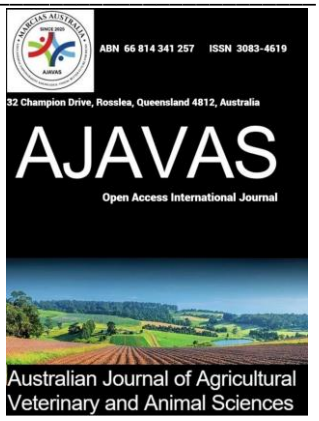

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Review

Microalgal supplements and SNP molecular markers for enhancing long chain omega-3 content and meat quality in beef cattle: A critical narrative review

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ABSTRACT: *Microalgae provide preformed long chain omega-3 polyunsaturated fatty acids (LC n-3 PUFA), particularly docosahexaenoic acid (DHA), and eicosapentaenoic acid (EPA). Their inclusion in cattle diets may increase the nutritional value of beef, but responses vary according to microalgal species, fatty acid composition, processing method, dietary inclusion level, feeding duration, basal diet and animal characteristics. Ruminal lipolysis and biohydrogenation substantially limit the transfer of dietary unsaturated fatty acids into muscle, while excessive lipid supplementation may reduce feed intake or compromise ruminal function. Although beef studies generally demonstrate increased muscle EPA, DHA or total LC n-3 PUFA following microalgal supplementation, the magnitude of deposition is inconsistent and may not always be sufficient to support nutrition content claims. Enrichment may also increase susceptibility to lipid oxidation, colour deterioration or undesirable flavour, although these effects depend on antioxidant protection, postmortem ageing, packaging, retail display and product format. Genetic variation contributes to intramuscular fat, fat melting point and fatty acid composition. Associations involving FASN, SCD, FABP4, FADS2, FADS3 and THRSP genes provide a biological basis for genetic improvement, but candidate gene effects can be population specific and should increasingly be complemented by genome wide prediction. Direct evidence that genotype modifies the response to microalgal supplementation remains scarce. Integrating microalgal nutrition, rumen protection technologies, repeated phenotyping, genomics, metabolomics and microbiome analysis therefore appears promising rather than established. Commercial translation will require adequately powered multibreed studies, standardised reporting of fatty acids in edible portions, comprehensive meat quality assessment, validated genomic predictions and evidence of economic return across feedlot and supply chain settings.*

Keywords: Functional beef; genomic prediction; nutrigenomics; precision feeding; ruminal biohydrogenation; intramuscular lipid; microalgal omega-3; meat quality

Highlights

- Microalgae can increase beef LC n-3 PUFA, but transfer efficiency and productive responses vary substantially.
- Ruminal biohydrogenation, dose, processing, basal diet and animal characteristics influence tissue deposition.
- Nutritional enrichment must be evaluated against oxidation, sensory quality, regulatory thresholds and cost.
- Candidate genes account for variation in lipid traits and polygenic improvement is by genome-wide prediction.
- Genotype x microalgae interactions remain an important but largely unvalidated research opportunity.

1.0 Introduction

Beef quality has traditionally been evaluated using carcass yield, marbling, tenderness, juiciness, flavour, colour and consistency (Kongsro et al., 2026). These attributes remain commercially important because nuances between different management systems may support differentiated marketing to promote quality or health related attributes specific to a target market (Weldy et al., 2026). However, consumer interest has expanded to include the nutritional composition and environmental sustainability of beef production (da Silva et al., 2026). From post-harvest to retail display, beef consumers increasingly encounter meat products differentiated by sustainable production system (Mukta et al., 2026), environmental provenance, animal welfare, nutrient composition, and value addition (Li et al., 2026). Therefore, beef quality is no longer judged solely by conventional carcass and sensory attributes such as dressing percentage, tenderness, juiciness, colour, and flavour alone (Motoyama et al., 2026). Consequently, improving healthy beef fatty acid composition without impairing eating quality or production efficiency has become an important research objective (Malau-Aduli et al., 2026).

