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Inter-annual and site-specific variability in greenhouse gas emissions from linseed genotypes

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Agriculture contributes significantly to global greenhouse gas (GHG) emissions. With increasingly diverse rotations, interest is growing in break crops such as linseed (*Linum usitatissimum* L.) to support soil health, pest and disease control, and reduce nitrogen inputs. However, the controls on GHG emissions (CO₂, CH₄, N₂O) from linseed, particularly genotypic variation, remain poorly understood. This study investigated genotypic variations in GHG emissions among four elite linseed genotypes (Empress, Omegalin, Richess, VT50) at two UK field sites: Leicestershire (Ashby-de-la-Zouch) in 2024 and Derbyshire (near Elvaston) in 2025. Using closed static chambers connected to a Gasmet GT5000 portable FTIR analyser, weekly GHG fluxes, soil temperature, volumetric soil moisture, and crop height were measured in randomised plot designs under commercial fertiliser regimes. Cumulative emissions were calculated by trapezoidal integration of daily mean fluxes, and data were analysed with ANOVA and linear mixed-effects models. Significant site- and year-driven differences in overall GHG emissions were observed ($P < 0.05$), with markedly higher cumulative CO₂, N₂O and CH₄ fluxes in the warmer, wetter 2024 season. No significant genotypic differences were found in cumulative CO₂ or N₂O emissions. However, genotype VT50 exhibited a significant CH₄ sink (-2.83 g ha^{-1}) in 2025. Crop height varied significantly between sites ($P < 0.001$) and positively influenced CO₂ fluxes ($P < 0.05$), with interactive effects of height $\times$ soil temperature on CO₂ and height $\times$ volumetric moisture on CH₄ and N₂O fluxes ($P < 0.05$). Environmental factors (site, climate, and management) dominated over genotype in determining GHG emissions from linseed under field conditions. VT50 showed strong potential for low-emission production, particularly as a CH₄ sink in certain years. These findings highlight the value of integrated genetic and environmental strategies, including growth-optimised genotypes, to enhance break crops like linseed for net-zero and sustainable agriculture.

KEYWORDS

agricultural management, agronomy, carbon dioxide, cultivar variation, methane, nitrous oxide, soil moisture, fertiliser

Introduction

Agriculture is a major producer of greenhouse gas (GHG) emissions. The food sector accounts for approximately 34% of all emissions, and the agriculture sector alone accounts for approximately 71% of those emissions (Crippa et al., 2021). In the United Kingdom agriculture accounts for 11% of total GHG emissions, which includes 69% of total N₂O and 48% of total CH₄ emissions (DEFRA, 2022). Transitioning to Net Zero agriculture thus plays a significant role in climate change mitigation (Lynch et al., 2021). Although livestock systems dominate agricultural GHG emissions, primarily through enteric methane from ruminants, cropping systems also contribute substantially to soil-to-atmosphere GHG fluxes, particularly through soil N₂O losses and carbon-cycle feedbacks associated with fertiliser use, soil organic matter (SOM) turnover, and crop residue management (Shcherbak et al., 2014; Paustian et al., 2016; IPCC, 2023). For instance, cropland fertilisation alone accounts for ~60% of agricultural N₂O emissions globally (Tian et al., 2020). Sustainable cropland nitrogen (N) management and N fertilisation practices are thus necessary for climate change mitigation, but require careful balancing with food security (Zhang et al., 2015).

N₂O production, being microbially mediated through nitrification and denitrification, is particularly sensitive to genotypic variations that alter soil N availability and microbial communities (Philippot et al., 2013; Girkin and Cooper, 2023). Genotypes can vary in their ability to transport N₂O from the soil via root uptake and release through the stomata, potentially reducing byproduct emissions (Verma et al., 2006; Baruah et al., 2010). Plants can also produce N₂O directly via N assimilation (Smart and Bloom, 2001), and different genotypes can have variable N₂O production during N assimilation (Oszwald et al., 2022). In contrast, CH₄ emissions are more likely affected by genotypic differences in aerenchyma and oxygen transport, while CO₂ fluxes relate primarily to soil respiration and crop management practices such as tillage and cropping intensity (Aulakh et al., 2000; Paustian et al., 2000; Girkin et al., 2018). These differences suggest that N₂O may exhibit more pronounced genotypic-driven variation than CO₂ or CH₄, particularly when modulated by crop growth traits such as height and biomass that influence plant-soil interactions and microbial activity (Behnke et al., 2022).

Crop growth traits, such as height, may also mediate GHG emissions by influencing rhizosphere microbial activity, soil microclimates, and resource allocation (Shenton et al., 2016; Si et al., 2023). Taller plants can enhance CO₂ efflux through increased biomass and root respiration, or alter CH₄ dynamics via rooting depth and aeration effects, although these relationships may vary inter-annually with environmental conditions like temperature and moisture (Thorup-Kristensen et al., 2020).

Another promising mitigation strategy involves selecting crop genotypes for greater yield and lower GHG emissions (Shcherbak et al., 2014; Swarbreck et al., 2019). Research has established that cash crops such as wheat and rice show genotypic differences in N₂O and CH₄ emissions, largely driven by variation in N uptake efficiency, root architecture and plant-soil-microbial interactions

(Gogoi and Baruah, 2012; Chen et al., 2021; Walthall et al., 2025). Other characteristics which can vary between genotypes such as N accumulation at anthesis and flag-leaf senescence have also been closely linked to GHG emission output and could further impact GHG emission rates (Gaju et al., 2011).

Agricultural management can also influence GHG dynamics, and rotational strategies that incorporate break crops such as linseed have been widely promoted to improve soil structure, nutrient cycling and pest suppression while supporting climate mitigation (Smith et al., 2007). Cereal crops such as wheat (*Triticum aestivum* L.) cannot be grown continuously, requiring the inclusion of break crops to maintain soil function and reduce pest and disease pressures (Yamini et al., 2025). Break crops such as linseed and oilseed rape (*Brassica napus* L.) deliver multiple agronomic and environmental benefits, including improved N cycling, enhanced soil physical structure and increased SOM accumulation (Moukanni et al., 2022). These processes directly support Net Zero strategies by promoting soil carbon sequestration, reducing reliance on synthetic N fertilisers and thereby lowering N₂O emissions, the dominant agricultural GHG in many cropping systems (Smith, 2004; Cusworth et al., 2021; Rumpel et al., 2022). In the context of GHG emissions, these processes are especially relevant to linseed cultivation: the crop's characteristically low nitrogen requirement can markedly reduce N₂O emissions by limiting substrate availability for nitrification and denitrification, while its contribution to SOM build-up supports net carbon sequestration and may help offset CO₂ and CH₄ fluxes (Cui et al., 2022; Nasser et al., 2025). Recent life-cycle assessments confirm that linseed possesses one of the lowest carbon footprints among common oilseeds (0.9–11 kg CO₂eq per kg fibre), driven largely by minimal synthetic inputs and favourable residue management (Stavropoulos et al., 2023). Consequently, linseed offers a practical opportunity to integrate break crop benefits with measurable GHG reductions under real world field conditions.

