Mitigation of Methanogenesis in Ruminants Using Wheatgrass Compounds as Methyl Coenzyme M Reductase Inhibitors: An *In Silico* Study

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Ruminants are significant contributors to methane (CH₄) emissions due to methanogenesis by their gut microbiomes. The enzyme methyl coenzyme M reductase (MCR) is crucial for this process in rumen archaea. Targeting MCR via computational tools has emerged as a novel approach to reduce CH₄ emissions in ruminants by inhibiting methanogenesis. This study focused on evaluating wheatgrass (Thinopyrum intermedium) compounds as potential MCR inhibitors using in silico methods. Initially, 21 wheatgrass compounds were selected, and their drug-likeness traits were assessed using Lipinski's rule of five. Five compounds, namely 2,4,6-trimethyl-1,3phenylenediamine, Caryophyllene oxide, Caryophyllene, tetramethylene-.alpha.-(aminomethylene) glutaconic anhydride, and nhexadecanoic acid met all criteria. These compounds were further analysed for absorption, distribution, metabolism, and excretion (ADME) properties using the Swiss ADME tool, confirming their drug-likeness traits with no Lipinski's violation. Molecular docking analysis was performed using the CB-Dock2 tool to assess binding interactions with MCR. The compounds showed binding affinities in the following order: N,Ntetramethylene-.alpha.-(aminomethylene) glutaconic anhydride (-7.3 kcal/mol) > Caryophyllene (-6.8 kcal/mol) > Caryophyllene oxide (-6.7 kcal/mol) > n-hexadecanoic acid (-6.3 kcal/mol) > 2,4,6-trimethyl-1,3phenylenediamine (-6.0 kcal/mol). These findings suggest that the selected wheatgrass compounds have potential as anti-methanogenic agents, positioning them as promising MCR inhibitors for mitigating CH₄ emissions in ruminants.

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INTRODUCTION

There is no doubt that ruminants are crucial for human life as they convert indigestible plant biomass into digestible products like milk and meat (Kamra *et al.* 2012). With rising global demand for these products due to population growth and improved lifestyles (Lan and Yang 2019), the number of domesticated ruminants has significantly

increased. However, this surge raises concerns among ecologists and veterinarians about the associated greenhouse gas emissions, especially methane (CH₄) production. As a matter of fact, the emission of CH₄ from ruminants is directly proportional to the ruminants' population (Islam and Lee 2019). Methane is a potent greenhouse gas, revealing a 25 times higher global warming effect than that of carbon dioxide (CO₂), and ruminants contribute to 16% of global greenhouse gas emissions, accounting for 33% of anthropogenic CH₄ emission (Lan and Yang 2019).

The rumen, an anaerobic fermenter, hosts a diverse microbial community, including bacteria, protozoa, fungi, and archaea (Islam and Lee 2019). Protozoa can constitute up to 50% of the rumen's microbial biomass (Newbold *et al.* 2015), while fungi typically make up around 8%, potentially reaching 20% in sheep (Orpin 1981; Rezaeian *et al.* 2004). Archaea account for a smaller fraction, about 0.3 to 4% (Janssen and Kirs 2008), with bacteria comprising the majority of the microbial biomass (Tapio *et al.* 2017). This microbiome is crucial for fermenting carbohydrates-based feed, producing volatile fatty acids (acetic acid, propionic acid, butyric acids, *etc.*), CO₂, and hydrogen (H₂), which are essential for the ruminant's energy metabolism (Lan and Yang 2019).

Methanogenesis is the process by which CH₄ is produced in the rumen, primarily through the reduction of CO₂ by H₂, facilitated by methanogenic archaea. This process is crucial for clearing H₂ from fermentation (Islam and Lee 2019). Methanogenesis occurs *via* two main pathways: the hydrogenotrophic and methylotrophic pathways (Fig. 1). In the hydrogenotrophic pathway, H₂ and CO₂ are converted into CH₄ by rumen microorganisms, such as bacteria, protozoa, and fungi (Martin *et al.* 2010). Formate, which can be utilized by most ruminal archaea similarly to H₂ and CO₂, is also included in this category (Janssen 2010). The methylotrophic pathway, on the other hand, involves the conversion of methyl groups from substrates like methylamines and methanol into CH₄ (Poulsen *et al.* 2013).