Long chain omega-3 polyunsaturated fatty acids (LC n-3 PUFA) include eicosapentanoic acid (EPA), docosapentaenoic acid (DPA) and docosahexaenoic acid (DHA), which all contribute to membrane structure, cell signalling and regulation of inflammatory and cardiovascular processes (Cloward et al., 2026). DHA is also important in neural and retinal tissues for protection against diseases involving retinal oxidative stress and age related macular degeneration (Foshe et al., 2026). Whilst seafood remains the principal dietary source of EPA and DHA (Sprague et al., 2026), intake is below recommended levels in many populations (Sun et al., 2025). Terrestrial animal products may therefore provide complementary sources, particularly for consumers who eat little seafood, hence the increasing interest in identifying plant-livestock based hybrid strategies that can enhance the LC n-3 PUFA content of meat and thereby improve its functional nutritional value (Théron et al., 2026). Beef contains EPA, DPA and DHA, but their concentrations are usually modest and vary with diet, production system, breed, age, sex, adiposity and muscle type (Nogoy et al., 2022). Thus, enhancing the LC n-3 PUFA content of beef has emerged as a promising strategy for improving the health profile and marketability of beef products (Ponnampalam et al., 2024). The most relevant LC n-3 PUFA in beef are EPA, DPA, and DHA, but their concentrations are typically modest and strongly influenced by diet, rumen metabolism, genotype, and finishing system (Malau-Aduli et al., 2022). Contemporary reviews on enhancing productivity, muscle gain, and meat quality in livestock production systems utilising forages, supplements, and agricultural by-products, show that

beef fatty acid composition is not fixed (Ponnampalam et al., 2025). Rather, it is nutritionally plastic and biologically complex (Burnett et al., 2020), making it amenable to targeted manipulation through feeding and genetic strategies since the fatty acid profile of beef is biologically modifiable (Malau-Aduli et al., 2022). Pasture rich diets commonly increase α-linolenic acid and improve the n-6:n-3 ratio relative to high concentrate diets (Nogoy et al., 2022), although responses vary and may occur alongside differences in growth rate, carcass fatness and flavour (Daley et al., 2010). Oilseeds and plant oils can increase dietary α-linolenic acid, but their capacity to substantially increase tissue EPA and DHA is constrained by ruminal biohydrogenation and limited endogenous elongation and desaturation (Steiner-Zitzenbacher et al., 2026). Providing preformed LC n-3 PUFA through marine or microalgal ingredients is therefore a more direct strategy (Zhang et al., 2026a). Among the strategies currently under investigation, microalgal supplementation is especially promising.

Microalgae and related heterotrophic microorganisms are primary producers of marine LC n-3 PUFA (Zhu et al., 2024). DHA-rich products derived from *Schizochytrium* or *Aurantiochytrium* species have received particular attention in animal nutrition, whereas species such as *Nannochloropsis* may contain relatively more EPA (Zhao et al., 2026a). Microalgal biomass can also provide protein, pigments, carotenoids, vitamins and antioxidant compounds, although composition varies substantially with species, strain, cultivation conditions, harvesting and processing (Madeira et al., 2017; Mavrommatis et al., 2023). Microalgae may reduce reliance on wild fish resources, but their overall environmental advantage depends on cultivation inputs, energy use, drying, processing, transport and feeding efficiency and should not be assumed without life cycle evaluation (Boukrouh et al., 2026). Mechanistically, microalgae alter the rumen microbiome, suppress methanogenic archaea, and protect fatty acids from degradation, ultimately modulating host lipid metabolism to improve milk and meat quality (Zhao et al., 2026b). Microalgae may influence lipid metabolism through mechanisms extending beyond their fatty acid content, and reported mechanisms include changes in ruminal microbial communities, antioxidant status and the regulation of lipid metabolism pathways (Catrett et al., 2025). Differences in these responses may contribute to the variability observed among algal species and formulations. Beef cattle studies indicate that DHA-rich microalgae can increase muscle LC n-3 PUFA, but the evidence is heterogeneous, because some studies reported reduced dry matter intake or increased oxidative susceptibility (Phelps et al., 2016a; Phelps et al., 2016b; Carvalho et al., 2018), while others found neutral performance, improved antioxidant status or acceptable sensory outcomes (Rodriguez-Herrera et al., 2018; Phelps et al., 2020; Xu et al., 2021; Catrett et al., 2025). Responses are likely influenced by the microalgal product, actual EPA and DHA intake, inclusion level, physical form, diet composition, exposure period and animal phenotype (Radican et al., 2026). The term microalgae therefore describes a diverse group of feed ingredients rather than a uniform intervention. Whilst nutritional intervention also occurs against a genetically variable background, intramuscular fat (IMF), fatty acid synthesis, desaturation, transport and storage are polygenic traits (Malau-Aduli et al., 2026). Therefore, nutritional strategies alone may not fully explain variation in beef quality traits including IMF, marbling, fatty acid composition, and tenderness (Felizari et al., 2025), as genetic influence must also be considered (Souf et al. 2026; Jiang & Wang 2026) . This has led to growing interest in molecular markers, particularly single nucleotide polymorphisms (SNP), associated with lipid metabolism and meat quality biology (Malau-Aduli et al., 2026). Candidate genes such as *fatty acid synthase* (*FASN*), *stearoyl CoA desaturase* (*SCD*), and *fatty acid binding protein 4* (*FABP4*) have repeatedly been implicated in fat deposition and fatty acid composition in cattle (Gao et al., 2022), making them highly relevant to any strategy aiming to improve both the nutritional and eating quality of beef (Romero et al., 2024). Accordingly, the present topic sits at the intersection of animal nutrition, meat science, and molecular genetics. A comprehensive review of the literature is needed to clarify