Break crops are expected to support carbon sequestration and reduce N losses (West and Post, 2002; Powlson et al., 2011), but their direct contributions to soil CO₂, CH₄, and N₂O fluxes are not well understood and genotypic variation in these emissions is unexplored. This knowledge gap is notable given evidence from cereals demonstrating substantial genotype-driven differences in GHG emissions (Walthall et al., 2025). Break crop breeding programmes increasingly focus on enhancing root traits, stress tolerance and resource use efficiency (Kell, 2012; Calleja-Cabrera et al., 2020), yet the extent to which different genotypes contribute to or mitigate GHG emissions under real field conditions is unknown. Addressing this gap is essential for positioning linseed as a climate-positive component of future crop rotations and for identifying genotypes that align with Net Zero farming systems. Here, we present the first multi-site assessment of soil-to-atmosphere GHG fluxes (CO₂, CH₄ and N₂O) across contrasting linseed genotypes in field conditions. Our aim was to quantify inter-annual and genotypic variation in CO₂, CH₄ and N₂O fluxes to provide empirical evidence to guide genotype selection and management strategies for climate-smart linseed production, whilst providing a greater understanding of how different linseed genotypes vary in GHG outputs.

Methods

Experimental design and site descriptions

Field trials were conducted at two commercial farm sites in the UK. In 2024 the trial was located at Eurofins Ashby-de-la-Zouch, Leicestershire (52°45' N, 1°27' W). The soil was a slowly permeable seasonally wet acidic loamy and clayey soil in the upper profile. Mean air temperature during the study period was 15.2 °C and mean monthly precipitation was 66.2 mm. In 2025 the trial was located near Elvaston, Derbyshire (52°52' N, 1°24' W). The soil was a slightly acid loamy and clayey soil with impeded drainage in the upper profile. Mean temperature during the study period was 11.2 °C and mean monthly precipitation was 26.46 mm. Both sites had been under continuous crop cultivation for at least 20 years in a typical rotation of wheat, barley (*Hordeum vulgare* L.), and peas (*Pisum sativum* L.).

The same four elite breeding linseed genotypes (Omegalin, VT50, Empress, Richess) were used in both years. These genotypes were selected because they are among the most widely grown linseed varieties in the UK, having all been introduced within the last 10 years (Premium Crops, 2022). They were sourced from Premium Crops, Hampshire, UK. VT50 was bred in Canada; the other three were bred in France. Control plots were included only at the 2024 site. No unfertilised control plots for the linseed genotypes were included in either year. GHG flux measurements were not taken from the blank control plots present at the 2024 site, as the study focused on genotypic variation under realistic commercial fertiliser regimes (Table 1).

Linseed treatments were established at Eurofins Ashby-de-la-Zouch, Leicestershire, UK during the 2024 season (Figure 1). The mean air temperature during the study period was 15.2 °C and the mean monthly precipitation was 66.2mm. Weather data for the site was collected using the ACCUR8 Weather Station labelled IASHBY15 located approximately 2 kilometres from the field site. The soil at the site was a slowly permeable seasonally wet acidic loamy and clayey soil in the topsoil layer (approximately 0 – 30cm). The site had been continuously used for crop cultivation for at least 20 years. Wheat, barley and peas are grown in a typical rotation. Seeds were sown at a rate of 800 per m² at a depth of 2cm. Each of the plots were ploughed, power harrowed, drilled and rolled to a

depth of 10cm approximately 1 week prior to the crop being sown. The crop was sown on the 1st of May and was harvested on the 9th of September. Plots measured 1.8 × 12 m in a randomized block design (Supplementary Figure 1B). Soil temperature, volumetric moisture, and crop height (mean of three stems per plot) were measured concurrently. Fertiliser and herbicide application applications followed standard agronomic practice and differed between years (Table 1).

Linseed treatments were established a year later in 2025 at a farm site managed by Eurofins located near Elvaston, Derbyshire (Figure 1). The mean temperature during the study period was 11.2 °C and the mean monthly precipitation over the study period was 26.46mm. Weather data for the site was collected via the StowmarketDriveTempest Weather Station labelled IDERBY296, which is located approximately 12 miles from the site. The soil at the site was a slightly acid loamy and clayey soil with impeded drainage in the topsoil layer (approximately 0 – 30cm). The site had been continuously used for crop cultivation for at least 20 years. Wheat, barley and peas are grown in a typical rotation. The crop was sown on the 1st of April 2025 and weekly GHG flux measurements continued until the final sampling date, after which no further measurements were taken (the crop had not yet reached harvest).

Unlike the field site in the first year, the field site used in the second year of this study was also being used as a wider linseed crop variety trial. Therefore, plots associated with this study were not directly next to each other (Supplementary Figure 2B). All four genotypes used were the same as the ones used in the previous year. Seeds were sown at a sowing rate of 800 per m², and they were drilled at a depth of 2cm. Each of the plots were ploughed, power harrowed, drilled and rolled to a depth of 10cm approximately 1 week prior to the seeds being sown. No reports from the trial managers or farmers indicated that any pesticides were applied at any point during the experiment taking place. Fertiliser and herbicide application followed standard agronomic practice and differed between years (Table 1). Yield data was unavailable due to harvesting difficulties from the growers. Both sites had broadly similar loamy and clayey textures in the upper profile. However, detailed soil properties relevant to GHG emissions such as particle-size distribution with clay and sand percentages, bulk density, soil

TABLE 1 Summary of experimental set up at each field site.

Location	Plots per genotype	Collars per genotype (collars per plot)	Number of blocks	Fertiliser application	Herbicide application	Pesticide application
Ashby-de-la-Zouch, Leicestershire, 52°45' N, 1°27' W	4	12 (3)	4	105 kg N ha ⁻¹ . 24N + 7.5S liquid fertiliser*. Fertiliser applied in a 65/40 kg N ha ⁻¹ split. 65 kg N ha ⁻¹ applied two weeks after planting and remaining fertiliser applied six weeks after planting.	0.5L/ha Callisto. 0.12L/ha Jubilee. 1L/ha Centurian Max. 2L/ha Glyphosate.	None.
Elvaston, Derbyshire, 52°52' N, 1°24' W	3	9 (3)	3	300kg N ha ⁻¹ AN fertiliser*. AN Fertiliser applied in a 150/150 kg N ha ⁻¹ split. First 150 kg N ha ⁻¹ applied 2 weeks after planting and remaining fertiliser planted six weeks after planting.	0.82L/ha SUa.	None.

* indicates that fertiliser application for that fertiliser was split between two days during the growing period. a indicates that exact name of herbicide was not provided by the trial managers. AN, Ammonium nitrate; AS, Ammonium sulfate.