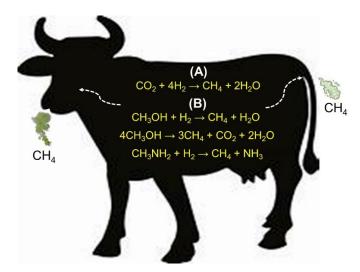


Fig. 1. Methane production from ruminants through (A) hydrogenotrophic pathway and (B) methylotrophic pathway

A variety of methanogens, including species, such as *Methanobacterium* spp., *Methanobrevibacter* spp., and *Methanosarcina* spp., are involved in the final stage of carbohydrate degradation in the rumen, where they convert H₂ and other compounds like formate, CO₂, or methyl donors into CH₄ (Poulsen *et al.* 2013). The final step in biological CH₄ synthesis is catalyzed by the enzyme methyl-coenzyme M reductase (MCR;

EC 2.8.4.1), a membrane-associated enzyme that is unique to methanogens and play a central role in CH₄ biogeochemistry (Khusro *et al.* 2022a). The enzyme is composed of three subunits: α (*mcrA*), β (*mcrB*), and γ (*mcrG*). The α -subunit, encoded by the *mcrA* gene, is highly conserved across all methanogens. This enzyme catalyzes the reduction of methyl coenzyme M (methyl-S-CoM) to CH₄, with coenzyme B serving as the electron donor and coenzyme F₄₃₀ (a nickel-containing tetrahydrocorphin) acting as the prosthetic group (Casañas *et al.* 2015).

In recent years, plethora of *in vitro* studies has been carried out to suppress CH₄ production from ruminants by adding disparate dietary supplements in the feed (Khusro *et al.* 2022b; Elghandour *et al.* 2023, 2024; Santillán *et al.* 2023). However, mitigating CH₄ emission by manipulating the biochemical pathway of methanogenesis process spotlights a new dimension in addressing anti-methanogenic trait in ruminants. Surprisingly, the mitigation of CH₄ emission from ruminants by targeting MCR receptor *via* computational tool is limited. In view of this, the present context was assessed to predict the anti-methanogenic attribute of wheatgrass (*Thinopyrum intermedium*)-associated compounds against MCR receptor in ruminants *via in silico* tools.

EXPERIMENTAL

Compounds of interest

A total of 21 compounds were identified from wheatgrass leaf extract based on previous studies (Durairaj *et al.* 2014; Shakya *et al.* 2014). The chemical structures of these compounds were obtained from PubChem (https://pubchem.ncbi.nlm.nih.gov/) in SDF format and were used for the subsequent analyses (Fig. 2).

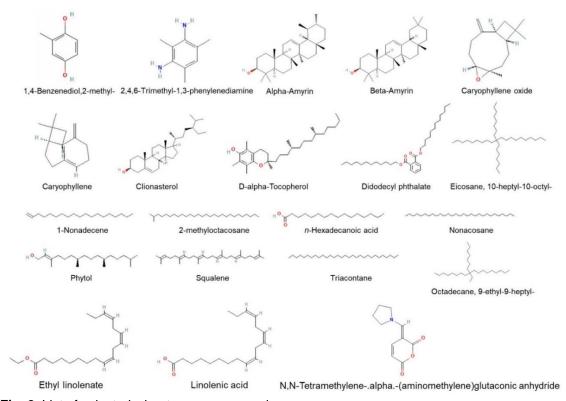


Fig. 2. List of selected wheatgrass compounds

Ligands Selection

Lipinski's rule of five

Lipinski's rule of five was applied to assess the drug-likeness of all the ligands (http://www.scfbio-iitd.res.in/software/drugdesign/lipinski.jsp). This rule evaluates the drug's viability by considering factors, such as molecular weight, logP, number of hydrogen bond acceptors, hydrogen bond donors, and molar refractivity (Lipinski 2004).