how microalgal supplementation may influence LC n-3 PUFA deposition and meat quality in beef cattle, how breed and sex differences affect these responses, and how SNP-based selection may complement nutritional intervention. Associations have been reported between beef lipid traits and variants in FASN, SCD, FABP4, thyroid hormone responsive protein (THRSP) and fatty acid desaturases (FADS2 and FADS3) (Dawood et al., 2021; Mwangi et al., 2022a; Otto et al., 2022; Pećina & Ivanković, 2021; Romero et al., 2024). These findings raise the possibility that cattle differ genetically in their capacity to absorb, partition and retain dietary LC n-3 PUFA. Nevertheless, microalgal feeding and genomic association studies have mostly been conducted independently. Their convergence provides a rationale for testing genotype by nutrition interactions, but does not demonstrate that marker informed supplementation is currently effective. This is a major research gap that needs to be filled.

Previous reviews (Madeira et al., 2017; Toral et al., 2018; Demeda et al., 2020; Xu et al., 2021; Pećina & Ivanković, 2021; Gadzama et al., 2024; Ponnampalam et al., 2024) have generally considered microalgae as livestock feed ingredients, feed based modification of ruminant fatty acids, ruminal lipid metabolism or the genetic determinants of beef quality as separate topics. The distinctive contribution of this review is to integrate dietary LC n-3 PUFA supply, ruminal metabolism, muscle deposition, conventional meat quality outcomes, live animal phenotyping, candidate genes and genomic selection within one translational framework. Accordingly, this critical narrative review aims to evaluate: (a) the nutritional and regulatory relevance of LC n-3 PUFA enriched beef; (b) the biological barriers to enrichment; (c) evidence regarding microalgal supplementation, animal performance, fatty acid deposition and meat quality; (d) genomic determinants of beef lipid traits; and (e) the scientific and commercial requirements for integrating nutrition and genomics. Therefore, this literature review examines the scientific basis, current evidence, and unresolved issues surrounding the use of microalgae and SNP markers to enhance beef quality.

2. Review methodology

This manuscript was developed as a critical narrative review using a structured approach to literature identification and synthesis. Electronic searches were conducted on PubMed, Scopus, Web of Science and CAB Abstracts using combinations of the following concepts: *microalgae*, *algae meal*, *Schizochytrium*, *Aurantiochytrium*, *Nannochloropsis*, *docosahexaenoic acid*, *eicosapentaenoic acid*, *omega-3*, *fatty acid composition*, *ruminal biohydrogenation*, *meat quality*, *oxidative stability*, *sensory quality*, *single-nucleotide polymorphism*, *candidate gene*, *genome-wide association* and *genomic selection, beef cattle*, *steer*, *heifer*. Reference lists of relevant reviews and primary studies were screened and priority was given to peer-reviewed beef cattle intervention studies that report microalgal species or commercial product, supplementation level, feeding duration and at least one productive, metabolic, carcass, fatty acid or meat quality outcome. *Inclusion criteria*: Cattle genomic studies were included when fatty acid composition, IMF, fat melting point, carcass quality or relevant lipid metabolism pathways were evaluated. *Exclusion criteria*: Studies in other ruminants where beef specific evidence was unavailable were identified as indirect evidence, hence excluded. Articles from bulletins, newsletters, conference abstracts and other non-peer reviewed publication sources were also excluded. Since available studies differed substantially in animal population, microalgal composition, dose, dietary context, outcome definitions and analytical methods, a narrative synthesis was considered more appropriate than quantitative pooling. Evidence was compared according to microalgal product, dietary inclusion, actual LC n-3 PUFA intake, duration, breed, sex, basal diet, productive response, tissue deposition, oxidative stability, sensory quality and genomic pathway. The literature search was restricted to a 10-year window from 2016 to 2026 to capture the most recent decade of technological advancements in microalgal supplementation. A total of 175 studies were identified comprising 85 in PubMed, 40 in