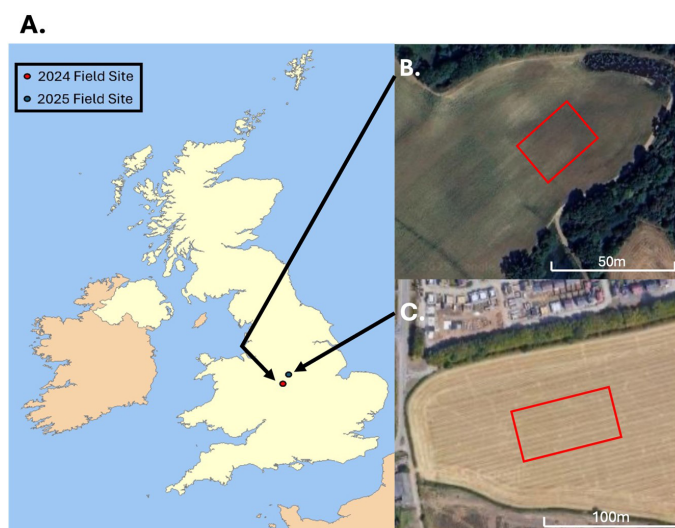


FIGURE 1

Location of the linseed genotype field sites (A) Ashby-de-la-Zouch, Leicestershire, UK in 2024 [red symbol; (B) and Elvaston, Derbyshire, UK in 2025 (blue symbol; (C)]. Source: Map image reproduced from Prioryman, Wikimedia Commons, https://commons.wikimedia.org/wiki/File:Uk_outline_map.png, available under CC BY-SA 3.0 license.

organic carbon or SOM content and precise pH values were not provided by farm managers and were not measured as part of the study.

Field measurements

Three stainless steel soil collars with a diameter of 40cm were inserted into the soil to a depth of 10cm within each plot approximately 1 week prior to the first GHG measurements taking place. This was done to allow the collars to settle into the ground, as insertion of collars followed quickly by GHG measurements can cause inaccurate results. All soil collar insertion techniques, materials and size requirements were found using the industry standard closed static chamber measurement guidelines (de Klein and Harvey, 2013), and the closed static chamber was constructed by the paper authors in line with these specifications.

Measurements were taken weekly using a closed static chamber (with a volume of 61.6dm³) connected to a Gasmeter GT5000 Terra portable gas analyser designed in Finland (Gasmeter Technologies, 2026), calibrated for CO₂, CH₄ and N₂O. A random, single soil collar from each plot was measured for 5 minutes during each weekly field site visit as measuring more collars per plot was not viable due to the optimal time for gas analyser measurements being 10:00am until 4:00pm and battery life constraints (Pavelka et al., 2018). A 5 minute closure time is standard practice for portable FTIR analysers and gas analysers and provides sufficient data points for reliable linear regression flux calculations while minimising chamber-induced artifacts (de Klein and Harvey, 2013; Pavelka et al., 2018; Gasmeter Technologies, 2026). The standing linseed crop vegetation was left intact inside the collar and chamber during measurements to capture total ecosystem fluxes (soil + plant-mediated). No measurements were made between the 4th and 17th of July and between the 30th of July and the 13th of August due to heavy rainfall in 2024, which prevented the use of the Gasmeter analyser due to its sensitivity to high moisture. No measurements

were taken between the 22nd of May and the 9th of June in 2025 for the same reason. Overall, GHG fluxes were measured on 9 days in 2024 across 11 weeks, whilst the 2025 site had 10 measurements conducted across 8 weeks.

In both years, soil temperature was measured using a Fisher Scientific temperature probe at a depth of approximately 5cm, and it was measured for each 5-minute period in which the portable gas analyser was attached to the chamber on a new collar. Soil volumetric moisture was measured using a Delta-T Devices SM150T soil moisture probe at a depth of approximately 5cm, which expresses water content of the soil as a percentage. Crop height was measured using a tape measure, and three stems were measured from soil to the top of the plant and then an average of the three measurements was recorded. Weather conditions were also recorded as either 'sunny', 'overcast' or 'drizzle' depending on if measurements were taking place with clouds overhead, no clouds overhead or a light amount of rainfall in-which the Gasmeter gas analyser could remain operational, however, this categorical weather data was never used for any analysis.

Flux calculations

The Gasmeter analyser provided a concentration measurement for CO₂, CH₄ and N₂O in ppm (parts per million) every 5s. A calculator was constructed using Microsoft Excel which converted these raw measurements into flux (μg m⁻² hr⁻¹). The flux (F) was calculated as:

$$F = \frac{V}{A} \times \frac{\Delta C}{\Delta t} \times \frac{P \times M}{R \times T} \times 10^6$$

Where V is the chamber volume (m³), A is the soil collar surface area (m²), ΔC/Δt is the rate of change in gas concentration (ppm h⁻¹) obtained by linear regression, P is atmospheric pressure (Pa), M is the molar mass of the gas (g mol⁻¹), R is the ideal gas constant (8.314 J mol⁻¹ K⁻¹), and T is the air temperature inside the

chamber (K). These calculations followed standard closed static chamber protocols (de Klein and Harvey, 2013; Pavelka et al., 2018).

To derive seasonal cumulative emissions, daily mean fluxes were first calculated for each genotype by averaging across all available collars and replicates on each measurement date. Because only one randomly selected collar per plot was measured each week (out of three installed per plot), cumulative emissions were computed individually for each collar before averaging to plot and genotype levels. Gaps between sampling dates, including periods when no measurements were possible due to heavy rainfall, were filled by linear interpolation. Seasonal cumulative emissions (Kg ha⁻¹ or g ha⁻¹) were then derived using trapezoidal integration of these daily mean fluxes over the measurement periods in each year, from sowing to harvest in 2024 (1st May to 9th September 2024) and from sowing to the final sampling date prior to harvest in 2025 (1st April 2025 to 25th June 2025) (Somers et al., 2019). Negative daily CH₄ fluxes, indicating net soil uptake (a CH₄ sink), were retained as negative values during integration and therefore contributed to a reduction in seasonal cumulative CH₄ emission. Global warming potential (GWP, kg CO₂-equivalents ha⁻¹) was calculated using 100-year IPCC conversion factors (CO₂ = 1, CH₄ = 27.9, N₂O = 273) (IPCC, 2023).

Statistical analysis

All data summary and statistical analyses were conducted in R v4.5.1 (R Core Team, 2025). Data inspection and cleaning included visual inspections of flux distributions via histograms and Q-Q plots, Shapiro-Wilk tests for normality and Leven's tests for homogeneity of variance. When necessary, GHG fluxes were log-transformed using $\log(y + c)$ where c was a small constant to accommodate negative CH₄ fluxes. Model residuals were checked for normality and homoscedasticity.

To test whether linseed genotype influenced GHG emissions within this study, we compare daily and cumulative CO₂, CH₄ and N₂O fluxes among genotypes were compared separately for each site-year using one-way ANOVA. For the 2025 trial, which followed a randomised complete block design with four blocks, the ANOVA model included Genotype as the main factor and Block as an additional fixed factor to account for the blocking structure. In contrast, for the 2024 trial, where plots associated with this study were dispersed among unrelated variety trial plots and not arranged in contiguous blocks (despite three replicates being used), the design was treated as completely randomised; therefore, Block was not included in the model and a standard one-way ANOVA

on Genotype alone was performed. In contrast, daily fluxes were analysed using a linear mixed-effect models (LMMs) with Genotype as the fixed effect (and Block included as appropriate for 2024). Random effects were included for collar nested within plot (or block) to properly account for the repeated measurements on the same collars across weekly sampling dates.

