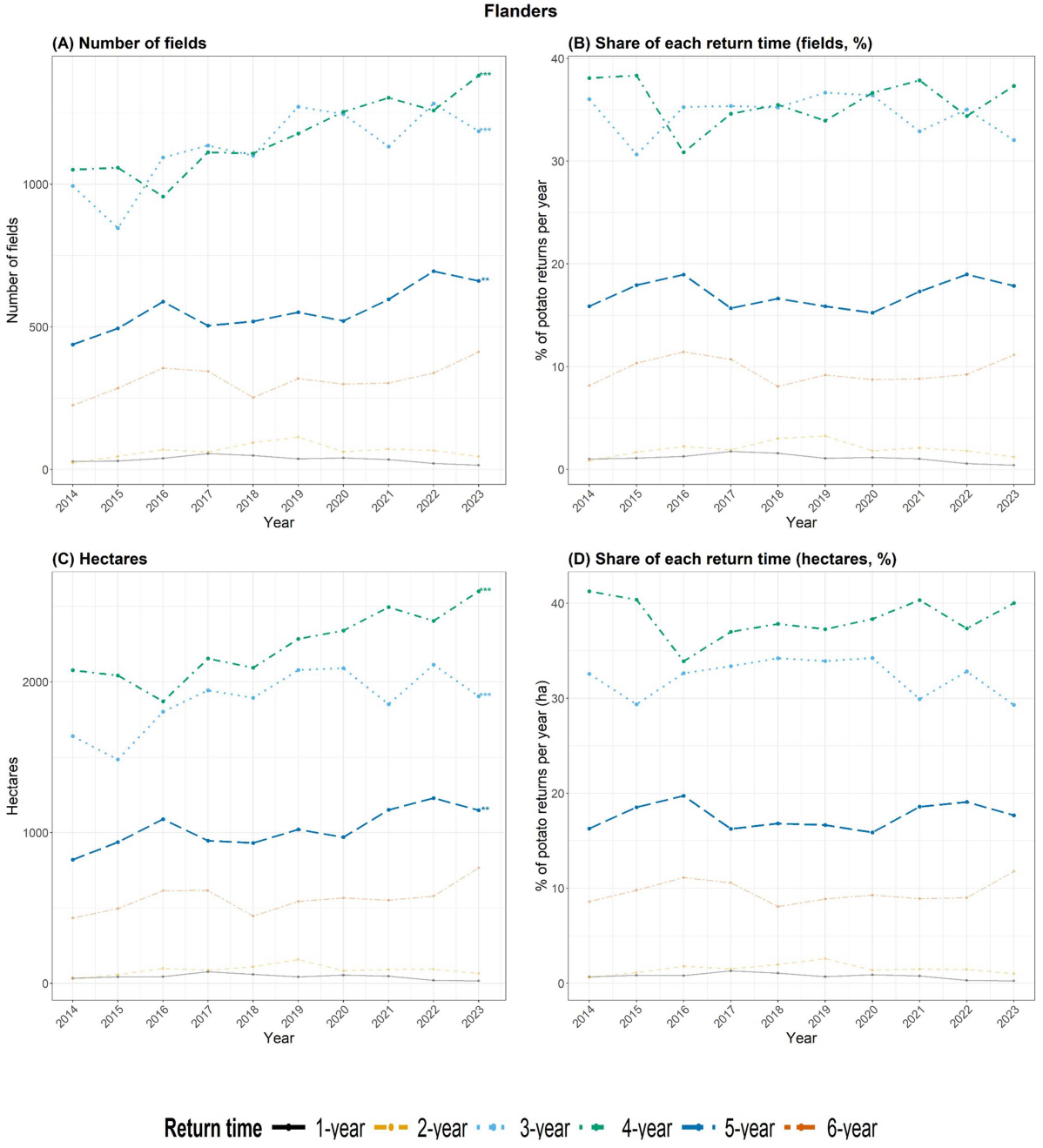


Figure 5. Changes in the return time of potatoes between 2014 and 2023 for all fields. The y-axis shows (A) the number of fields in which a particular return time between two potato occurrences was observed, (B) the share of fields over the total in which a particular return time between two potato occurrences was observed, (C) the number hectares in which a particular return time between two potato occurrences was observed, and (D) the share of hectares over the total in which a particular return time between two potato occurrences was observed. Absolute values indicate that longer return times became more frequent over time; however, because the total area under potato cultivation also increased, relative shares changed only modestly. Both absolute and relative values should therefore be considered when interpreting return time dynamics. ** denotes a p-value < 0.01 and *** denotes a *p*-value < 0.001 based on the modified Mann-Kendall test.

with the 4-year return time consistently representing approximately 35–40% of all potato returns and the 3-year return time approximately 30-35%. This apparent contradiction between significant trends in absolute values and stable relative shares reflects the overall expansion of potato cultivation in Flanders over the study period, which increased the absolute frequency of all return times simultaneously. Therefore, the significant trends in absolute values indicate that longer return times are becoming more common, but not at the expense of shorter ones, as the overall potato cultivation area has expanded.