ADME properties analysis

Ligands that satisfied Lipinski's rule of five were further analysed for ADME (absorption, distribution, metabolism, and excretion) properties analysis using the Swiss ADME tool from the Swiss Institute of Bioinformatics (http://www.swissadme.ch/). Canonical SMILES for the ligands were retrieved from PubChem and evaluated for properties such as water solubility (Log mol/L), lipophilicity (Log $P_{o/w}$), gastrointestinal (GI) absorption, blood brain barrier (BBB) permeant, and P-gp substrate status. The Swiss ADME tool, based on a support vector machine algorithm, efficiently analyses datasets of known inhibitor/non-inhibitor and substrate/non-substrate (da Silva *et al.* 2006). These selected compounds were then advanced to molecular docking analysis.

In silico Molecular Docking

Target receptor

The structure of the MCR receptor was obtained from the RCSB PDB (Research Collaboratory for Structural Bioinformatics Protein Data Bank - IMRO) (http://www.rscb.org/pdb) and saved in PDB format. Prior to docking, non-essential components, such as water molecules and bound inhibitors, were removed from the receptor structure to ensure accurate docking results (Fig. 3).

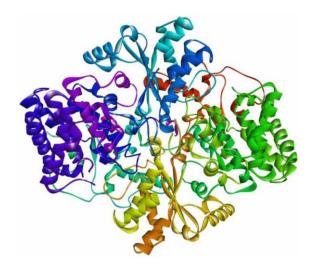


Fig. 3. 3D structure of MCR receptor

Molecular docking and visualization

The interaction between the selected protein and ligands was analyzed using the Cavity detection-guided Blind Docking2 (CB-Dock2) tool (Liu *et al.* 2020). This webbased tool automatically identifies protein cavities, calculates their centers and sizes, and focuses on the top five cavities by default. Blind docking was used to explore potential binding sites and ligand-binding modes by scanning the entire protein surface (Bultum *et*

al. 2022). CB-Dock2 customizes the docking box based on the query ligand and performs molecular docking using AutoDock Vina (Liu *et al.* 2020). The lowest vina score (kcal/mol), typically associated with the largest cavity, was selected as the optimal result for each ligand.

RESULTS AND DISCUSSION

Lipinski's Rule of Five for Compounds

The use of diversified additives in expensive feed formulations, along with the need to assess their CH₄ mitigation potential through *in vitro* or *in vivo* experiments, can be both time-consuming and costly. To address this, researchers are exploring alternative strategies for rapid screening of anti-methanogenic agents. Computational tools have emerged as an effective alternative for veterinarians, helping save time and resources. These short-term *in silico* approaches aim to identify suitable additives without the high cost or duration of traditional testing methods. Through developing cost-effective and efficient screening techniques, it becomes possible to find viable solutions for reducing CH₄ emissions in ruminants while maintaining productivity.

In this investigation, all selected wheatgrass compounds were initially evaluated for drug-likeness properties using Lipinski's rule of five. According to drug-likeness criteria, an ideal ligand should have a molecular mass under 500 Da, fewer than 5 hydrogen bond donors, fewer than 10 hydrogen bond acceptors, lipophilicity (log p) below 5, and molar refractivity between 40 and 130 (Abhishek Biswal *et al.* 2019). Table 1 presents key parameters, such as molecular weight, logP, hydrogen bond acceptors, hydrogen bond donors, and molar refractivity of each compound. Among the tested compounds, 2,4,6-trimethyl-1,3-phenylenediamine, Caryophyllene oxide, Caryophyllene, N,N-tetramethylene-.alpha.-(aminomethylene)glutaconic anhydride, and *n*-hexadecanoic acid met the essential criteria of Lipinski's rule of five, indicating potential for further analyses.