Because the two field trials were conducted at different sites in different years and used slightly different experimental designs (randomised complete block design in 2024 versus dispersed plots in 2025), site and year effects are confounded. Models including the factor "Year" (the LMM for daily fluxes and the two-way ANOVA for cumulative fluxes) were therefore used in an exploratory manner. Results involving year should be interpreted with caution, as they reflect the combined influence of site, year, climate, management and fertiliser regime rather than purely isolated temporal effects.

To evaluate genotype performance across years, two-way ANOVA models (Genotype x Year) were used to assess cumulative emissions for each GHG, with post-hoc Tukey HSD tests conducted for pairwise comparisons where significant effects were found.

Crop height trajectories were analysed using LMMs using the lme4 package, with days since planting, genotype, year and their interactions as fixed effects, and collar nested within plot as a random effect to account for repeated measurements. Fixed-effect significance was assessed via F-tests and estimated marginal means, slopes and 95% confidence intervals obtained using emmeans. To test whether above-ground growth predicted GHG fluxes, separate LMMs were fitted for daily log-transformed CO₂, CH₄ and N₂O fluxes. Fixed effects included crop height, year, soil temperature, volumetric soil moisture and their interactions. Random effects included genotype, block, plot and collar. Backward step-wise model selection removed non-significant interactions, with significant terms interpreted using estimated marginal means and model-derived slopes. Across all models, significance was assessed at $\alpha = 0.05$. Where appropriate, partial η^2 values were calculated to assess effect sizes.

Results

Genotypic variation in GHG fluxes

Across both field sites and growing seasons, no significant differences were observed in daily or cumulative GHG fluxes

TABLE 2 Mean $\pm$ standard error of daily and cumulative GHG fluxes (CO₂, N₂O, CH₄) by genotype across both sites.

Genotype	Daily CO ₂ (mg m ⁻² h ⁻¹)	Daily N ₂ O (μ g m ⁻² h ⁻¹)	Daily CH ₄ (μ g m ⁻² h ⁻¹)	Cumulative CO ₂ (kg ha ⁻¹)	Cumulative N ₂ O (g ha ⁻¹)	Cumulative CH ₄ (g ha ⁻¹)
Empress	23.34 $\pm$ 24.40	3.10 $\pm$ 0.92	6.64 $\pm$ 3.61	412 $\pm$ 29.16	5.88 $\pm$ 2.92	7.92 $\pm$ 1.61
Omegalín	22.49 $\pm$ 22.07	3.62 $\pm$ 1.14	3.40 $\pm$ 0.74	365 $\pm$ 32.25	6.47 $\pm$ 3.02	6.86 $\pm$ 2.11
Richess	25.30 $\pm$ 26.50	3.77 $\pm$ 1.04	4.00 $\pm$ 0.86	408 $\pm$ 26.60	7.84 $\pm$ 3.55	8.86 $\pm$ 1.07
VT50	21.04 $\pm$ 21.06	2.30 $\pm$ 0.58	4.55 $\pm$ 1.24	382 $\pm$ 26.75	5.09 $\pm$ 1.75	10.40 $\pm$ 4.98

among the four linseed genotypes (Table 2). Mean daily CO₂ fluxes ranged from 21.04 ± 21.06 to 25.30 ± 26.50 mg m⁻² h⁻¹, with no genotype effect detected (ANOVA, $p > 0.05$). Similarly, daily N₂O fluxes varied between 2.30 ± 0.58 and 3.77 ± 1.04 μg m⁻² h⁻¹, and daily CH₄ fluxes between 3.40 ± 0.74 and 6.64 ± 3.61 μg m⁻² h⁻¹, with no statistically significant differences (Supplementary Table 1). Patterns in cumulative emissions mirrored those of daily fluxes. Cumulative CO₂ emissions ranged from 365 ± 32.25 to 412 ± 29.16 kg ha⁻¹, cumulative N₂O from 5.09 ± 1.75 to 7.84 ± 3.55 g ha⁻¹, and cumulative CH₄ from 6.86 ± 2.11 to 10.40 ± 4.98 g ha⁻¹, with no significant genotypic effects ($p > 0.05$ for all gases). Genotype was not a major determinant of GHG emissions in the two field sites studied, potentially due to a stronger influence of environmental conditions between growing seasons on flux variability.

Environmental variation between sites and associated GHG fluxes

Environmental conditions differed markedly between the two growing seasons (Table 3). Mean soil temperature was significantly higher in 2024 (19.9 ± 0.24 °C) than in 2025 (17.6 ± 0.14 °C; $p < 0.05$), while cumulative rainfall was 2.5-fold greater (66.2 vs. 26.5 mm in 2024 and 2025 respectively, $p < 0.05$). Soil volumetric moisture was similar between years (15.8 ± 0.67% in 2024 vs. 16.7 ± 0.37% in 2025, $p < 0.05$).

These comparisons between site-years should be interpreted qualitatively, as the two locations shared broadly similar loamy and clayey soil textures in the upper profile and comparable long-term crop rotations (wheat, barley, peas), but differed substantially in N fertiliser regime (105 kg N ha⁻¹ liquid fertiliser in 2025 versus 300 kg N ha⁻¹ ammonium-based fertiliser in 2025; Table 1) and other unmeasured factors such as exact soil physicochemical properties (e.g., bulk density, SOM/SOC content, pH). These environmental differences were reflected in GHG fluxes, indicating that intra-annual variation strongly shaped GHGs with warmer and wetter conditions in 2024 associated with high cumulative CO₂, N₂O and CH₄ compared to 2025 (Table 3, Figure 2).

TABLE 3 Mean ± standard error of environmental variables (ST, soil temperature; VSM, volumetric soil moisture; P, precipitation; CH, crop height) and daily and cumulative GHG fluxes by site.

Environmental variable	2024	2025
ST (°C)	19.9 ± 0.24*	17.6 ± 0.14*
VSM (%)	15.8 ± 0.67	16.7 ± 0.37
P (mm)	66.2 [†]	26.5 [†]
CH (cm)	31.45 ± 0.52*	35.88 ± 0.61*
Mean daily CO ₂ (mg m ⁻² h ⁻¹)	16.02 ± 1.64*	32.16 ± 1.24*
Mean Cumulative CO ₂ (Kg ha ⁻¹) (SE)	413.8 ± 29.3*	341.2 ± 19.7*
Mean daily N ₂ O (μg m ⁻² h ⁻¹) (SE)	4.84 ± 0.80*	1.06 ± 0.16*
Mean Cumulative N ₂ O (g ha ⁻¹) (SE)	10.2 ± 1.9*	1.15 ± 0.20*
Mean daily CH ₄ (μg m ⁻² h ⁻¹) (SE)	3.47 ± 0.49	5.13 ± 2.16
Mean Cumulative CH ₄ (g ha ⁻¹) (SE)	12.8 ± 1.9*	2.74 ± 1.43*

*indicates that results were significantly different using either independent-sample t-tests for environmental variables, two-way ANOVA for cumulative fluxes and t-tests for mean daily fluxes. [†]indicates that significance tests were not conducted due to data being aggregated.