Scopus, 25 in Web of Science and 25 in CAB Abstracts. After screening records for duplicates and assessment of full-text articles for eligibility, 168 were discarded, resulting in a final inclusion of 7 studies. Table 1 summarises the studies, animals and intervention, principal fatty acid findings, performance and meat quality findings and interpretation, while Table 2 summarises genes and genomic approaches relevant to beef fatty acid composition and meat quality including principal biological role, reported associated traits, potential applications and major limitations.

Table 1. Beef cattle studies evaluating microalgal supplementation, findings and interpretation

Study	Animals and intervention	Principal fatty acid findings	Performance and meat quality findings	Interpretation
Phelps et al. (2016a, 2016b)	Finishing heifers fed DHA-rich microalgae meal	Increased PUFA and LC n-3 PUFA in beef	Some adverse effects on flavour and colour stability	Demonstrated enrichment but identified sensory and retail display trade-offs
Carvalho et al. (2018)	Finishing steers fed DHA-rich microalgae	EPA and DHA percentages increased approximately fourfold and 6.25-fold, respectively	Reduced dry matter intake; greater oxidative susceptibility after prolonged ageing	Strong biological response, but productive and oxidative costs require consideration
Rodriguez-Herrera et al. (2018)	Charolais cross finishing heifers receiving 0, 15 or 30 g microalgae/kg diet for 95 days	Increased long-chain n-3 fatty acid content	Relatively small sensory effects	Suggests enrichment can be achieved without severe sensory impairment under some conditions
Demeda et al. (2020)	Beef steers supplemented with a commercial *Schizochytrium limacinum* product	Increased meat omega-3 content	Study specific productive and quality outcomes require comparison using full reported data	Supports incorporation but requires cautious interpretation because evidence is from a single experimental context
Phelps et al. (2020)	DHA-rich microalgae with antioxidant strategies	Increased unsaturated fatty acid exposure	Antioxidant treatment influenced colour and sensory outcomes	Demonstrates that enrichment and oxidative protection should be evaluated jointly
Xu et al. (2021)	Cattle receiving *Schizochytrium* at graded daily amounts of 0, 100 and 200 g microalgae/day	Increased selected n-3 fatty acids and altered volatile profiles	Changes in antioxidant status and physicochemical traits	Indicates metabolic and flavour related effects beyond simple deposition
Catrett et al. (2025)	Flaxseed and *Nannochloropsis oculata*-based supplementation evaluated in ground beef sources	Improved LC n-3 PUFA composition in patties	Effects assessed for colour stability and palatability	Highlights product format and blending as possible commercial pathways

Table 2. Genes and genomic approaches relevant to beef fatty acid composition and meat quality

Gene or approach	Principal biological role	Reported associated traits	Potential application	Major limitation
FASN	*De novo* fatty acid synthesis	IMF, marbling, saturated and monounsaturated fatty acids, selected LC n-3 traits	Biological marker and component of genomic prediction	Associations may be indirect or population-specific
SCD	Desaturation of saturated fatty acids	Fat melting point, MUFA:SFA balance, IMF and fatty acid composition	Selection for fat quality and composition	Effects depend on breed, allele frequency and lipid phenotype
FABP4	Intracellular fatty acid transport and adipocyte metabolism	Marbling, carcass fatness and selected fatty acids	Marker of lipid partitioning and adiposity	Limited transferability without external validation
THRSP	Regulation of lipogenesis	Marbling and fatty acid traits	Biological candidate in genomic models	Usually small individual effect
FADS2 and *FADS3*	PUFA desaturation pathways	Variation in PUFA composition	Mechanistic and genomic prediction candidates	Functional effects in cattle require further validation
SREBF1	Transcriptional control of lipogenic pathways	IMF and fatty acid composition	Network level marker	Pleiotropy and environmental sensitivity
LEP	Appetite, energy balance and adiposity	Feed intake, fatness and marbling	Multitrait selection	May affect production traits beyond fatty acid composition
Candidate gene selection	Selection using specific variants	Trait-specific associations	Mechanistic interpretation and targeted validation	Captures only a small component of polygenic variation
GWAS	Genome-wide detection of associated regions	Multiple fatty acids and carcass traits	Discovery of loci and pathways	Requires large samples and independent replication
Genomic selection	Genome-wide prediction of breeding value	Polygenic improvement across lipid and production traits	Most appropriate long-term breeding strategy	Requires large, relevant reference populations and affordable phenotyping