Return times also varied across agricultural regions (see from Figure A2 and Figure A5 in the Appendix). In the Sandy region, significant increasing trends were detected for 3-year, 4-year, and 5-year return times in both fields and area ($p < 0.01$, $p < 0.001$, and $p < 0.01$ for fields, $p < 0.001$, $p < 0.001$, and $p < 0.01$ for hectares, respectively), while 1-year return times showed a significant decreasing trend in area ($p < 0.05$), suggesting a reduction in consecutive potato cultivation. The Sandy Loam region showed a similar pattern, with significant increasing trends for 3-year and 4-year return time ($p < 0.01$ for fields in both cases, $p < 0.05$ and $p < 0.01$ for hectares, respectively), while the 5-year return time was significant only in field counts ($p < 0.05$). The Loam region was the only one where a significant increasing trend was detected for the 6-year return time ($p < 0.01$ for fields, $p < 0.05$ for hectares), alongside significant increases for 4-year and 5-year return times ($p < 0$ .001 and $p < 0.01$ for fields, $p < 0.05$ and $p < 0.001$ for hectares, respectively), indicating a shift towards extended return times. The Campine region showed significant decreasing trends for 1-year and 2-year return times ($p < 0.01$ for fields in both cases, $p < 0.05$ for hectares in the case of 2-year return times), significant increasing trends for 4-year and 5-year return times ($p < 0.001$ and $p < 0.01$ for fields, $p < 0.05$ and $p < 0.01$ for hectares, respectively), and a significant increasing trend in area for the 6-year return time ($p < 0.001$). Finally, the Polder region showed no statistically significant trends for any return time.

4. Discussion

This study examines changes in crop sequence typologies and their complexity over a 16-year period in Flemish agriculture, with a particular focus on the evolution of return times of potatoes. Three complementary analytical approaches were employed. First, following the framework developed by Peltonen-Sainio et al. (2017), crop sequence typologies were identified and their distribution over time was analysed. Second, the RCI, developed by Socolar et al. (2021), was used to assess changes in sequence complexity. Third, a more detailed analysis of return time—the interval between two occurrences of the same crop—was conducted specifically for potatoes.

The results reveal substantial restructuring of crop sequence typologies, with an important share of the agricultural area transitioning between a limited number of dominant typologies, particularly sequences dominated by cereals and root crops. However, these structural shifts are not matched by strong increases in crop sequence complexity, which, although statistically significant, remain limited in magnitude. In parallel potato return times indicate that farmers continue to operate within tight agronomic constraints, with most rotations maintaining intervals of three to four years, despite a slight tendency towards longer return times.

4.1. Structural change without substantial increases in crop sequence complexity

The analysis reveals that Flemish agriculture is dominated by a limited number of crop sequence typologies, namely 'Permanent grassland', 'Root crop sequences', and cereal-dominated sequences. Although almost 40% of the agricultural area underwent a change in typology between the two study periods, these transitions occurred largely within a restricted set of dominant systems, particularly those centred on root crops and cereal sequences with a break crop. These findings are consistent with those reported by Desmarez et al. (2026) for the Belgian region of Wallonia, where distinct production areas were identified, including systems characterised by intensive crop patterns with high-value crops, areas dominated by cereals with occasional break crops and others with a high share of grassland or continuous maize cultivation. Notably, the first type of system—characterised by the presence of high-value crops—is located at the border with Flanders, in the Loam and Sandy Loam regions, where we also observe the highest share of 'Root crop sequences'. Similarly, the Liège Grassland region corresponds to areas in Wallonia dominated by grassland-based systems, as highlighted by Vandevoorde and Baret (2023). In both contexts, a substantial share of the simplest sequences is dominated by maize grown in rapid succession, mirroring the patterns observed in Flanders for 'Monospecific cereal sequences' and 'Cereal monocultures'. This pattern is not unique to Belgium; similar dynamics have been documented in Germany by Jänicke et al. (2022) and Stein and Steinmann (2018), where maize-dominated systems have been linked to the demand for animal feed in livestock-intensive regions. However, between the two study periods, the share of highly cereal-

dominated sequences in Flanders declined, with a corresponding increase in root crop-dominated sequences and, to a lesser extent, more diversified cereal systems.

Looking at the evolution of crop sequence complexity provides an important nuance to the structural changes observed in Flemish agriculture. Although sequences became more complex between the two study periods, the magnitude of this increase remains very limited. This suggests that, while a substantial share of sequences shifted typology, structural change alone does not necessarily translate into meaningful improvements in complexity. A similar pattern has been documented in Sweden, where changes in crop sequences coexisted with only limited improvements in diversity, and where gains in agronomic performance were driven by specific crop combinations rather than broader diversification (Chopin et al., 2026). This is consistent with earlier findings showing that, despite some shifts in cropping patterns, cereals remain dominant in the most productive regions, which are also characterised by relatively low levels of diversity (Peltonen-Sainio et al., 2017; Reumaux et al., 2023). More broadly, studies from Germany highlight how regional differences in pedo-climatic conditions, cropping history, and market incentives, lead to varying levels of temporal diversification (Jänicke et al., 2022; Palka et al., 2026; Schiller et al., 2024; Stein & Steinmann, 2018).

Some authors suggest that an increase in temporal diversification, as reflected in this study by a greater sequence complexity, is partially influenced by CAP measures promoting spatial diversification (Bertoni et al., 2018; Mahy et al., 2015), tough exceptions exist (e.g. Peltonen-Sainio et al., 2017; Schaak et al., 2023). However, assessing the impact of the CAP on temporal diversification, and consequently on sequence complexity, falls beyond the scope of this study. Future research could explore causal relationships between successive CAP reforms and changes in crop sequence complexity. This will be facilitated by the continuous expansion of the GAS dataset with data covering the ongoing 2023-2027 and future CAP reforms, and by the progressively harmonisation and availability of IACS datasets at the EU level (Claverie et al., 2026).