Cumulative GHG fluxes differed strongly between years (Table 3, Figure 2), with values integrated over the respective measurement periods described in the Flux Calculations section (full season to harvest in 2024 versus the monitored period prior to harvest in 2025). Mean cumulative CO₂ flux decreased by ~15% from 413 ± 29 to 341 ± 19 kg ha⁻¹, N₂O flux declined by ~89%, from 10.2 ± 1.9 to 1.15 ± 0.20 g ha⁻¹ and CH₄ flux decreased ~79% from 12.8 ± 1.4 to 2.74 ± 1.43 g ha⁻¹ between 2024 and 2025 (Table 3). Despite lower cumulative CO₂ in 2025, mean daily CO₂ flux was significantly higher (32.16 ± 1.24 mg m⁻² h⁻¹ vs. 16.02 ± 1.64 mg m⁻² h⁻¹; $p < 0.01$). Daily N₂O flux followed the cumulative trend, decreasing from 4.84 ± 0.80 to 1.06 ± 0.16 μg m⁻² h⁻¹ ($p < 0.01$), while daily CH₄ flux showed no significant year effect.

Inter-annual comparison of cumulative GHG fluxes between genotypes

Two-way ANOVA (Genotype × Year) revealed no significant genotypic differences in cumulative CO₂ ($p = 0.58$) or N₂O ($p = 0.88$) emissions (Table 2, Figures 2A; B). However, year had a significant effect on both gases, with higher emissions in 2024 than in 2025 (CO₂: $p < 0.05$; N₂O: $p < 0.05$) (Figure 2A, B). No Genotype × Year interaction was detected for CO₂ ($p = 0.62$) or N₂O ($p = 0.94$). In contrast, CH₄ flux was strongly influenced year and by a highly significant Genotype × Year interaction ($p < 0.05$) (Figure 2C; Supplementary Table 3), however the main effect of genotype was not significant (Table 2; Figure 3C). *Post-hoc* Tukey tests showed that VT50 was the strongest CH₄ source in 2024 (10.8 g ha⁻¹ > Empress, $p < 0.05$), but in 2025 it became a net sink (mean -2.83 g ha⁻¹), differing significantly from its 2024 emissions (diff = -23.2 g ha⁻¹, $p < 0.05$) and from all other genotypes in 2024 ($p < 0.05$) (Figure 3C; Supplementary Table 4).

Crop growth dynamics and height variations

Crop height increased steadily at both sites over the growing season, with a mean growth rate of 0.45 cm day⁻¹ across all genotypes and years ($b = 0.448$, SE = 0.032, $P < 0.05$, Supplementary Figure 5). Growth trajectories were well explained by a LMM with fixed effects for days since planting, genotype, year and their interactions, and collar as random effects ($R^2_m = 0.852$; $R^2_c = 0.856$, Supplementary Table 2), indicating that time since planting explained the majority of variation in crop height.

A significant main effect of genotype on height was observed ($P < 0.05$), driven by differences in growth rates rather than initial heights (Figure 4). The interaction between days since planting and genotype was significant ($P < 0.05$), with VT50 exhibiting a faster growth rate relative to Empress ($b = 0.118$ cm day⁻¹, SE = 0.045, $P < 0.05$) (Figures 4A; D), while Richess grew slower ($b = -0.091$ cm day⁻¹, SE = 0.045, $P < 0.05$) (Figure 4C). No significant differences were found for Omegalin relative to Empress ($P = 0.792$) (Figures 4A; B). *Post-hoc* pairwise comparisons revealed no significant differences in predicted heights among genotypes within each year (all $P > 0.19$), suggesting that genotypic effects on overall height trajectories were subtle and not detectable after multiple-testing correction.

Inter-annual variability was pronounced, with a marginal main effect of year ($P = 0.1$) and a highly significant interaction between

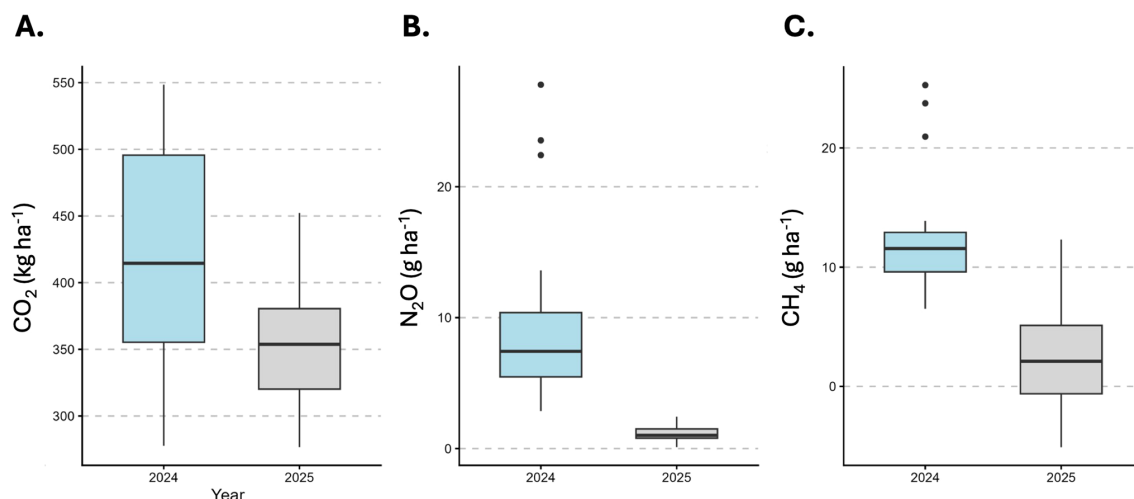


FIGURE 2

Cumulative GHG fluxes aggregated across all linseed genotypes for two years (2024 and 2025). Panels show CO₂ fluxes in kg ha⁻¹ (A), N₂O fluxes in g ha⁻¹ (B), and CH₄ fluxes in g ha⁻¹ (C). Light blue boxes represent data from 2024 (Leicestershire site), while grey boxes represent data from 2025 (Derbyshire site).

days since planting and year ($P < 0.05$) (Supplementary Table 2). Crops in 2025 exhibited approximately 0.31 cm day⁻¹ faster than in 2024 ($b = 0.305$, $SE = 0.072$, $P < 0.001$). *Post-hoc* comparisons confirmed that, for each genotype, predicted heights were significantly higher in 2025 than in 2024 (differences ranging from 25.4 to 27.8 cm, all $P < 0.05$). No three-way interaction was detected ($P > 0.9$), indicating that genotypic differences in growth rates were consistent across years.

Influence of crop height on GHG fluxes

We investigated whether crop height, as a proxy for above-ground growth, predicted variation in daily GHG fluxes (CO₂, N₂O and CH₄) (Figure 5). LMMs included fixed effects for height, year, soil temperature, and volumetric soil moisture, and their

interactions, with random effects for genotype, block, plot and collar. Backward selection was used to remove non-significant terms from this full model (Supplementary Table 1).

For CO₂ fluxes, there was a highly significant main effect of height ($P < 0.05$) and year ($P < 0.05$), alongside soil temperature ($P < 0.05$) and a height $\times$ soil temperature interaction ($P < 0.05$) (Supplementary Table 1). *Post-hoc* comparisons confirmed a steeper positive slope in 2024 ($b = 0.036$, $SE = 0.005$, $P < 0.001$) than in 2025 ($b = 0.007$, $SE = 0.005$, $P = 0.204$; difference = 0.030, $SE = 0.007$, $P < 0.001$) (Figure 5B). Fluxes increased with height in both years, with a steeper slope in 2024, aligning with the significant height $\times$ year interaction (Figure 5B).

