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METHANE FLUX DYNAMICS IN AGRICULTURAL ECOSYSTEMS: ROLE OF EXTREME WEATHER EVENTS AND MOLECULAR MARKERS

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ABSTRACT

Methane (CH_4) is the second most potent anthropogenic greenhouse gas after CO_2, with an atmospheric concentration exceeding 1,923 ppb in 2024 — a 160% increase above pre-industrial levels (~722 ppb) — and a global warming potential 27–30 times greater than CO_2 over a 100-year horizon. Agriculture contributes approximately 40% of total anthropogenic CH_4 emissions (~145–155 Tg CH_4 yr^{-1}), with rice paddies alone accounting for 28–32 Tg CH_4 yr^{-1} (8–10% of global totals) through prolonged anaerobic methanogenesis. Net CH_4 flux from agricultural soils is governed by the balance between anaerobic methanogenesis and aerobic methane oxidation (methanotrophy). Under continuously flooded conditions, soil redox potential (Eh) falls below −150 mV, driving daily emissions of 150–350 mg CH_4 m^{-2} day^{-1}, while well-aerated upland soils act as net CH_4 sinks (−0.5 to −3.5 mg CH_4 m^{-2} day^{-1}). Extreme weather events — including flooding, drought, and heatwaves — alter these dynamics non-linearly: flooding can accelerate methanogenesis by 200–500% while concurrently reducing methane oxidation efficiency by 40–80%, whereas drought reduces CH_4 production by 50–90% through increased soil aeration. Temperature sensitivity of methanogenesis (Q_{10} = 2.0–4.2) further amplifies emissions under warming scenarios. At the molecular level, the functional genes mcrA and pmoA are frequently utilized as molecular markers to assess methanogenic and methanotrophic community abundance (10^6–10^8 and 10^5–10^7 copies g^{-1} dry soil, respectively) and their functional activity. The mcrA/pmoA ratio serves as a reliable proxy for the source–sink balance, with ratios of 2.0–2.5 under continuous flooding versus 1.2–1.6 under alternate wetting and drying (AWD) — the latter reducing seasonal emissions by ~30%. This review synthesizes current quantitative understanding of how extreme weather events modulate CH_4 flux in agricultural ecosystems and highlights the utility of molecular markers in developing targeted mitigation strategies.

KEYWORDS: Agricultural soils, Extreme weather events, Methane flux, Methanogenesis, pmoA gene

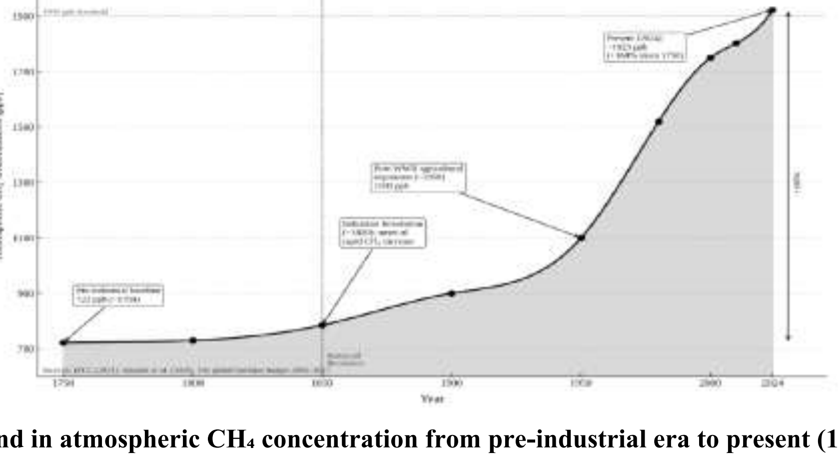

Fig. 1. Trend in atmospheric CH_4 concentration from pre-industrial era to present (1750–2024).

INTRODUCTION

Methane (CH_4) is the second most significant anthropogenic greenhouse gas, following CO_2. Over a century, it can contribute to global warming 27 to 30 times more than CO_2. The atmospheric concentration has exceeded 1,900 ppb, representing an increase of almost 160 per cent compared to pre-Industrial Revolution levels (IPCC 2021; Saunois et al. 2020; Ming et al. 2025). Methane is a transient climate forcer contributing around 0.54 W m^{-2} of radiative forcing, accounting for roughly 17–20 per cent of total greenhouse gas forcing (IPCC 2021; Nisbet et al. 2019). The atmospheric concentration of nitrous oxide (N_2O), another potent greenhouse gas, has increased to approximately 335 ppb, primarily due to agricultural practices and increased utilization of nitrogen-based fertilizers (IPCC 2021; Tian et al. 2020; Forster 2019).