Table 1. Wheatgrass Compounds Analysed by Lipinski's Rule of Five

Phytocomponents	Molecular Formula / Mass (g/mol)	logP	Number of Hydrogen Bond Acceptors	Number of Hydrogen Bond Donors	Molar Refractivity
1,4-benzenediol, 2-methyl-	C ₇ H ₈ O ₂ / 124.14	0.754	2	2	32.35
1-nonadecene	C ₁₉ H ₃₈ / 266.5	5.962	0	0	102.25
2,4,6-trimethyl-1,3- phenylenediamine	C ₉ H ₁₄ N ₂ / 150.22	1.794	0	4	48.2
2-methyloctacosane	C ₂₉ H ₆₀ / 408.8	9.138	0	0	160.6
Alpha-Amyrin	C ₃₀ H ₅₀ O / 426.7	7.826	1	1	153.43
Beta-Amyrin	C ₃₀ H ₅₀ O / 426.7	7.837	1	1	153.38
Caryophyllene oxide	C ₁₅ H ₂₄ O / 220.35	3.486	1	0	74.46
Caryophyllene	C ₁₅ H ₂₄ / 204.35	3.961	0	0	75.11

Clionasterol	C ₂₉ H ₅₀ O / 414.7	7.745	1	1	150.19
D-alpha-tocopherol	C ₂₉ H ₅₀ O ₂ / 430.7	7.658	2	1	150.71
Didodecyl phthalate	C ₃₂ H ₅₄ O ₄ / 502.8	8.34	4	0	164.91
Eicosane, 10-heptyl-10- octyl-	C ₃₅ H ₇₂ / 492.9	- 0.053	6	5	77.14
Ethyl linolenate	C ₂₀ H ₃₄ O ₂ / 306.5	5.297	2	0	103.6
Linolenic acid	C ₁₈ H ₃₀ O ₂ / 278.4	4.325	2	1	92.19
N,N-tetramethylenealpha (aminomethylene)glutaconic anhydride	C ₁₀ H ₁₁ NO ₃ / 193.2	1.056	3	0	48.07
n-hexadecanoic acid	C ₁₆ H ₃₂ O ₂ / 256.4	4.325	2	1	88.26
Nonacosane	C ₂₉ H ₆₀ / 408.8	9.128	0	0	160.65
Octadecane, 9-ethyl-9- heptyl-	C ₂₇ H ₅₆ / 380.7	8.536	0	0	149.61
Triacontane	C ₃₀ H ₆₂ / 422.8	9.434	0	0	166.12
Phytol	C ₂₀ H ₄₀ O / 296.5	5.721	1	1	109.16
Squalene	C ₃₀ H ₅₀ / 410.7	8.21	0	0	152.12

ADME Properties Analysis

Table 2 presents the ADME properties of five selected wheatgrass compounds, highlighting their drug-likeness traits. All compounds demonstrated favourable traits, including water solubility, high GI absorption, lipophilicity, BBB permeability, P-gp substrate status, and no Lipinski's rule violations. All the phytocomponents were reported as water-soluble in nature. The lipophilicity values (log $P_{o/w}$) of 2,4,6-trimethyl-1,3-phenylenediamine, Caryophyllene oxide, Caryophyllene, N,N-tetramethylene-.alpha.-(aminomethylene)glutaconic anhydride, and n-hexadecanoic acid were 1.64, 3.15, 3.25, 1.65, and 3.85, respectively. All compounds displayed high GI absorption, while 2,4,6-trimethyl-1,3-phenylenediamine, Caryophyllene oxide, Caryophyllene, and n-hexadecanoic acid showed BBB permeability. Caryophyllene and N,N-tetramethylene-.alpha.-(aminomethylene)glutaconic anhydride did not permeate the BBB. None of the compounds were P-gp substrates, and there were no violations of Lipinski's rule of five.