N₂O fluxes showed a highly significant effect of height $\times$ volumetric moisture ($P < 0.05$) and year $\times$ volumetric moisture ($P < 0.05$), but no effects from height, year, soil temperature, or

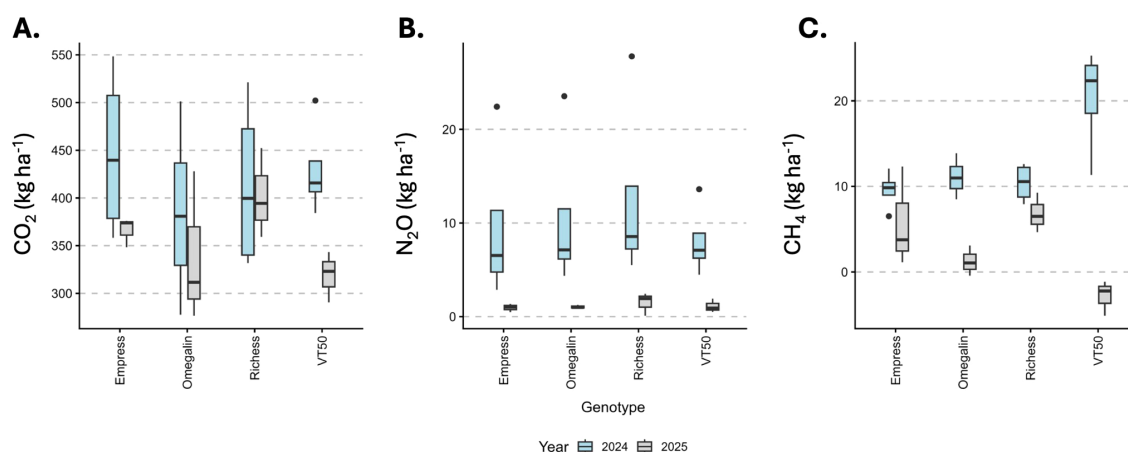


FIGURE 3

Cumulative GHG fluxes for four linseed genotypes (Empress, Omegalin, Richess, VT50) across two years (2024 and 2025). Panels show: CO₂ in kg ha⁻¹ (A), N₂O fluxes in g ha⁻¹ (B), and CH₄ fluxes in g ha⁻¹ (C). Light blue boxes represent data from 2024 (Leicestershire site), while grey boxes represent data from 2025 (Derbyshire site).

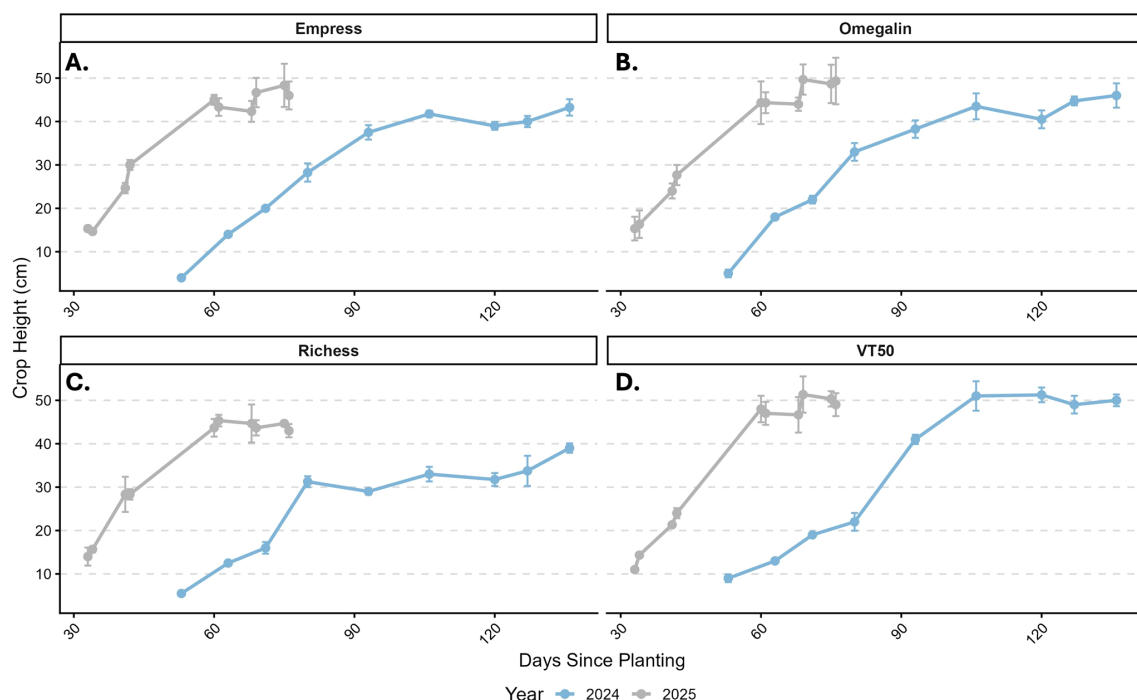


FIGURE 4

Mean crop height (cm; points represent means across replicates per measurement date) plotted against days since planting for each linseed genotype: Empress (A), Omegalin (B), Richess (C) and VT50 (D). Data derived from weekly measurements at the 2024 Leicestershire site (light blue line) and 2025 Derbyshire site (grey line). The 2024 season was measured over a greater period of time (11 weeks) compared to the 2025 season (2025). The 2025 measuring season also concluded prior to harvest.

the height $\times$ year interaction (all $P > 0.1$) (Supplementary Table 1). No significant trends were seen for N_2O fluxes increasing with crop height (Figure 5C).

CH_4 fluxes exhibited significant effects of height $\times$ volumetric moisture ($P < 0.05$), volumetric moisture ($P < 0.05$) and year $\times$ volumetric moisture interaction. None of year, soil temperature, or the interaction (all $P > 0.2$) were significant (Supplementary Table 1). There was a mild positive trend in both years for CH_4 flux which was consistent with the significant height effect (Figure 5A).

Discussion

This two-year field experiment provides an initial assessment of GHG emissions from linseed genotypes under commercial farm conditions. We anticipated that genotypic differences would contribute to variation in CO_2 , CH_4 and N_2O fluxes, reflecting potential genetic control over plant-soil interactions (Smart and Bloom, 2001; Verma et al., 2006; Gogoi and Baruah, 2012; Chen et al., 2021). While clear genotypic effects were not observed for cumulative CO_2 and N_2O emissions, results indicate that environmental variation between seasons exerted much stronger influence on flux dynamics than genotype in this study. A notable exception was the significant genotype $\times$ year interaction for CH_4 emissions, exemplified by VT50's transition to a net CH_4 sink (-2.83 g/ha) in 2025 consistent

with studies suggesting that plant-mediated CH_4 dynamics may arise through root traits and oxygen transport to soils (Aulakh et al., 2000; Baruah et al., 2010; Girkin et al., 2018). This pattern warrants further investigation but given the confounding effects of site and year should be interpreted cautiously. Overall, our findings suggest that, under the environmental conditions tested, site-specific factors and seasonal climate variation played a dominant role in shaping soil GHG fluxes from linseed systems.