Total global methane emissions are estimated at 580–600 Tg yr^{-1}, of which approximately 60 per cent originate from anthropogenic sources (Smith et al. 2021; Searchinger et al. 2021). Enteric fermentation, manure management, and rice cultivation account for approximately 40% of agricultural sector emissions (Saunois et al. 2020; Jackson et al. 2020; Nisbet et al. 2019). Rice paddies contribute around 8–12% of global anthropogenic CH_4 emissions. Upland croplands serve as minor yet significant sinks for CH_4 and substantial sources of N_2O due to nitrogen fertilization and fluctuating wet–dry soil conditions (Saunois et al. 2020; Zhang et al. 2016; Tian et al. 2020).

Anaerobic methanogenesis and aerobic oxidation are the primary mechanisms affecting CH_4 fluxes. Environmental factors such as soil temperature, redox potential, water-filled pore space (WFPS), and substrate availability influence these processes (Nazaries et al. 2013; Yin et al. 2023). Extreme weather events, increasingly frequent due to climate change, can significantly alter soil conditions, resulting in intermittent methane emissions and influencing N_2O emissions (IPCC 2021; Seneviratne et al. 2021; Shakoor et al. 2020). The present review synthesizes current quantitative understanding of how extreme weather events modulate CH_4 flux in agricultural ecosystems and highlights the utility of molecular markers in developing targeted mitigation strategies.

Mechanistic Basis Of Methane Emissions In Agricultural Soils

The quantity of methane emitted from agricultural soils is contingent upon the interplay between anaerobic methanogenesis and aerobic methane oxidation. Methanogenesis occurs in the absence of oxygen, resulting in the production of CH_4 (Malyan et al. 2021; Conrad 2020). Methane oxidation occurs in the presence of oxygen, decomposing methane prior to its release into the atmosphere. Recent global analyses indicate that agriculture emits around 145–155 Tg CH_4 annually (Filonchyk et al. 2024; Saunois et al. 2020). Rice paddies emit approximately 28–32 Tg CH_4 annually, constituting 8–10% of total anthropogenic methane emissions (Singh et al. 2018; Roy et al. 2025).

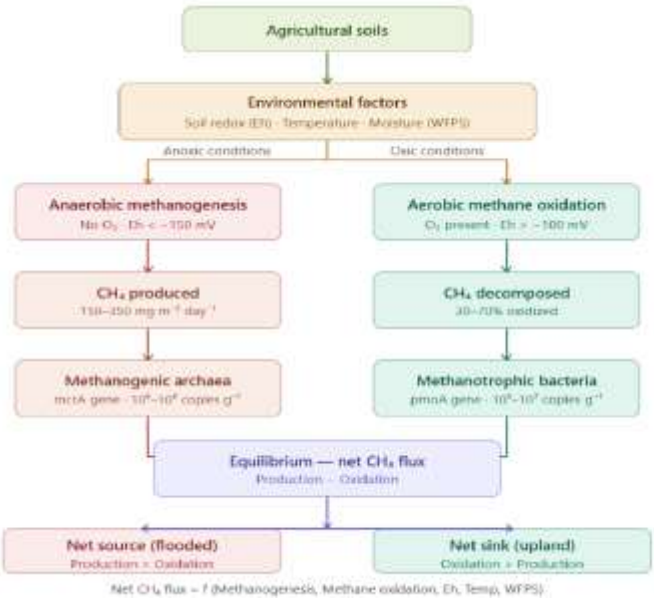

Fig. 2. Microbial pathways of organic matter degradation and methane production in the carbon cycle.

The main factor initiating methanogenesis is soil redox potential (Eh). Aerobic soils exhibit Eh values of +300 to +400 mV, with minimal methane production. Flooding depletes oxygen, causing Eh to fall below 0 mV within days; methanogenesis becomes thermodynamically favorable when Eh decreases to approximately −150 mV, with daily emissions reaching 200–350 mg CH_4 m^{-2} day^{-1} (Tian et al. 2020; Li et al. 2022; Zhang et al. 2024). Temperature significantly influences methane production, with Q_{10} values of 2.0–4.2 for methanogenesis (Liu et al. 2025; Fan et al. 2022). Water management strategies such as alternate wetting and drying (AWD) elevate soil redox potential to levels exceeding −100 mV and can decrease seasonal methane emissions by 30–60% relative to continuous flooding (IPCC 2021; Tian et al. 2020).