4.2. Regional contrasts in return times

Our findings indicate an overall increase in medium return times for potatoes, particularly three, four, and five years. This increase in absolute terms is associated with the growing number of fields cultivated with potato in recent years. When considering the proportion of fields exhibiting a given return time between two potato crops, it becomes evident that the most common return times—three and four years—have changed only marginally. Similarly, the proportions of 5 and 6-year return times have shown only modest increases. Longer return times are generally associated with benefits for soil health, production quality, and yields (Hills et al., 2020; Myers et al., 2008). However, as potatoes typically generate higher returns than other crops, farmers are incentivised to cultivate them more frequently, thereby reducing the interval between plantings (Hills et al., 2020), with return times often remaining close to the minimum agronomic requirements to avoid phytosanitary issues (Hills et al., 2020) and comply with the minimum 3-year return time mandated by the Flemish authorities (Conditionaliteit – Gewasrotatie op bouwland (GLMC 7) 2024, 2024). Nevertheless, some, though very few, instances of return times shorter than three years were observed. Similar patterns were reported by Desmarez et al. (2026) for the Walloon region, where potato return times are typically shorter than the recommended five years, indicating relatively intensive rotational practice.

When considering the return times characteristic of each agricultural region, a more nuanced picture emerges. In the Sandy region, 3-year return times were the most common, indicating a more intensive potato cultivation pattern, while in the Sandy Loam region, 4-year return times predominated, suggesting a slight tendency to extend the interval beyond the strict minimum. Importantly, both regions showed significant increasing trends for medium return times (3, 4 and 5-year) over the study period, indicating a gradual shift towards longer return times even in the most potato-intensive areas.

4.3. Limitations and opportunities for future research

First, the Flemish GSA data does not allow for farm-level traceability due to privacy restrictions, limiting the analysis to the field-level. While this does not compromise the validity of the results, which are presented at the field scale, it does restrict insights at the farm level—the scale at which farmers typically design their cropping plans (Dury et al., 2013). Future research could seek to integrate GSA data with other sources to overcome this limitation and explore factors associated with more or less complex sequences.

Second, the publicly available GSA dataset is limited by a lack of information on cover crops. Given the increasing emphasis on cover crops in the current CAP reform (2023–2027) as a strategy to enhance temporal diversity, their inclusion in the dataset could allow for more nuanced analyses of sequence complexity, as also suggested by Jänicke et al. (2022) and Vandevoorde and Baret (2023). This limitation could be overcome by incorporating remote sensing imagery into the analysis (see for example Lobert et al., 2025).

Third, the method used to derive crop sequences from GSA data is relatively straightforward to implement and replicate. However, it is susceptible to changes in field boundaries, which can result in data loss. A recent methodological development proposed by Pahmeyer et al. (2025), known as the *largest overlap* approach, reconstructs crop sequences by identifying the largest area overlap between field polygons in consecutive years. Thus, it preserves the field-level management unit but also account for splits and merges. Applying this methodology to the Flemish context could reduce data loss and provide a more comprehensive representation of crop sequence patterns in Flemish agriculture.

Fourth, as noted by Socolar et al. (2021), the RCI does not assess the agronomic quality of sequences or fully capture the benefits of including different functional groups, such as legumes. While increased sequence complexity is generally associated with agronomic and environmental benefits (Bennett et al., 2012; Isbell et al., 2011; Zhao et al., 2022), it is important to recognise that the RCI does not directly account for aspects such as soil health or biodiversity. This limitation does not affect the validity of our findings, as the study does not aim to rank sequences by their RCI value but rather to assess overall changes in complexity within the study region. Nonetheless, future research could benefit from combining the RCI with indices designed to evaluate agronomic quality, such as the one proposed by Bockstaller & Girardin, (1996) and refined by Desmarez et al. (2026), Leteinturier et al. (2006), and Vandevoorde and Baret (2023).

5. Conclusions

This study analysed the evolution of crop sequence complexity among potato-producing farms in Flanders between 2008 and 2023, using field-level GSA data. The results indicate a modest overall increase in complexity, with most sequences remaining within a moderate range. These findings provide an updated picture of cropping practices in Flemish agriculture and highlight that, despite structural changes in crop sequences, gains in temporal diversification remain limited. At a time when temporal diversification is increasingly emphasised in European agricultural policy, particularly within the framework of the Common Agricultural Policy (CAP), these results suggest that current developments only partially align with policy objectives aimed at promoting more diverse and resilient cropping systems. The methodological approach adopted in this study is flexible and transferable. The return time analysis, applied here to potato-based systems, can be extended to other crops and regions, offering a useful framework for monitoring changes in crop sequences using large-scale administrative datasets such as GSA. Future research could build on this work by investigating the drivers of observed changes in crop sequence complexity, including the role of agronomic constraints, economic incentives, and policy measures, as well as by assessing whether recent reforms lead to more substantial shifts in temporal diversification.

Author contributions

CRediT: **Marco Moretti:** Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Software, Visualization, Writing – original draft, Writing – review & editing; **Kato Van Ruymbeke:** Conceptualization, Investigation, Methodology, Supervision, Validation, Writing – review & editing; **Erik Mathijs:** Conceptualization, Funding acquisition, Project administration, Supervision, Validation, Writing – review & editing.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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Data availability statement

Data will be made available upon request.

Declaration of generative AI and AI-assisted technologies in the writing process

During the preparation of this work, the authors used CHAT GPT-5 in order to improve the readability. After using this tool, the authors reviewed and edited the content as needed and take full responsibility for the content of the published article.

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Appendix

Table A1. Crop sequence typologies in Flanders, as well as in the Campine, Liège Grassland, Loam, Polder, Sandy Loam, and Sandy regions. Flanders also include fields located in the Dune region and with no agricultural region assigned.