Phytocomponents	Water	Lipophilicity	GI	BBB	P-gp	Lipinski's	Drug
	Solubility	$(\text{Log } P_{\text{o/w}})$	Absorption	Permeant	Substrate	Violation	Likeness
	(Log mol/L)						
2,4,6-trimethyl-1,3-	-2.21	1.64	High	Yes	No	0	Yes
phenylenediamine	(Soluble)						
Caryophyllene	-3.45	3.15	High	Yes	No	0	Yes
oxide	(Soluble)						
Caryophyllene	-3.87	3.25	Low	No	No	0	Yes
	(Soluble)						
N,N-	-1.6 (Very	1.65	High	No	No	0	Yes
tetramethylene-	Soluble)						
.alpha							
(aminomethylene)gl							
utaconic anhydride							
n-hexadecanoic	-5.02	3.85	High	Yes	No	0	Yes
acid	(Moderate						
	soluble)						

Table 2. ADME Properties of Five Selected Compounds

Molecular Docking and Visualization

Molecular docking of specific ligands with target receptors has proved to be an ideal, cost-efficient screening technique in diverse areas (Khusro *et al.* 2020a; Lavanya *et al.* 2023; Ramasubburayan *et al.* 2023; Mukundh *et al.* 2024). Methanogens rely on MCR for the methanogenesis process, making MCR a prime target for computational approaches aimed at reducing CH₄ emissions in animals. In the present study, the binding affinity energies or docking score, cavity volume, interacting amino acid residues, docking centre, and docking size between selected wheatgrass compounds and receptor are shown in Table 3.

Table 3. Docking Score, Cavity Volume, Interacting Amino Acid Residues, Docking Centre, and Docking Size Between Five Selected Compounds and MCR Receptor

S.	Compounds	Docking	Cavity	Interacting Amino Acid	Docking	Docking
No.		Score	Volume	Residues	Centre	Size
		(kcal/mol)	(Å3)		(x, y, z)	(x, y, z)
1.	2,4,6-trimethyl-	-6.0	6348	Chain A: GLN147 MET150	23, 37, -	35, 25,
	1,3-			MET233 ILE236 ALA243	52	35
	phenylenediami			GLY244 THR248		
	ne			Chain D: VAL328 GLY329		
				PHE330 THR331 GLN332		
				TYR333 ALA334 PHE396		
				GLY397 GLY398 SER399		
				PHE443 TYR444		
				Chain E: PHE361 HIS364		
				SER365 ILE366 TYR367		
				Chain F: LEU117 ARG120		
2.	Caryophyllene	-6.7	6348	Chain A: VAL146 GLN147	23, 37, -	35, 25,
	oxide			ARG225 MET233 ILE236	52	35
				ALA243 GLY244 THR248		
				ALA252 TYR253 LYS256		
				ALA258 VAL260		
				Chain D: ARG270 TYR333		
				PHE443 TYR444		