Methane Cycling in Agricultural Soils
The cycling of methane in agricultural soils demonstrates the equilibrium between microbial methanogenesis and methane oxidation (methanotrophy), determining whether soils act as net sources or net sinks of atmospheric CH_4 (Lim et al. 2024; Obregon et al. 2023). Upland soils globally are considered net sinks, absorbing approximately 30–45 Tg CH_4 per year from the atmosphere (Li et al. 2025). Conversely, flooded rice cultivation systems are significant sources, emitting around 30–40 Tg CH_4 annually (Guo et al. 2023). Methane fluxes vary from net absorption rates as low as −3.5 mg CH_4 m^{-2} day^{-1} in well-aerated upland soils to significant emissions reaching 400 mg CH_4 m^{-2} day^{-1} in inundated agricultural environments.

Sources of Methane: Methanogenesis
Methanogenesis is an obligatory anaerobic metabolic activity performed exclusively by methanogenic archaea, representing the final stage in the decomposition of organic matter in anaerobic settings (Lyu et al. 2018; Getabalew et al. 2020). This process commences when soil redox potential decreases to approximately −150 mV, typically when WFPS exceeds 85–90% (Du et al. 2023; Anderson et al. 2019). Methanogenesis rates typically range from 0.5 to 6.0 mg CH_4 kg^{-1} soil day^{-1} at optimal temperatures of 25–35°C. In inundated rice systems, surface methane emissions typically range from 100 to 300 mg CH_4 m^{-2} day^{-1} (Saha et al. 2018; Chen et al. 2020).
Molecular analyses employing the mcrA gene indicate that methanogenic archaea abundance in inundated soils typically varies between 10^6 and 10^8 copies per gram of dry soil (Liu et al. 2018), compared to fewer than 10^4 copies g^{-1} in well-aerated soils.

Sinks of Methane: Methane Oxidation
Aerobic methanotrophic bacteria facilitate the oxidation of methane in soil environments, functioning as a biological filter. The enzyme methane monooxygenase (MMO), particularly the particulate variant encoded by the pmoA gene, initiates conversion of methane to methanol (Brasseur and Gaubert 2025). Typical methane oxidation rates in soils range from 0.1 to 2.5 mg CH_4 kg^{-1} soil day^{-1}, with net uptake rates of −0.5 to −3.5 mg CH_4 m^{-2} day^{-1} (Abernethy et al. 2023; Gao et al. 2022). Agricultural soils typically contain 10^5–10^7 pmoA gene copies g^{-1} dry soil. When WFPS exceeds 85–90%, the pmoA gene transcription may decrease by 40–80%, resulting in methane oxidation rates falling to below 30% of those observed under fully aerobic circumstances (Tentori et al. 2020; Tentori et al. 2022).

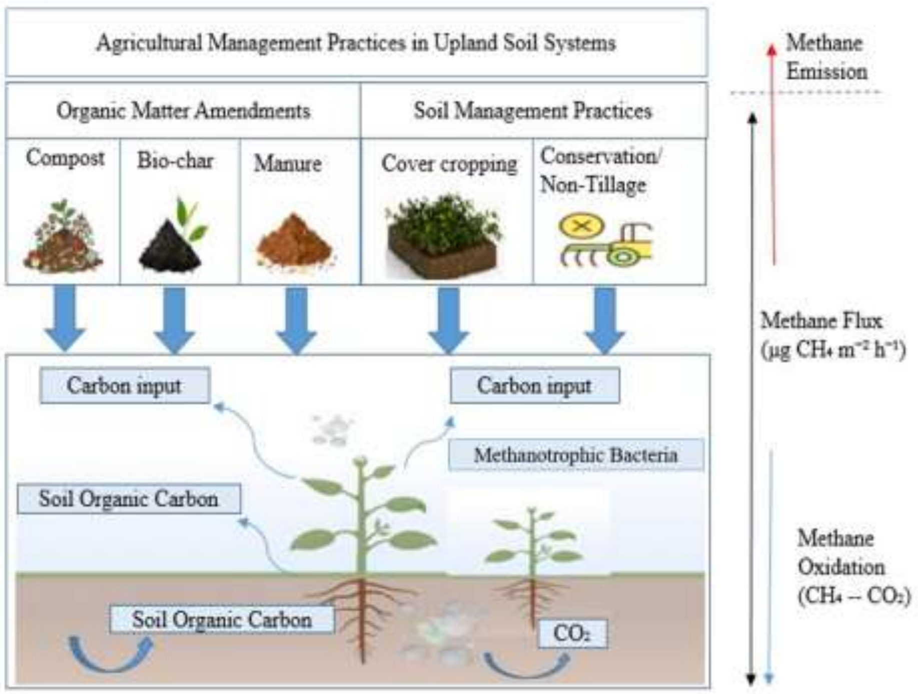

Fig. 3. Effects of agricultural management practices on CH_4 flux in upland soils.