	Flanders		Campine		Liège Grassland		Loam		Polder		Sandy Loam		Sandy	
Crop sequence typology	2008–2015	2016–2023	2008–2015	2016–2023	2008–2015	2016–2023	2008–2015	2016–2023	2008–2015	2016–2023	2008–2015	2016–2023	2008–2015	2016–2023
Monospecific cereal sequences	11,631.27	7,071.81	5,451.23	3,707.69	41.91	31.13	166.70	110.15	150.04	95.72	1,417.57	692.02	4,395.39	2,430.31
Cereal monocultures	8,625.79	6,995.64	1,175.47	1,206.94	26.14	26.07	922.28	660.59	835.90	518.40	2,982.32	2,635.17	2,670.39	1,940.29
Cereal sequences with one annual break crop	12,201.09	11,413.94	2,215.00	2,429.35	15.10	13.29	987.36	885.01	858.52	732.94	3,516.99	3,396.60	4,599.71	3,935.26
Cereal sequences with two or three annual break crops	3,601.56	4,023.23	492.94	645.36	4.06	2.23	296.98	258.04	575.84	583.91	1,162.11	1,191.69	1,068.84	1,339.52
Cereal sequences with perennial crops	8,341.49	8,785.02	4,220.32	4,236.21	33.47	37.26	164.23	195.36	610.12	728.63	929.90	1,071.66	2,380.07	2,511.39
Diverse sequences	1,720.23	3,135.78	649.94	1,035.27	1.69	0.00	49.36	78.15	167.02	359.52	322.82	545.50	529.40	1,111.16
Grassland sequences	352.34	582.02	132.73	249.19	0.00	0.00	7.40	8.30	20.38	35.26	70.49	65.85	121.35	223.41
Permanent grassland	32,559.01	31,637.57	6,082.24	6,009.45	357.14	360.77	1,672.58	1,671.37	3,498.35	3,361.32	10,256.24	10,040.33	10,651.67	10,153.55
Horticultural sequences	825.19	620.96	133.67	148.28	0.00	0.00	32.93	8.45	12.55	16.09	389.90	220.76	256.03	227.29
Root crop sequences	28,558.88	33,964.89	2,385.26	3,256.01	27.81	36.57	5,028.96	5,401.78	2,705.79	2,971.29	12,081.29	13,205.67	6,291.19	9,068.36
Fallow	5.84	141.03	0.00	14.16	0.00	0.00	3.40	43.57	0.00	22.14	2.44	40.70	0.00	20.46
Other	64.08	114.86	0.00	0.90	0.00	0.00	14.54	25.93	13.93	23.24	33.38	59.54	2.23	5.25

Table A2. Main transitions between crop sequence typologies in Flanders between 2008–2015 and 2016–2023.

Flanders			
Sequence typology in 2008–2015	Sequence typology in 2016–2023	Area (ha)	Area (%)
Cereal sequences with one annual break crop	Root crop sequences	4,578	4.2
Root crop sequences	Cereal sequences with one annual break crop	2,722	2.5
Monospecific cereal sequences	Cereal sequences with one annual break crop	2,180	2.0
Cereal monocultures	Cereal sequences with one annual break crop	2,116	2.0
Monospecific cereal sequences	Root crop sequences	1,708	1.6

Table A3. Main transitions between crop sequence typologies in the Sandy Loam region between 2008–2015 and 2016–2023.

Sandy Loam region			
Sequence typology in 2008–2015	Sequence typology in 2016–2023	Area (ha)	Area (%)
Cereal sequences with one annual break crop	Root crop sequences	1,470	4.4
Root crop sequences	Cereal sequences with one annual break crop	1,152	3.5
Cereal monocultures	Cereal sequences with one annual break crop	759	2.3
Cereal sequences with two or three annual break crops	Root crop sequences	639	1.9
Cereal sequences with one annual break crop	Cereal monocultures	585	1.8

Table A4. Main transitions between crop sequence typologies in the Sandy region between 2008–2015 and 2016–2023.

Sandy region			
Sequence typology in 2008–2015	Sequence typology in 2016–2023	Area (ha)	Area (%)
Cereal sequences with one annual break crop	Root crop sequences	1,786	5.4
Monospecific cereal sequences	Root crop sequences	930	2.8
Monospecific cereal sequences	Cereal sequences with one annual break crop	912	2.8
Cereal monocultures	Cereal sequences with one annual break crop	762	2.3
Permanent grassland	Cereal sequences with one annual break crop	676	2.1

Table A5. Main transitions between crop sequence typologies in the Campine region between 2008-2015 and 2016-2023.

Campine region			
Sequence typology in 2008–2015	Sequence typology in 2016–2023	Area (ha)	Area (%)
Monospecific cereal sequences	Cereal sequences with one annual break crop	902	3.9
Monospecific cereal sequences	Cereal sequences with perennial crops	807	3.5
Cereal sequences with perennial crops	Permanent grassland	677	3.0
Permanent grassland	Cereal sequences with perennial crops	608	2.7
Cereal sequences with one annual break crop	Cereal monocultures	551	2,4

Table A6. Main transitions between crop sequence typologies in the Loam region between 2008–2015 and 2016–2023.

Loam region			
Sequence typology in 2008–2015	Sequence typology in 2016–2023	Area (ha)	Area (%)
Cereal sequences with one annual break crop	Root crop sequences	485	5.2
Root crop sequences	Cereal sequences with one annual break crop	300	3.2
Cereal monocultures	Cereal sequences with one annual break crop	236	2.5
Cereal monocultures	Root crop sequences	201	2.2
Cereal sequences with two or three annual break crops	Root crop sequences	185	2.0

Table A7. Main transitions between crop sequence typologies in the Liège Grassland region between 2008–2015 and 2016–2023.