The absence of consistent genotypic differences in CO_2 and N_2O aligns with evidence that environmental conditions, including soil moisture, temperature and N availability, can override plant genetic controls on microbial pathways such as nitrification and denitrification (Philippot et al., 2013; Shenton et al., 2016; Guo et al., 2022; Girkin and Cooper, 2023). Warmer and wetter conditions in 2024 coincided with higher cumulative fluxes across all gases, consistent with well-established climate controls on microbial metabolism and GHG production (Shcherbak et al., 2014; Thorup-Kristensen et al., 2020; Tian et al., 2020). The observed CH_4 genotype response was variable but suggests the potential role of plant functional traits such as rooting depth, porosity, and exudation in modulating methane cycling (Baruah et al., 2010; Corneo et al., 2017; Griffiths et al., 2022). However, the magnitude and direction of effects differed between years, reinforcing the need for multi-year, multi-site studies to assess whether genotype-driven variation in GHG fluxes can be robustly detected in linseed systems subject to strong environmental forcing (Lynch et al., 2021; Rumpel et al., 2022).

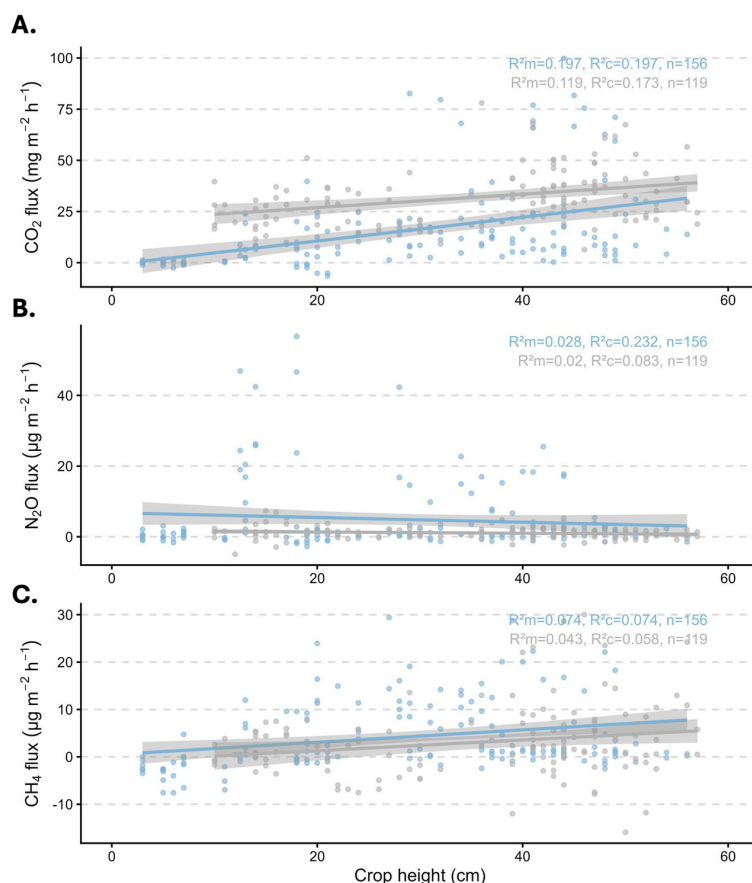


FIGURE 5

Relationships between crop height and GHG fluxes across two years. Panels show daily fluxes for CO_2 ($\text{mg m}^{-2} \text{h}^{-1}$) (A), N_2O ($\mu\text{g m}^{-2} \text{h}^{-1}$) (B), and CH_4 ($\mu\text{g m}^{-2} \text{h}^{-1}$) (C) plotted against crop height (cm). Data points represent individual chamber measurements from all genotypes and replicates ($n = 276$). Light blue points and lines correspond to 2024 (Leicestershire site), grey to 2025 (Derbyshire site). Solid lines indicate linear regression fits with 95% confidence intervals (shaded bands). Note differing y-axis scales across panels to accommodate flux ranges.

Environmental and site-specific drivers of emission variability

Site and year emerged as primary influencers of GHG emission patterns, with marked differences in fluxes underscoring the overriding impact of environmental conditions. The two experimental sites had broadly similar loamy and clayey soil textures in the upper profile and shared a comparable long-term rotation history of wheat, barley and peas with standard residue management. However, they differed in several key agronomic factors that likely contributed to the observed inter-annual differences in emissions. Most notably, N fertilisation was considerably lower in 2024 (105 kg N ha^{-1}) than in 2025 (300 kg N ha^{-1}), yet N_2O emissions were approximately 89% lower in the second year (Figure 3B). This counter-intuitive pattern is most plausibly explained by the substantially drier and cooler conditions in 2025, which would have limited denitrification rates despite the higher N input. For CO_2 fluxes, the lower cumulative emissions in 2025 coincided with faster crop growth (higher mean height) but drier conditions, potentially reflecting reduced soil respiration and altered root activity under lower moisture availability. Although detailed soil properties (bulk density, SOM/SOC content, pH) were not measured as part of the study, the similar broad soil texture classes suggest that differences

in initial organic matter or drainage characteristics may have played secondary roles. Soil tillage (ploughing, power harrowing, drilling and rolling to 10cm depth) occurred approximately one week prior to sowing in both years, minimising major differences in this regard. Chamber placement followed the same protocol in both trials, and crop height data (a proxy for above- and belowground biomass) were collected consistently. Overall, these site-specific agronomic and climatic interactions highlight that environmental conditions and management practices exerted stronger control over GHG fluxes than genotype in the present study.

From a practical perspective, our findings suggest that agronomic and environmental management currently offer greater scope for reducing GHG emissions from linseed systems than genotype choice alone. Approaches that optimise N inputs, improve soil structure and drainage, and synchronise fertiliser application with rainfall patterns are likely to have more immediate influence on fluxes than varietal selection, particularly under variable UK weather conditions (Smith et al., 2007; Zhang et al., 2015; Paustian et al., 2016; IPCC, 2023). As a break crop with typically lower fertiliser requirements and benefits for soil health and rotation resilience, linseed may still contribute to more climate-efficient cereal systems (Angus et al., 2015; Stavropoulos et al., 2023). However, resolving potential genotype-mediated mitigation

pathways will require multi-year, multi-site designs with greater replication, coordinated phenotyping of below-ground traits, and integration of yield and nitrogen-use-efficiency data to contextualise emissions outcomes (Lynch et al., 2021; Rumpel et al., 2022). Future work combining plot-scale chambers, continuous flux measurements, and trait-based breeding approaches could help identify whether specific genotypes consistently confer lower emissions under particular soil or climate regimes, supporting refined selection strategies as climate variability intensifies (Thorup-Kristensen et al., 2020; Hallett et al., 2022).

These site-driven patterns align with global syntheses showing environmental factors (e.g., moisture, aeration) dominate N_2O and CH_4 in oilseeds, often overriding genotypic impacts (Walthall et al., 2025). For linseed specifically, our results complement evidence of its low overall carbon footprint (0.9–11 kg CO_2 -eq per kg fiber), which is 2–3 times lower than cotton or sunflower equivalents, underscoring its potential as a sustainable break crop in rotations (Stavropoulos et al., 2023).