Source–Sink Balance in Soils
The net CH_4 flux from soils is the differential between gross methane production (methanogenesis) and gross methane oxidation (methanotrophy). When WFPS approaches 90%, soils can transition from a CH_4 sink of approximately −2 mg CH_4 m^{-2} day^{-1} to a substantial source exceeding 200 mg CH_4 m^{-2} day^{-1} (Deng et al. 2024). Severe flooding can accelerate methanogenesis by 200–500% while concurrently reducing methane oxidation efficiency by 40–80% (Moore 2018). Drought conditions generally reduce methane production by 50–90% due to increased soil aeration, with methane flows decreasing by 60–95% during dry conditions relative to flooding conditions (Raghav and Kumar 2021). Methane cycling in agricultural soils should therefore be regarded as a threshold-driven system, wherein minor fluctuations in weather can rapidly transform the soil from a methane sink to a methane source.

Extreme Weather Events and Their Direct Impacts

Drought and heatwaves

Heatwaves and drought significantly influence CH_4 emissions by altering soil moisture, temperature, and redox potential. When WFPS decreases from 80–90% to below 60%, soil redox potential increases to above −100 mV, inhibiting methanogenesis and reducing methane emissions by 20–40%. Under extremely arid conditions (WFPS 50–70%), methane emissions may decrease by 50–70% due to enhanced soil aeration (Yu et al. 2022). The response of methane emissions to temperature is non-linear; methanogenesis possesses a Q_{10} value of 2.0–3.0, indicating that a moderate temperature increase of +1 to +3°C with sufficient moisture can significantly augment methane synthesis. Severe heat events can reduce methane oxidation by 15–30%, particularly when accompanied by soil desiccation.

Crop development stage significantly influences methane quantities emitted. Heatwaves can reduce methane emissions by approximately 28% during booting and flowering phases and by 12–16% during the milky maturity phase, primarily due to disparities in root exudation and carbon substrate accessibility. Regional differences are notable: extreme heat events are associated with an 8% increase in methane emissions in mid-latitude regions, but may decrease emissions by 12% in low-latitude regions under current climatic conditions (Xiong et al. 2026; Lee et al. 2023; Yu et al. 2022).

Heavy rainfall and flooding

Intense precipitation and resultant flooding significantly impact soil hydrology and redox processes, prolonging anaerobic conditions and markedly enhancing CH_4 production (Das et al. 2025; Wang and Hu 2025; Zhang et al. 2021). When WFPS exceeds 80–90%, oxygen transport is significantly restricted, and soil Eh typically declines to −150 to −250 mV, favoring methanogenic archaea over other microbial respiratory pathways. Daily methane emissions in continuously flooded lowland rice fields typically range from 150 to 350 mg CH_4 m^{-2} day^{-1}, compared to 30–80 mg CH_4 m^{-2} day^{-1} in intermittently drained systems (Qian et al. 2022). In AWD systems, methane concentrations can increase severalfold within a few days following substantial rainfall, rising from approximately 60–90 mg CH_4 m^{-2} day^{-1} to 140–220 mg CH_4 m^{-2} day^{-1} (Zhang 2025).

Water table fluctuations play a critical role in methane variability. Analysis of over 30,000 daily water-table observations from six wetland types identified a robust nonlinear correlation between water-table position and CH_4 flux dynamics (Cui et al. 2024). As the water table ascends to within 0 to +5 cm of the soil surface, methanogenic bacteria exhibit increased activity, with methane fluxes in rice paddies potentially surpassing 150–300 mg CH_4 m^{-2} day^{-1}. When the water table descends to depths of −10 to −20 cm, soils may act as net CH_4 sinks with uptake rates of −1 to −5 mg CH_4 m^{-2} day^{-1} (Su et al. 2024). FLUXNET-CH_4 data indicate that intense rainfall can rapidly elevate the water table, transforming soils from oxic to anoxic conditions within 1–3 days, resulting in methane emissions increasing 30–70 times.