3. Nutritional and regulatory significance of long-chain omega-3 fatty acids in beef

LC n-3 PUFA are considered important components of a health promoting diet because of their physiological roles in cell membrane function, inflammatory regulation, cardiovascular health, and neural development (Sun et al., 2025). Although fish and marine foods remain the best known sources of EPA and DHA, there is increasing interest in terrestrial animal products as complementary dietary sources, especially for consumers who do not regularly consume seafood (Sprague et al., 2026). Red meat therefore, has the potential to contribute useful quantities of health enhancing fatty acids if its lipid composition can be strategically modified (Ponnampalam et al., 2024). The commercial relevance of LC n-3 PUFA enrichment is strengthened by food labelling frameworks. In Australia and New Zealand, Food Standards Australia New Zealand (FSANZ, 2005) regulates nutrition content claims relating to LC n-3 PUFA, including the conditions under which foods may be described as a "source" or "good source" of omega-3. Such standards mean that enrichment is not merely a scientific exercise in changing tissue biochemistry; it may also underpin product differentiation and consumer facing nutritional claims if tissue levels are sufficiently elevated (FSANZ, 2022). However, the nutritional value of enriched beef must be considered alongside its sensory and commercial attributes (Felizari et al., 2025). Any improvement in the LC n-3 PUFA profile must occur without unacceptable deterioration in colour stability, oxidation resistance, flavour, or tenderness (Phelps et al., 2020). This dual requirement has shaped recent research, which increasingly views fatty acid enhancement as part of a broader meat quality optimisation problem rather than as a single compositional target (Kongsro et al., 2026).

EPA, DPA and DHA are biologically active fatty acids, but their nutritional relevance in beef depends on the amount consumed rather than solely on their percentage of total fatty acids. Reporting an increase from a low baseline may demonstrate biological incorporation while still representing a small absolute contribution per serving. Consequently, studies should report individual EPA, DPA and DHA concentrations in mg/100 g edible meat, together with total LC n-3 PUFA, total lipid and the percentage of total identified fatty acids. DPA warrants explicit consideration. It is frequently present in ruminant meat at concentrations equal to or higher than EPA and DHA, yet some studies report only EPA and DHA. Excluding DPA can underestimate the LC n-3 PUFA contribution of beef and make comparisons across studies difficult. At the same time, total n-3 PUFA or the n-6:n-3 ratio should not be treated as substitutes for individual LC n-3 PUFA measurements. A favourable ratio can arise through lower n-6 PUFA without a nutritionally meaningful increase in EPA, DPA or DHA. Regulatory interpretation is jurisdiction specific. In Australia and New Zealand, nutrition content and health claims must satisfy the Australia New Zealand Food Standards Code. A statistically significant treatment difference does not itself establish eligibility for a "source" or "good source" claim. Product developers must evaluate nutrient concentration in the food as sold and consumed, serving size, compositional variability and all applicable labelling conditions. FSANZ distinguishes nutrition content claims from health claims and requires specified criteria to be met.

Nutritional enhancement must also be assessed in the context of the whole product. Increasing PUFA can increase the number of oxidation sensitive double bonds in muscle lipids. Lipid oxidation may contribute to rancid or warmed over flavours, while interactions between lipid derived radicals and myoglobin can accelerate discoloration. These responses depend on the amount and location of PUFA deposited, endogenous antioxidant capacity, dietary antioxidants, muscle type, postmortem ageing, oxygen exposure, packaging, retail display conditions and cooking (Burnett et al., 2020; Phelps et al., 2020). Nutritional value, therefore, cannot be separated from shelf life, sensory acceptance and product consistency. The practical significance of enrichment should be judged against at least four criteria:

1. Nutrient delivery: Does a customary portion contain a meaningful amount of EPA, DPA and DHA?
2. Regulatory eligibility: Does the final product meet the requirements for the intended claim?
3. Product quality: Are colour, oxidation, flavour, tenderness and shelf life acceptable?
4. Economic value: Does the achievable market premium exceed supplementation, processing, testing and segregation costs?