	T	ı	1		1	
				Chain E: PHE361 HIS364 SER365 ILE366 TYR367		
				GLY368 GLY369 HIS379		
				Chain F: LEU117 ARG120		
				SER154 VAL155		
3.	Caryophyllene	-6.8	6348	Chain A: GLN147 MET150	23, 37, -	35, 25,
				ARG225 ALA243 ALA252	52	35
				TYR253		
				Chain D: MET324 TYR333		
				PHE396 GLY397 GLY398		
				SER399 GLY442 PHE443 TYR444		
				Chain E: PHE362 GLY368		
				GLY369 VAL381		
				Chain F: LEU117 SER118		
				GLY119 ARG120 VAL155		
				HIS156 GLY157 HIS158		
				SER159		
4.	N,N-	-7.3	6348	Chain A: GLN147 MET150	23, 37, -	35, 25,
	tetramethylene-			ARG225 TYR253 LYS256	52	35
	.alpha			Chain D: LEU320 MET324		
	(aminomethyle			SER325 GLY329 PHE330		
	ne)glutaconic			THR331 GLN332 TYR333 PHE396 GLY397 GLY398		
	anhydride			SER399 GLY442 PHE443		
				ASN474 ALA479 MET480		
				ASN481 VAL482		
				Chain E: PHE361 PHE362		
				TYR367 GLY368 GLY369		
				ILE380 VAL381		
				Chain F: LEU117 SER118		
				GLY119 ARG120 VAL155		
5.	n-	-6.3	6348	HIS156 HIS158 Chain A: PRO268 ARG270	24, 38, -	34, 35,
J.	hexadecanoic	-0.3	0340	TRP319 LEU320 MET324	14	35
	acid			SER325 PHE330 TYR333		
				GLY397 GLY398 SER399		
				LEU441 GLY442 PHE443		
				TYR444 PRO473 ASN474		
				ALA479 MET480 ASN481		
				VAL482		
				Chain B: GLU186 PHE361 PHE362 HIS364 SER365		
				ILE366 TYR367 GLY368		
				GLY369 GLY370 ILE374		
				HIS379 ILE380 VAL381		
				Chain C: LEU117 SER118		
				GLY119 ARG120 VAL155		
				Chain D: GLN147 ARG225		
				MET229 MET233 ILE236		
				ALA243 GLY244 TYR253		
				LYS256		

The compound 2,4,6-trimethyl-1,3-phenylenediamine, Caryophyllene oxide, Caryophyllene, N,N-tetramethylene-.alpha.-(aminomethylene)glutaconic anhydride, and *n*-hexadecanoic acid predicted binding energy score of -6.0, -6.7, -6.8, -7.3, and -6.3

kcal/mol, respectively. Figure 4 shows the 3D interaction views between compounds and MCR receptor. This is the first *in silico* investigation to predict the CH₄-mitigating potential of wheatgrass-derived bioactive compounds by targeting MCR as the receptor.

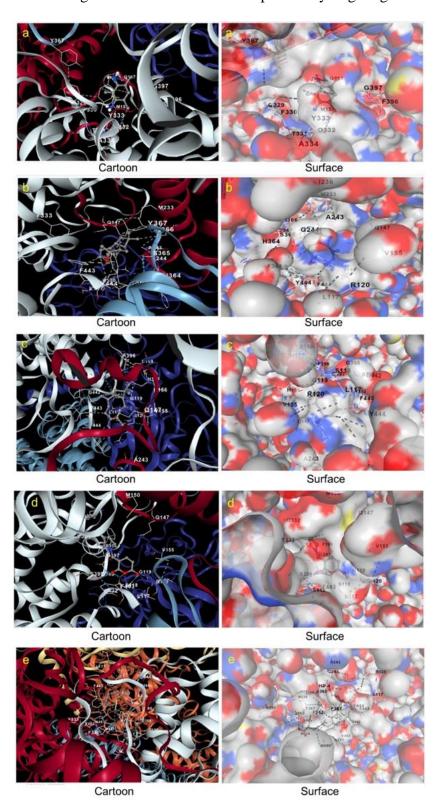


Fig. 4. Molecular docking visualization of: **(a)** 2,4,6-trimethyl-1,3-phenylenediamine, **(b)** Caryophyllene oxide, **(c)** Caryophyllene, **(d)** N,N-tetramethylene-.alpha.-(aminomethylene)