Soil physical properties, particularly texture, significantly influence gas diffusivity and anaerobic microsite formation. When WFPS exceeds 60–70%, gas diffusivity may decrease to below 10% of its value under fully aerated conditions, significantly impeding oxygen movement (Niu et al. 2024; Burke et al. 2019). Clay-rich soils can retain high WFPS for 3–5 days following 50–80 mm precipitation, compared to sandy soils, creating persistent anoxic microsites that inhibit methane degradation (Vallotton et al. 2025). Flooding elevating WFPS beyond 70% can decrease Eh to below −150 mV within 24–48 hours, facilitating rapid growth of methanogenic archaea (Sulman et al. 2022). Conversely, drainage can elevate Eh to exceed +200 mV within 12–36 hours, enabling aerobic methanotrophic bacteria to consume accumulated methane at rates of approximately 20–60 mg CH_4 m^{-2} day^{-1} (Das et al. 2025; Wang et al. 2025).

In irrigated rice systems, plant aerenchyma establishes low-resistance pathways facilitating methane transfer from anaerobic soils to the atmosphere, increasing total methane emissions by 2–5 times relative to diffusion under perpetual inundation (Villa et al. 2020; Jeffrey et al. 2019). Spatial variability is substantial: low-lying depressions frequently maintaining WFPS above 70% for over 72 hours emerge as methane emission hotspots, discharging 3–8 times more methane than adjacent upland areas (Yang et al. 2025). Flux studies frequently exhibit coefficients of variation of 60–100%, indicating significant disparities between saturated microtopographic depressions (10–120 mg CH_4 m^{-2} day^{-1}) and well-aerated upland regions (<5 mg CH_4 m^{-2} day^{-1}) (Nisbet et al. 2025).

Quantitative Role of the pmoA Gene in Methanotrophic Activity

Particulate methane monooxygenase (pMMO) accelerates the rate-limiting phase in aerobic methane oxidation; the pmoA gene encodes the alpha subunit of this enzyme, initiating conversion of CH_4 to methanol (Sabrekov et al. 2020). The gene is present in various methanotrophic groups, including Alphaproteobacteria (Type II), Gammaproteobacteria (Type I), and members of the phylum Verrucomicrobia (Tentori et al. 2020; Li et al. 2020). The quantity of pmoA gene copies in surface paddy soils typically ranges from 10^5 to 10^7 copies g^{-1} dry soil, with peak concentrations at oxic–anoxic interfaces (Chu et al. 2020; Sun et al. 2017; Bhardwaj et al. 2020). Soils rich in pmoA can oxidize methane at rates of 0.12–2 µmol CH_4 m^{-2} h^{-1}, compared to 0.01–0.05 µmol CH_4 m^{-2} h^{-1} in soils with fewer gene copies (Knief et al. 2015; Su et al. 2024). The abundance of Type I methanotroph pmoA copies can increase by approximately 240–380% following flooding, indicating enhanced microbial growth in favorable methane and oxygen gradients. Experimental investigations utilizing pure cultures demonstrate a significant correlation between pmoA transcription levels and methane oxidation activity, with rates per cell ranging from 0.005 to 3.8 µmol CH_4 $cell^{-1}$ (Tentori and Richardson 2020). Recent advances in metagenomics, quantitative PCR (qPCR), and transcriptomics have significantly facilitated the correlation between pmoA gene abundance and ecosystem methane oxidation capacity (Kharitonov et al. 2021).

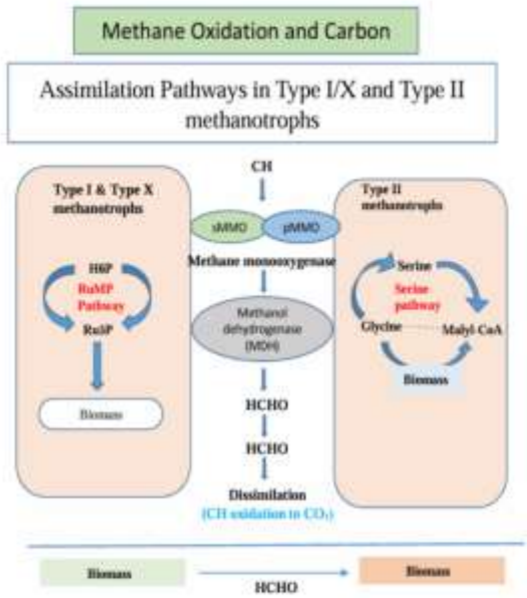

Fig. 4. Methane oxidation and carbon assimilation pathways in methanotrophic bacteria.