4. Ruminant lipid metabolism and strategies for improving postruminal long chain omega-3 delivery

A major obstacle in enriching beef with LC n-3 PUFA lie in the unique digestive physiology of ruminants. Dietary unsaturated fatty acids entering the rumen are subject to extensive microbial lipolysis and biohydrogenation, which convert a substantial proportion of polyunsaturated fatty acids into more saturated forms before absorption (Calder et al., 2026). This metabolic barrier limits the efficiency with which dietary LC n-3 PUFA are deposited in muscle and adipose tissue, making the manipulation of beef fatty acid composition more difficult in cattle than in monogastric species (Toral et al., 2018). Toral et al. (2018) also argued that attempts to improve the fatty acid composition of ruminant meat must address ruminal metabolism directly, either by increasing the amount of desirable fatty acids that escape biohydrogenation, modifying microbial pathways, or using feed ingredients whose structural properties alter the fate of lipids in the rumen. This challenge explains why feeding plant derived omega-3 precursors such as α-linolenic acid, often produces limited gains in tissue EPA and DHA (Chen et al., 2026). Conversion of shorter chain n-3 PUFA

into their longer chain forms is constrained in cattle, making direct dietary provision of EPA and DHA more attractive (Phelps et al., 2016a). Microalgae are particularly relevant in this context because they provide preformed LC n-3 PUFA and may possess cellular structures or associated compounds that influence how lipids are processed in the rumen (Boukrouh et al., 2026). This means that microalgal supplementation must be viewed as a biologically nuanced intervention rather than a simple additive strategy since response to supplementation remains strongly dependent on the specific algal species, inclusion level, and dietary context (Radican et al., 2026).

4.1 Ruminal lipolysis and biohydrogenation

A principal biological barrier to LC n-3 PUFA enrichment is the extensive metabolism of dietary lipids in the rumen. Esterified lipids are hydrolysed by microbial lipases, releasing free fatty acids, and unsaturated fatty acids are subsequently isomerised and hydrogenated by rumen microorganisms (Zhao et al., 2026). These processes reduce the flow of intact dietary PUFA to the small intestine and alter the fatty acid intermediates available for absorption (Toral et al., 2018). EPA and DHA can inhibit or alter some biohydrogenation pathways, but they are not completely protected from ruminal metabolism. High concentrations of unsaturated lipids may also inhibit fibre digesting microorganisms, reduce fibre digestion or modify fermentation (Souza et al., 2026). Thus, increasing dietary supply does not necessarily produce a proportional increase in muscle deposition as transfer efficiency may decline at higher inclusion levels because of ruminal losses, reduced intake, altered digestion or metabolic regulation (Singh et al., 2026). After intestinal absorption, fatty acids are incorporated into circulating lipoproteins and partitioned among tissues, and muscle concentration is affected by phospholipid content, neutral lipid deposition, IMF and fatty acid turnover (Kandasamy et al., 2026). Malau-Aduli et al. (2022) opined that lean muscle phospholipids contain a greater proportion of PUFA than triglycerides, but animals with more IMF may have greater total lipid and lower PUFA percentages because neutral lipids are enriched in saturated and monounsaturated fatty acids. Therefore, results expressed only as a percentage of total fatty acids may differ from those expressed as mg/100 g tissue.

4.2 Direct provision of preformed LC n-3 PUFA

da Silva et al. (2026) in their study on intensified tropical pasture based beef cattle production systems and their effects on carcass traits, meat quality and methane emissions in steers opined that oilseeds and forages can increase α-linolenic acid supply, but conversion to EPA and DHA is limited after ruminal losses and mammalian elongation and desaturation. Microalgae on the other hand, provide preformed EPA or DHA and can therefore bypass the need for conversion from shorter chain precursors (Madeira et al., 2017). They do not, however, automatically bypass the rumen, as their effectiveness depends on the accessibility of intracellular lipids and the degree to which the biomass or formulation protects fatty acids from microbial metabolism (Jiang &Wang, 2026).