Liège Grassland region			
Sequence typology in 2008–2015	Sequence typology in 2016–2023	Area (ha)	Area (%)
Permanent grassland	Cereal sequences with perennial crops	15.3	3.0
Cereal sequences with perennial crops	Permanent grassland	7.8	1.5
Cereal sequences with one annual break crop	Permanent grassland	7.5	1.5
Cereal sequences with perennial crops	Cereal monocultures	6.1	1.5
Monospecific cereal sequences	Cereal sequences with perennial crops	5.2	1.2

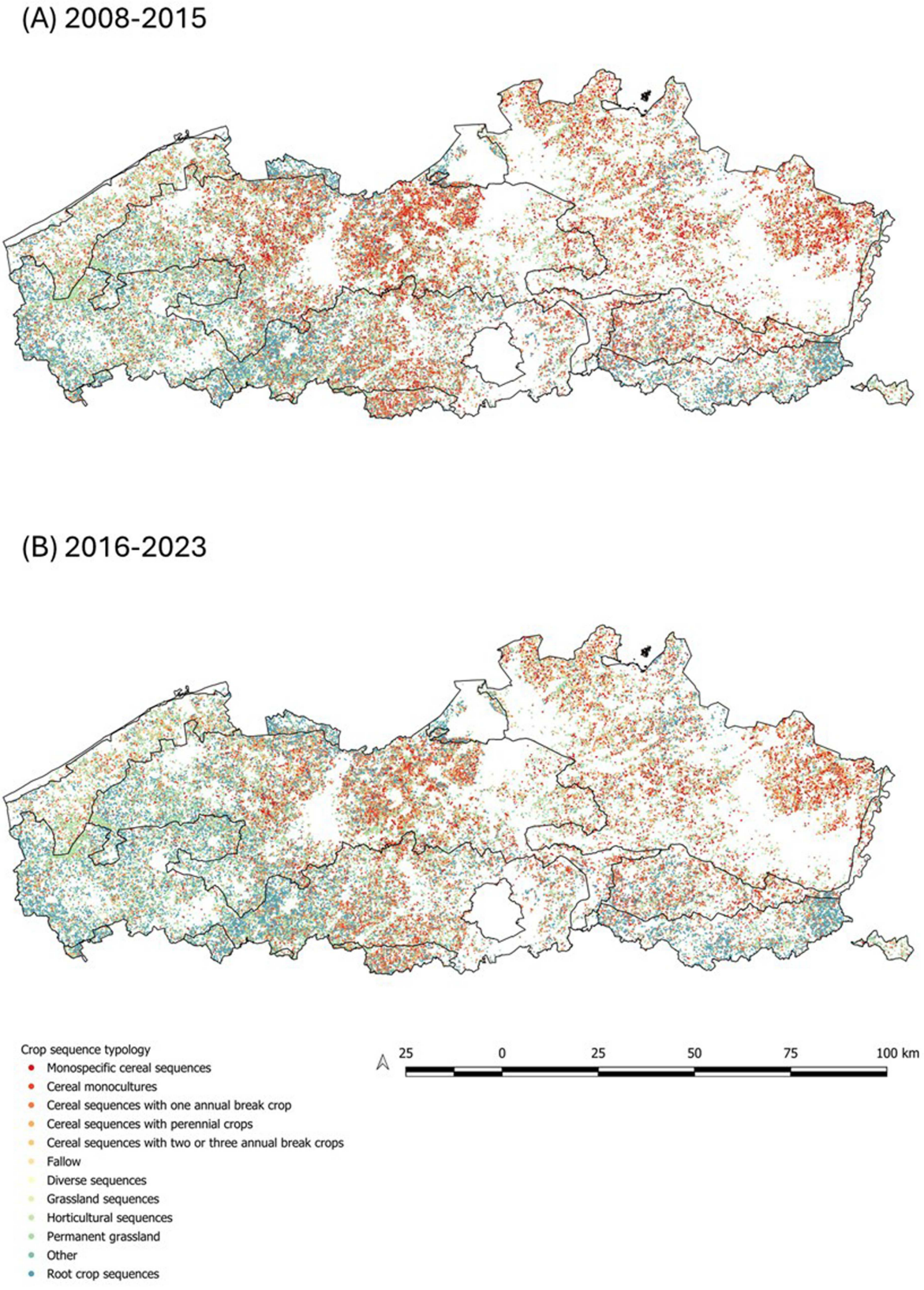


Figure A1. Spatial representation of the crop sequence typologies for the period (A) 2008–2015 and (B) 2016–2023 in Flanders, Belgium.