Molecular Applications of pmoA in Soil Methane Dynamics

Quantitative PCR (qPCR) amplification of the pmoA gene is a prevalent molecular technique for determining the abundance of aerobic methanotrophs in soil. Research indicates that pmoA is more prevalent in conditions enhancing soil aeration, such as during temporary drainage of rice fields or afforestation, conditions that typically indicate increased methane oxidation rates and decreased net methane emissions (Sabrekov et al. 2020; Shinjo et al. 2023). Conversely, prolonged soil saturation can diminish pmoA levels and impede the capacity of soils to function as methane sinks (Xu et al. 2024).

Amplicon sequencing of the pmoA gene provides substantial insights into the ecological diversity and functional specialization of methanotrophic communities. Type I methanotrophs are frequently located in environments rich in methane, such as inundated agricultural soils, exhibiting rapid growth in elevated methane concentrations (Knief et al. 2015). Type II methanotrophs, including USCα and USCγ clusters, are predominantly located in well-drained soils with low atmospheric methane concentrations and can oxidize atmospheric methane, enhancing the capacity of highland soils to function as methane sinks (Kharitonov et al. 2021). Alterations in community structure in response to soil moisture fluctuations, nutrient availability, and temperature stress significantly influence net methane oxidation rates (Silva et al. 2022; Meena et al. 2023).

Table 1. Relationship between mcrA/pmoA ratio and seasonal soil methane flux under different management systems

Soil System/Management Practice	mcrA/pmoA Ratio	Seasonal Methane Flux (mg CH_4 m^{-2} $season^{-1}$)	Interpretation	Reference
Continuous Flooded Paddy (CF)	2.0–2.5	300–400	Methanogenesis dominates: Strong source	Xiao et al. 2015; Hou et al. 2025
Alternate Wetting and Drying (AWD)	1.2–1.6	180–260	Reduced production; enhanced oxidation	Kumar and Rajitha 2019; Alauddin et al. 2020
Tree-based/Agroforestry Soil	0.8–1.0	80–150	Shift toward CH_4 sink strength	Li et al. 2025
Well-drained Upland Agricultural Soil	0.4–0.8	-20 to 60 (net uptake possible)	Oxidation dominates; net CH_4 sink	Cheng et al. 2021

Linkages Between pmoA, mcrA, and Methane Flux

The net methane flux in soils is determined by the balance between methane production (methanogenesis) and methane oxidation (methanotrophy). The mcrA gene, encoding the enzyme methyl coenzyme-M reductase, is utilized for identification of methanogenic archaea; the pmoA gene is utilized for methanotrophic bacteria (Kong et al. 2019). The mcrA/pmoA ratio indicates source–sink dynamics of methane; elevated ratios indicate increased methane production, while diminished ratios suggest predominant methane oxidation (Ouyang et al. 2024; Wang et al. 2023). Research in rice paddies employing AWD irrigation revealed that a 1.5-fold reduction in the mcrA/pmoA ratio corresponded to an estimated 30% drop in seasonal methane emissions, whereas under continuous flooding the ratio typically ranges from 2.0–2.5 (Rana et al. 2023; Xiao et al. 2015; Hou et al. 2025).

CONCLUSION

The quantity of methane emitted by croplands is contingent upon the equilibrium between anaerobic methane production (methanogenesis) and aerobic methane consumption (methanotrophy), both of which are highly susceptible to environmental changes occurring during extreme weather events. Droughts and heatwaves typically inhibit methane production by increasing soil aeration and altering redox potential, restricting the activity of anaerobic microorganisms. Intense precipitation and flooding render the soil highly anaerobic, promoting methanogenesis and frequently resulting in transient increases in methane emissions. The alteration of methane dynamics in response to extreme weather events is significantly influenced by cropland type, soil texture, drainage methods, land management practices, climatic region, and the timing and duration of weather events. The

The pmoA gene serves as an effective molecular marker for methanotrophic activity, and the mcrA/pmoA ratio provides a reliable proxy for methane source–sink balance. Future research should prioritize long-term, multi-site observations, the incorporation of microbial functional gene dynamics into process-based models, and more precise characterization of compound climatic extremes to improve predictions of methane emissions from agricultural ecosystems and to develop climate-resilient agriculture strategies in a rapidly changing climate.

Authorship Contribution Statement

S.Kokilavani,R.Vennila: Conceptualization, data curation, writing–original draft.
T.Kalaiselvi , Periyar Ramasamy, V.Karunakaran: Review and editing, supervision.

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