4.3 Intact algal biomass and processing

Intact algal cells may provide partial physical protection, but the extent varies with cell wall composition and processing (Boukrouh et al., 2026). Drying, grinding, extrusion, oil extraction or cell disruption may improve digestibility while simultaneously exposing lipids to ruminal lipases. Conversely, highly resistant cell structures may protect lipids in the rumen but reduce intestinal availability (Mavrommatis et al., 2023). Processing should therefore be evaluated using both ruminal escape and total tract digestibility rather than assuming that greater protection is always beneficial.

4.4 Encapsulation and rumen protected lipid matrices

Microencapsulation, lipid coating and other rumen protected matrices aim to restrict lipid release in the rumen and permit digestion in the abomasum or small intestine (Malau-Aduli et al., 2020). These technologies may increase post ruminal EPA and DHA supply, but protection can be incomplete and highly dependent on ruminal pH, particle integrity and manufacturing consistency (Théron et al., 2026). Additional processing also raises cost and may limit large scale feedlot adoption. It is important to compare protected and unprotected lipid forms at equivalent intakes of EPA and DHA. Without such standardisation, improved deposition cannot be attributed confidently to the protection technology rather than to differences in nutrient supply (Toral et al., 2018).

4.5 Calcium salts and other protected fats

Calcium salts are widely used to reduce the ruminal effects of supplemental fatty acids (Malau-Aduli et al., 2020). Their effectiveness is influenced by fatty acid profile and ruminal pH, and highly unsaturated marine lipids may not be protected as consistently as long chain saturated fats (Lewis et al., 2025). Calcium salts can also affect palatability and mixing characteristics (Demartini et al., 2026). Although they remain commercially familiar, they should not be assumed to provide complete protection for EPA and DHA rich oils. Protein associated lipids (Wulandari et al., 2024), formaldehyde treated matrices (Kumar et al., 2026) and other chemically protected systems have also been investigated, and findings indicate that their use requires consideration of feed regulation, processing safety, consumer perception and cost (Bionaz et al., 2020).

4.6 Oilseeds, emulsification and feed processing

Advancements in oilseeds, emulsification, and feed processing for cattle have focussed heavily on optimising fat digestibility, avoiding rumen driven fat depression, and upcycling oilseed processing byproducts (Kadam et al., 2026; Burtnett et al., 2026;) Whole or processed oilseeds provide lipids within a plant matrix, may slow release in the rumen and are useful for increasing α-linolenic acid, but generally provide little preformed EPA or DHA (Rakita et al., 2023). Extrusion, micronisation, pelleting and emulsification can alter lipid release, microbial exposure and intestinal digestion, but the effect is product specific and should be established empirically (Chetia et al., 2026). Although processing changes the structural and chemical availability of proteins and lipids within cattle rations and these byproducts are excellent for loading cattle diets with essential fatty acids, mechanical extraction levels must be tightly controlled because varied residual oil content triggers opposing animal performance outcomes (Rakita et al., 2023). Manipulating the rumen microbiome provides an added biological advantage for balancing and sustaining productivity.

4.7 Manipulation of the rumen microbiome

Modifying biohydrogenating microbial communities through diet, plant secondary compounds, direct fed microorganisms, bacteriocins or other additives is biologically attractive as a means of balancing animal productivity with environmental sustainability (Sing et al., 2026). However, the rumen microbiome is functionally redundant and responsive to the whole diet, therefore, effects observed under controlled conditions may not persist across animals or production systems (Chen et al., 2026). Therefore, microbial manipulation should be considered within an emerging complementary approach focussed on reducing the impact of ruminant populations on environmental degredation and enhancement of human health rather than a reliable replacement for physical protection (Bueno de Mesquita et al., 2026). Singh et al. (2026) highlights the need to integrate multi-omics datasets, computational modelling, and precision livestock technologies to develop robust, scalable, and economically viable microbiome management strategies. A deeper understanding of host-microbiome interactions and microbial functional dynamics remains essential for

translating scientific advances into practical approaches that support sustainable livestock production, environmental stewardship, and overall global food security (Singh et al., 2026).