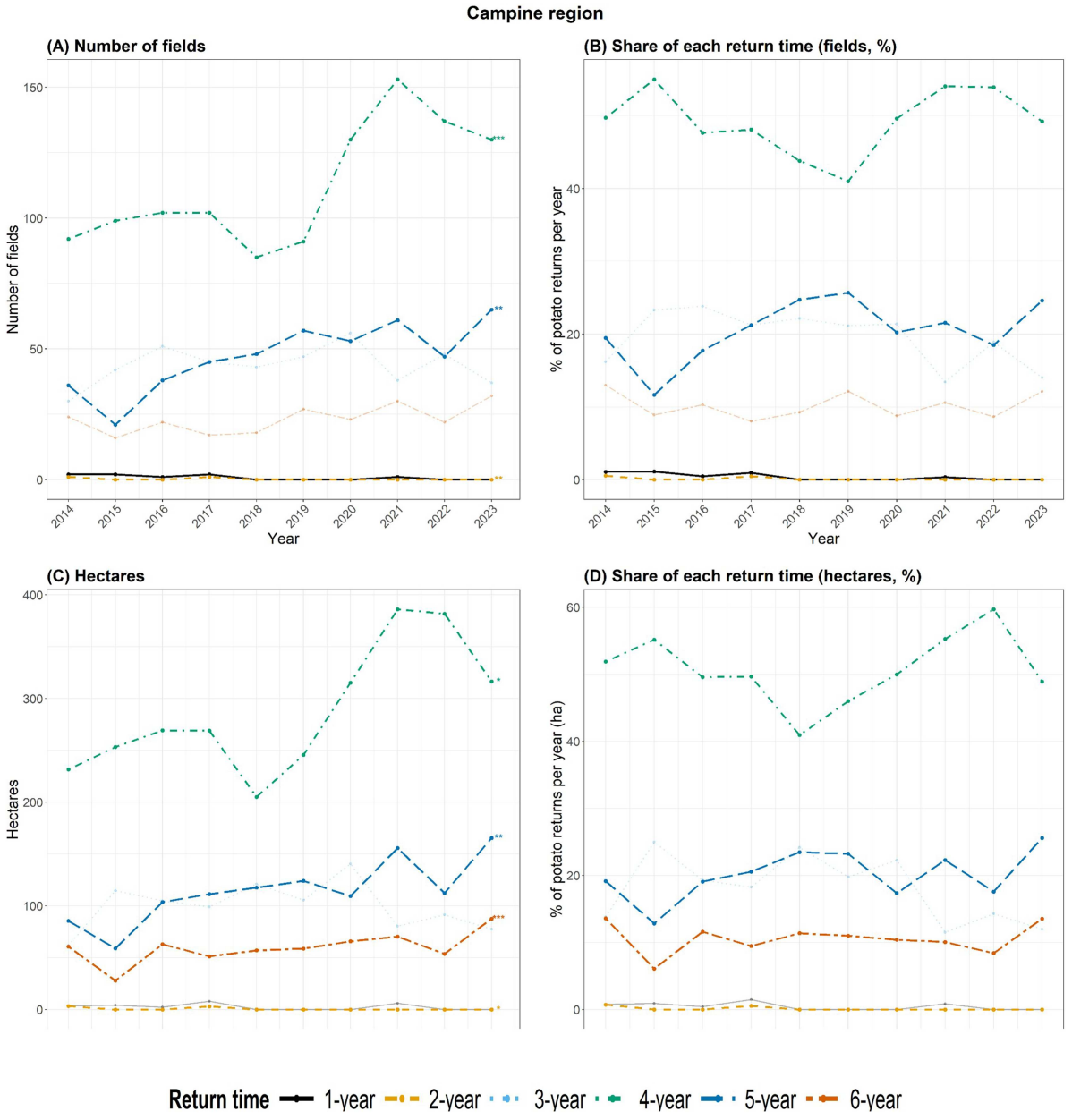


Figure A2. Changes in the return time of potatoes between 2014 and 2023 in the Campine region. The y-axis shows (A) the number of fields in which a particular return time between two potato occurrences was observed, (B) the share of fields over the total in which a particular return time between two potato occurrences was observed, (C) the number hectares in which a particular return time between two potato occurrences was observed, and (D) the share of hectares over the total in which a particular return time between two potato occurrences was observed. Absolute values indicate that longer return times became more frequent over time; however, because the total area under potato cultivation also increased, relative shares changed only modestly. Both absolute and relative values should therefore be considered when interpreting return time dynamics. ** denotes a p-value < 0.01 and *** denotes a *p*-value < 0.001 based on the modified Mann-Kendall test.