glutaconic anhydride, and (e) n-hexadecanoic acid with MCR receptor

Previous in silico studies highlighted the anti-methanogenic potential of varied plant metabolites by targeting MCR. For instance, Arokiyaraj et al. (2019) identified 9,10anthracenedione, 1,8-dihydroxy-3-methyl, phthalic acid isobutyl octadecyl ester, and diisooctyl phthalate from *Rheum* sp. as promising anti-methanogenic agents in ruminants through molecular modeling. Similarly, Dinakarkumar et al. (2021) analyzed 168 compounds from 11 plants, targeting MCR to mitigate CH₄ emissions in ruminants. The study identified rosmarinic acid, biotin, α-cadinol, and 2,4,7,9-tetramethyl-5decyn4,7diol as the most effective MCR inhibitors. Khusro et al. (2020b) further demonstrated the pivotal role of compounds like 3,5-bis(1,1-dimethylethyl)-phenol, kaempferol, moringyne, niazimisin, and tetradecanoic acid from Moringa oleifera in reducing CH₄ emissions in horses by showing strong binding interactions with MCR using Hex 8.0.0 software. Moreover, bioactive compounds, such as acacetin, matairesinol, methyl tetradecanoate, cis-6-nonenal, syringic acids, limonene, trans-2,4-decadienal, 3-isopropyl-6methylenecyclohex-1-ene, and 2,5-octanedione, from safflower oil also exhibited strong interaction with MCR, indicating their potential as anti-methanogenic agents in the equine industry (Khusro et al. 2022a).

Methanogenesis occurs in natural anaerobic environment and within the digestive tracts of animals, particularly ruminants (Alvarado *et al.* 2014). During this process, methanogens convert varied substrates into CH₄ to obtain energy for their growth and metabolism. Annually, approximately 600 million metric tons of CH₄ are released into the ecosystem through methanogenesis (Khusro *et al.* 2022a). The global warming potential of CH₄ is about 25 times greater than that of CO₂, making CH₄ production a significant environmental threat (Lan and Yang 2019). In agriculture, CH₄ emission from enteric fermentation in ruminants are the largest single source of greenhouse gases and one of the most significant anthropogenic contributors (Palangi and Lackner 2022). Given its detrimental impact, reducing CH₄ emissions from ruminants has become a key focus for researchers worldwide, driven by the urgent need to mitigate the release of this potent greenhouse gas (Khusro *et al.* 2022a). Various strategies, such as altering feed consumption and using dietary additives, are being explored to curb CH₄ production, presenting a promising area of study for environmental conservation and climate change mitigation efforts (Khusro *et al.* 2022b).

In recent years, various *in vitro* strategies have been employed to reduce CH₄ emissions from livestock, with dietary manipulation emerging as one of the most effective approaches. As global demand for meat, milk and other ruminant-derived products continue to rise, incorporating feed additives presents a promising solution to mitigate CH₄ emissions (Khusro *et al.* 2022b). Additives, such as plant extracts, probiotics, plant metabolites, exogenous enzymes, and organic acids, can alter the gut microflora of ruminants, thereby influencing fermentation kinetics and reducing CH₄ emissions (Elghandour *et al.* 2019). Additionally, these supplements enhance feed quality and adjust the dietary proportions, ultimately affecting gut microbial metabolism and further altering fermentation processes (Haque 2018).

Previous research demonstrated that wheatgrass can enhance the growth performance and flesh quality of common carp (Barbacariu *et al.* 2021; Burducea *et al.* 2022), suggesting its potential as a feed additive for other animals, particularly ruminants. The current findings open new avenues for exploring wheatgrass as an additive to reduce CH₄ emissions in livestock.

CONCLUSIONS

- 1. In summary, among the 21 selected compounds of wheatgrass, five compounds met Lipinski's rule of five criteria.
- 2. *In silico* analysis revealed strong binding potential of these compounds with the MCR receptor, with N,N-tetramethylene-.alpha.-(aminomethylene)glutaconic anhydride showing the highest docking score of -7.3 kcal/mol using CB-Dock2 tool. The other compounds had lower binding affinities.
- 3. This study suggested that 2,4,6-trimethyl-1,3-phenylenediamine, Caryophyllene oxide, Caryophyllene, N,N-tetramethylene-.alpha.-(aminomethylene)glutaconic anhydride, and *n*-hexadecanoic acid could be promising anti-methanogenic agents in ruminants.

ABBREVIATIONS

MCR: Methyl coenzyme M reductase

ADME: Absorption, Distribution, Metabolism, and Excretion

PDB: Protein Data Bank

CB-Dock2: Cavity detection-guided Blind Docking2

CH₄: Methane

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