Genotype-specific patterns in GHG fluxes

Breaking down results by GHG reveals genotype-specific patterns that partially validate our hypothesis. CO_2 fluxes, reflecting plant and soil respiration, were higher in 2024 for VT50 (Figure 3A), likely due to greater biomass and root exudation under favourable temperatures, enhancing decomposition and carbon cycling (Bardgett et al., 2014; Hallett et al., 2022). CH_4 showed the most striking genotypic variation, with reductions in 2025 for Omegalin and VT50, the latter exhibiting a negative cumulative flux (-2.83 g/ha) (Figure 3C), indicating a soil CH_4 sink possibly driven by root specific traits like aerenchyma or oxygen leakage, which support methanotrophic bacteria in drier, better-aerated soils (Aulakh et al., 2000; Girkin et al., 2018). Such sinks are uncommon in arable systems but align with findings in rice, where root porosity modulates CH_4 transport (Baruah et al., 2010). N_2O emissions showed no significant genotypic differences (Figure 3B), suggesting uniform N assimilation and limited NUE (nitrogen use efficiency) variability among these linseed varieties, possibly due to their recent breeding history (all introduced in the UK within the last decade) or fertilizer forms overriding genetic controls (Smart and Bloom, 2001; Verma et al., 2006).

Crop growth and its relationship to emissions

In 2024, VT50's greater height compared to Empress and Richess aligns with its elevated CH_4 emissions (Figures 3, Figure 4C), suggesting trade-offs where vigorous growth enhances nutrient cycling but increases respiratory losses (Gaju et al., 2011; Corneo et al., 2017). Positive correlations between height and fluxes for CO_2 and CH_4 across genotypes indicate that root traits, such as length, hairs, and rhizodeposits, drive ecosystem functions, including GHG fluxes, emphasizing the need for root phenotyping in break crop assessments (Obara et al., 2010; Griffiths et al., 2022). Linear mixed models, accounting for covariates, confirmed these links persist independently of temperature and moisture (Figure 5).

This integration of growth data reinforces height's utility in genotype selection for break crops, promoting varieties that balance productivity and emissions under inter-annual variability (Thorup-Kristensen et al., 2020).

Implications for sustainable agriculture and net zero in UK and global contexts

These findings carry significant implications for sustainable linseed production and agricultural net zero strategies. No unfertilised control plots for the linseed genotypes were included in either year, as the experiment was deliberately conducted under realistic commercial farm conditions using standard farmer-applied fertiliser rates (Table 1). As a break crop in cereal rotations, linseed enhances soil health, nutrient cycling, and carbon sequestration (Robson et al., 2002; Cusworth et al., 2021; Moukanni et al., 2022). Our results suggest that selecting genotypes like VT50 for CH_4 sinks in drier regions could further mitigation efforts, while broader NUE improvements could reduce N fertilizer dependency, addressing food security and environmental concerns (Zhang et al., 2015; Reay, 2020). This supports evidence that linseed has potential to reduce GHG emissions via low-input farming, allowing for improved NUE and soil health (Stavropoulos et al., 2023). In the UK, where agriculture accounts for 11% of GHG emissions (DEFRA, 2022), targeted breeding aligns with the 2050 Net Zero roadmap, emphasizing soil carbon and sustainable N management (Smith, 2004; Department for Energy, Security & Net Zero, 2021; Rumpel et al., 2022). However, the lack of pertinent genotype effects suggests that varietal selection alone is insufficient, advocating for integrated approaches combining genetics with site-specific management in the context of linseed.

Challenging field conditions and data analyses

Some limitations constrain the outcomes of the study and highlight areas for practical improvements. Because the two growing seasons (2024 and 2025) were located at different sites, site and year effects are partially confounded and environmental drivers cannot be entirely separated from year effects. Using different field sites across years confounds genetic and environmental effects, as unpaired replicates (12 collars per genotype in 2024 vs. 9 in 2025) reduce statistical power for detecting subtle genotypic differences (Bayuelo-Jiménez et al., 2011). Weather interruptions, such as unexplored measurements during rainfall (July–August 2024 and May–June 2025), created data gaps, potentially underestimating peak fluxes during high-moisture periods when denitrification and methanogenesis peak (de Klein and Harvey, 2013). The closed static chamber method, while standard, assumes linear gas accumulation and may miss diurnal or spatial variability, especially in heterogeneous plots (Shenton et al., 2016). The lack of direct NUE, root trait, or microbial community measurements limits mechanistic insights into inferred processes like aerenchyma effects or exudation (Bardgett et al., 2014). Low replication and the focus on a few recently introduced genotypes restrict applicability to broader linseed diversity or other break crops.

Additionally, although three collars were installed per plot, only one randomly selected collar per plot was measured on each sampling date due to practical constraints of the portable analyser. While this approach is common in manual chamber studies, it limits the capture of within-plot spatial heterogeneity in GHG fluxes, which can be substantial even in visually uniform plots due to micro-scale variation in soil properties, root distribution, or residue management (Parkin, 1987; Chadwick et al., 2014). Both sites shared similar long-term rotations of wheat, barley and peas with standard residue management, but the absence of detailed soil physicochemical data (e.g., bulk density, pH, SOC content) further constrains interpretation of inter-annual differences. Omitting yield data precludes emission intensity assessments per unit production, a key metric for sustainable intensification (Smith et al., 2007).

Conclusion and future research directions

Our data, although covering only four genotypes indicate possible benefits from crop selection for lower emitting traits, however, future research should prioritize a controlled environment e.g. glasshouse based pot experiments, to isolate genotypic effects, coupled with advanced phenotyping (e.g., root imaging, metagenomics) to more appropriately link traits to emissions (Corneo et al., 2017; Hallett et al., 2022). Multi-year, multi-site trials with increased replications and continuous monitoring (e.g., eddy covariance) could better capture climate interactions, while integrating yield and NUE data would direct breeding for low-emission, high-productivity varieties (Swarbreck et al., 2019; Si et al., 2023). Expanding to diverse linseed germplasm and other break crops like oilseed rape with reduced GHG characteristics would significantly improve ecosystem service evaluations, supporting global net zero agriculture efforts (Lynch et al., 2021; Griffiths et al., 2022).

Data availability statement

The original contributions presented in the study are included in the article/Supplementary Material. Further inquiries can be directed to the corresponding authors.

Author contributions

CW: Investigation, Visualization, Software, Data curation, Validation, Writing – review & editing, Formal analysis, Conceptualization, Methodology, Writing – original draft, Project administration. AS: Methodology, Data curation, Conceptualization, Supervision, Software, Writing – review & editing, Formal analysis, Project administration. ZK: Project administration, Methodology, Writing – review & editing, Conceptualization, Supervision. NP:

Supervision, Conceptualization, Writing – review & editing, Resources, Funding acquisition. NG: Funding acquisition, Supervision, Writing – review & editing, Methodology, Conceptualization, Project administration.

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Conflict of interest

The author(s) declared that this work was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Generative AI statement

The author(s) declared that generative AI was not used in the creation of this manuscript.

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Supplementary material

The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fagro.2026.1748086/full#supplementary-material>

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