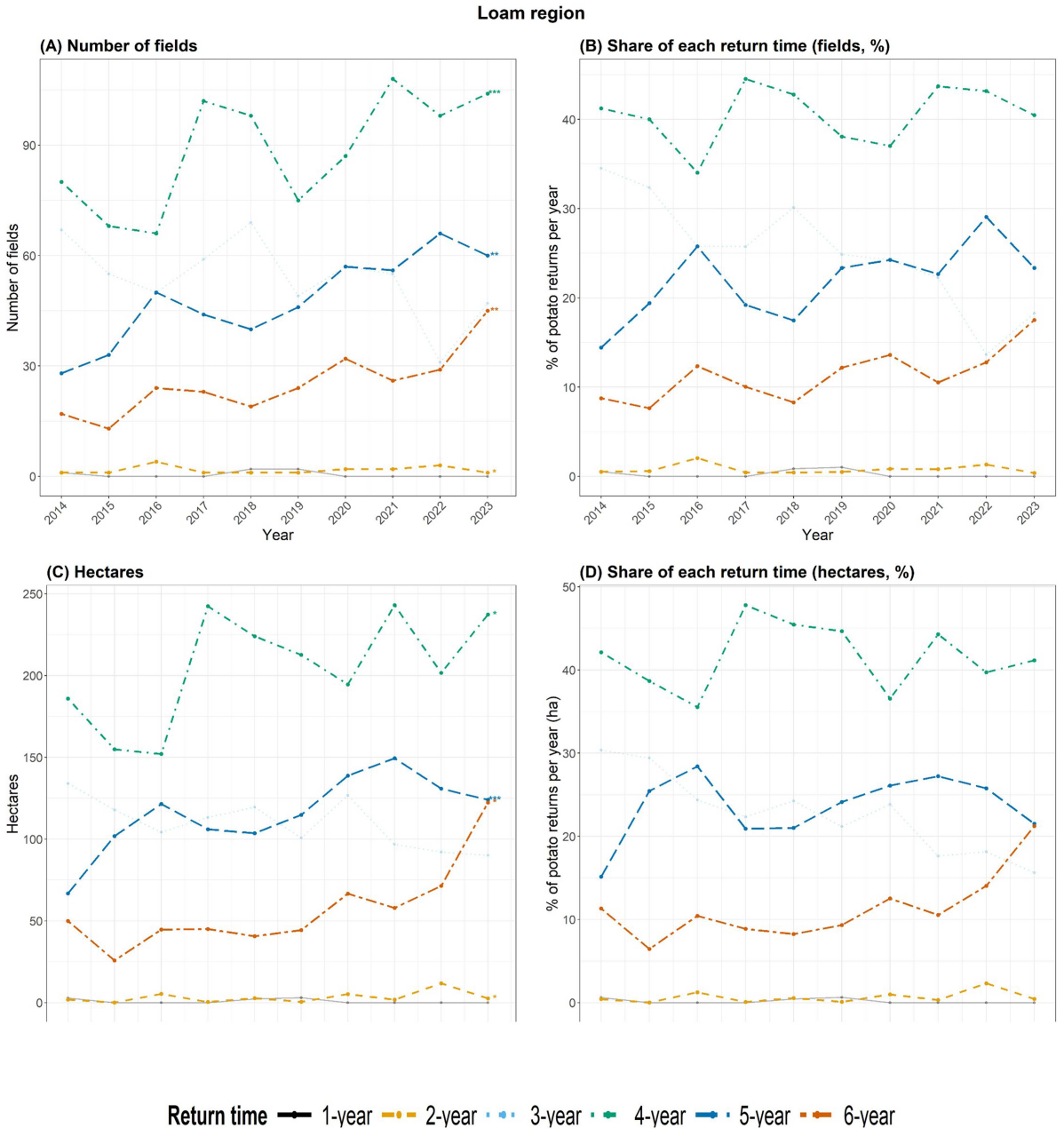


Figure A3. Changes in the return time of potatoes between 2014 and 2023 in the Loam region. The y-axis shows (A) the number of fields in which a particular return time between two potato occurrences was observed, (B) the share of fields over the total in which a particular return time between two potato occurrences was observed, (C) the number hectares in which a particular return time between two potato occurrences was observed, and (D) the share of hectares over the total in which a particular return time between two potato occurrences was observed. Absolute values indicate that longer return times became more frequent over time; however, because the total area under potato cultivation also increased, relative shares changed only modestly. Both absolute and relative values should therefore be considered when interpreting return time dynamics. ** denotes a p-value < 0.01 and *** denotes a *p*-value < 0.001 based on the modified Mann-Kendall test.

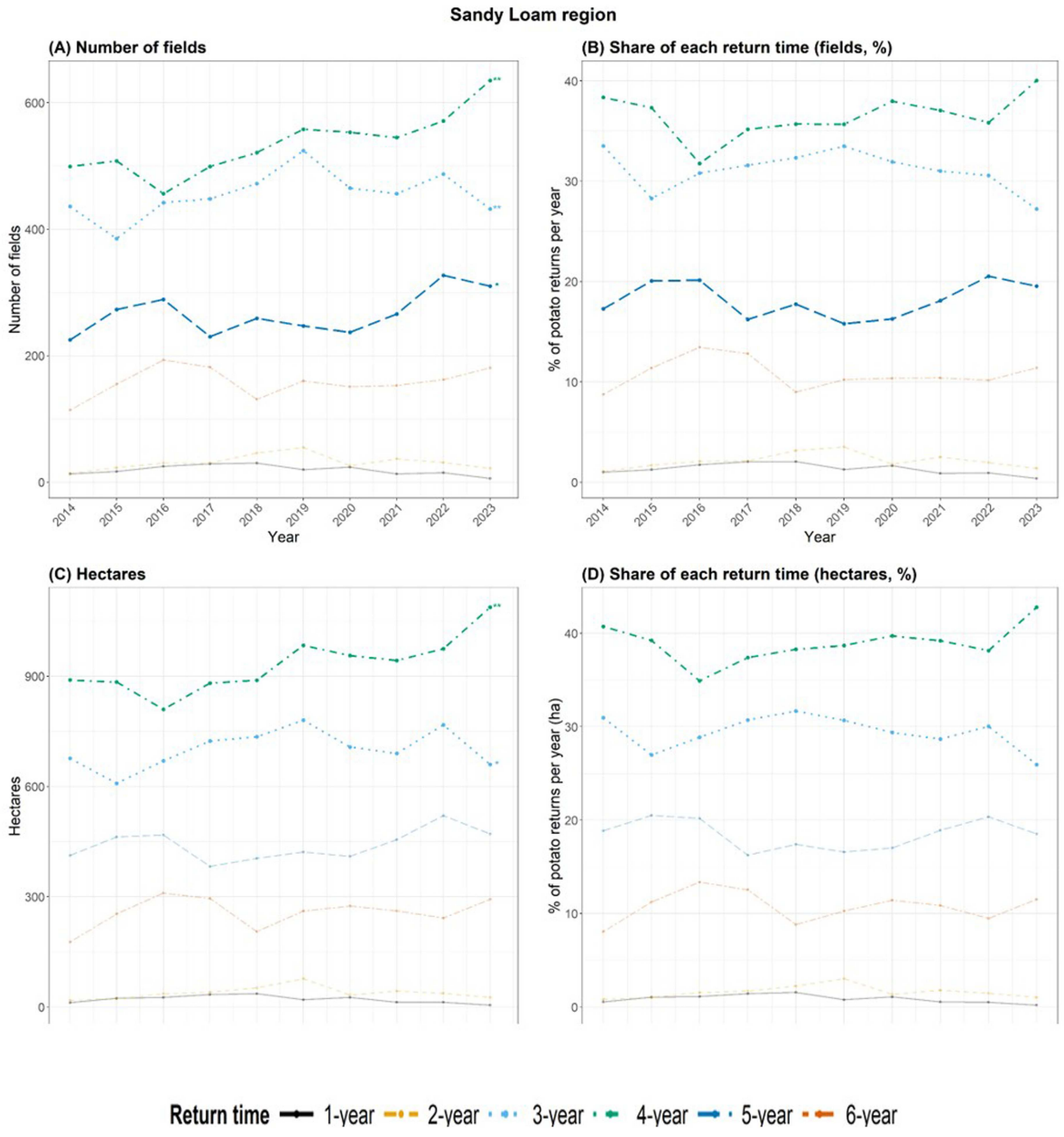


Figure A4. Changes in the return time of potatoes between 2014 and 2023 in the Sandy Loam region. The y-axis shows (A) the number of fields in which a particular return time between two potato occurrences was observed, (B) the share of fields over the total in which a particular return time between two potato occurrences was observed, (C) the number hectares in which a particular return time between two potato occurrences was observed, and (D) the share of hectares over the total in which a particular return time between two potato occurrences was observed. Absolute values indicate that longer return times became more frequent over time; however, because the total area under potato cultivation also increased, relative shares changed only modestly. Both absolute and relative values should therefore be considered when interpreting return time dynamics. ** denotes a p-value < 0.01 and *** denotes a *p*-value < 0.001 based on the modified Mann-Kendall test.

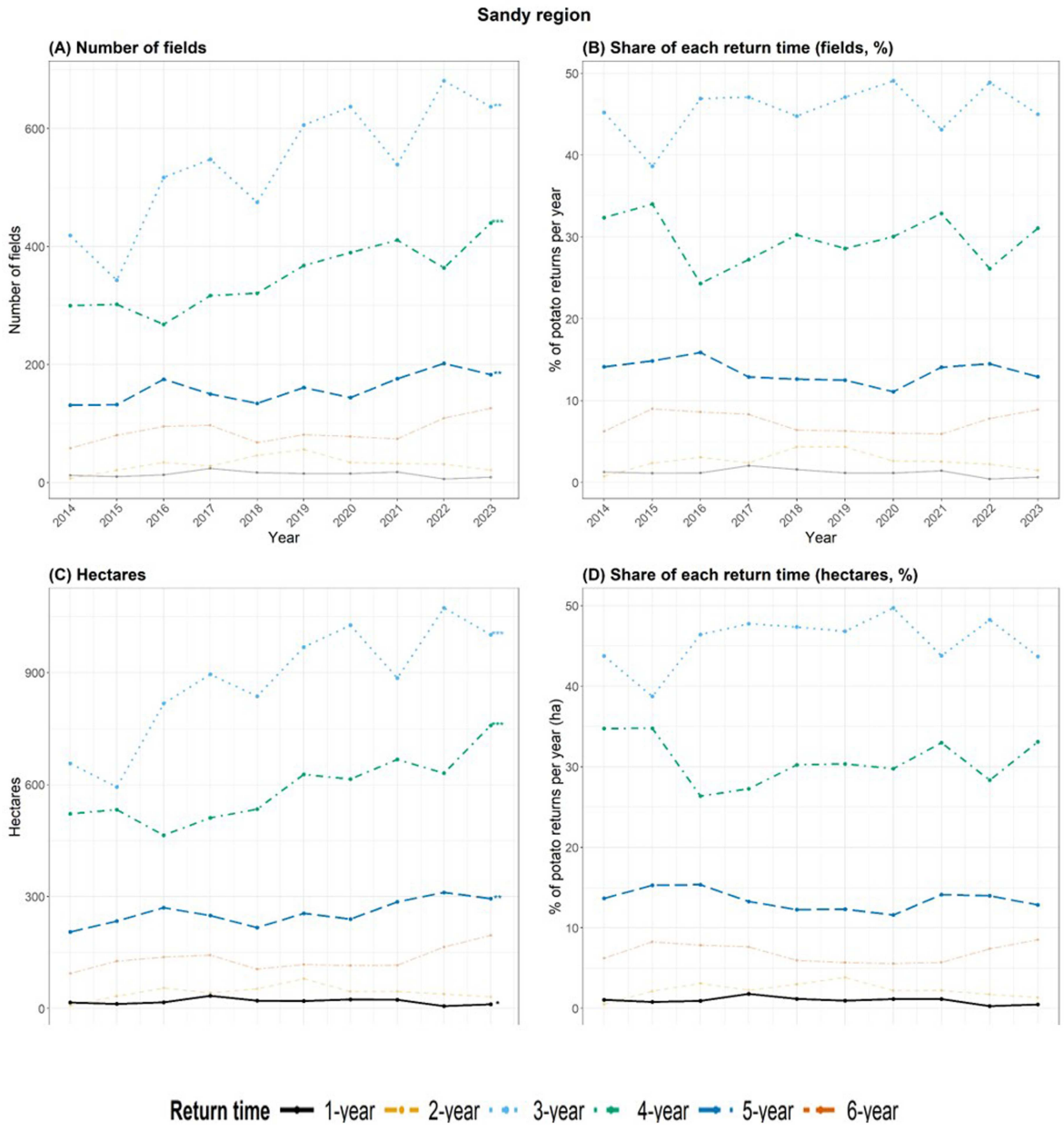


Figure A5. Changes in the return time of potatoes between 2014 and 2023 in the Sandy region. The y-axis shows (A) the number of fields in which a particular return time between two potato occurrences was observed, (B) the share of fields over the total in which a particular return time between two potato occurrences was observed, (C) the number hectares in which a particular return time between two potato occurrences was observed, and (D) the share of hectares over the total in which a particular return time between two potato occurrences was observed. Absolute values indicate that longer return times became more frequent over time; however, because the total area under potato cultivation also increased, relative shares changed only modestly. Both absolute and relative values should therefore be considered when interpreting return time dynamics. ** denotes a p-value < 0.01 and *** denotes a *p*-value < 0.001 based on the modified Mann-Kendall test.