4.8 Comparative assessment

A comparative assessment is necessary because microalgae have the distinctive advantage of supplying preformed LC n-3 PUFA (Madeira et al., 2017), whereas many terrestrial strategies supply precursors (Jiang & Wang, 2026). The limitations to both microalgal and terrestrial supplementation strategies include costs, variable compositions, susceptibility to ruminal metabolism, potential palatability effects and supply constraints (Boukrouh et al., 2026). Encapsulation may improve transfer efficiency but increases processing costs (Carreno et al., 2026). Calcium salts are operationally familiar but may incompletely protect highly unsaturated fatty acids (Malau-Aduli et al., 2020). Microbiome manipulation may eventually improve biological efficiency but remains difficult to standardise (Petrosino et al., 2026). Therefore, the most promising strategy may involve moderate microalgal inclusion, effective but digestible rumen protection, appropriate antioxidant support and selection of cattle capable of efficiently depositing LC n-3 PUFA. This proposition requires direct comparative testing.

5. Microalgal species, composition and characteristics as a feed-based strategy for enriching beef

Microalgae have emerged as promising livestock feed ingredients because they combine nutritional functionality with sustainability potential (Mavrommatis et al., 2023). They may contain substantial concentrations of DHA and EPA, as well as proteins, vitamins, carotenoids, antioxidants, and other metabolites that can influence animal metabolism and product quality (Radican et al., 2026)). Zhu et al. (2024) described microalgae as an emerging class of feed additives for ruminants with relevance to productivity, product composition, environmental sustainability, and feed diversification. One of the chief advantages of microalgae over traditional terrestrial lipid supplements is that they can provide the specific LC n-3 PUFA of greatest nutritional interest. Pasture based or flaxseed based strategies may increase shorter chain n-3 PUFA, but direct enrichment of beef with EPA and DHA is generally more difficult to achieve unless marine derived or algal sources are used (Catrett et al., 2025). This makes microalgae highly attractive where the goal is to increase nutritionally valuable LC n-3 PUFA rather than simply improve the overall unsaturation of fat. However, the literature also indicates that microalgae are not a uniform category of feed ingredient, as different species have different lipid profiles, cell wall structures, digestibility characteristics, and antioxidant properties (Mavrommatis et al., 2023). There are also practical considerations relating to cost, availability, consistency of biomass composition, and palatability. Zhu et al. (2024) emphasised that these practical and biological factors currently constrain wider commercial adoption, despite the strong scientific rationale for microalgae in ruminant feeding. While microalgae offer a strong conceptual basis for LC n-3 PUFA enrichment, their effective use in beef production depends on optimisation of species, dose, formulation, and delivery system (Catrett et al., 2025).

Microalgal species used in animal feeding differ markedly in their lipid profiles and non-lipid components. Treating them as a single class obscures biologically important variation. The various microalgal species and products commonly available include:

5.1 DHA-rich Schizochytrium and Aurantiochytrium products

Heterotrophic thraustochytrid products marketed under *Schizochytrium* or *Aurantiochytrium* designations are generally rich in DHA and have dominated cattle studies (Rinttila et al., 2022; Hao et al., 2026; Zhang et al., 2026b; Poaty Ditengou et al., 2026). Their biomass may contain substantial lipid, with DHA constituting a large proportion of total

fatty acids, but EPA concentrations are frequently lower. Such products are well suited to experiments targeting DHA deposition but should not be described as equivalent sources of all LC n-3 PUFA (Rinttila et al., 2022). Study to study differences may reflect strain, culture substrate, total lipid, DHA concentration, carrier material and processing (Zhang et al., 2026b). Reporting only grams of product per animal or percentage of dietary dry matter is therefore insufficient. Investigators should report product proximate composition, total fatty acids, individual EPA, DPA and DHA concentrations, oxidation status and the actual daily intake of each target fatty acid (Hao et al., 2026).

5.2 EPA-rich Nannochloropsis

Nannochloropsis possesses a rigid, naturally protective cell wall structure (Vitor et al. 2021). This architectural trait allows its high EPA content (often bound as bioavailable phospholipids) to naturally bypass standard rumen degradation far more effectively than processed fish oils (Alves et al., 2018), enabling a higher deposition rate of omega-3 directly into bovine tissues and milk (Halim et al., 2022). *Nannochloropsis* species are recognised for relatively high EPA concentrations, although composition varies. Their robust cell walls may affect digestibility and lipid availability. However, beef specific evidence is more limited than for DHA-rich thraustochytrids. Results from *Schizochytrium* cannot be extrapolated directly to *Nannochloropsis*, particularly where the nutritional target is EPA rather than DHA. A recent study involving a *Nannochloropsis oculata* based product evaluated fatty acid composition, retail colour and palatability in ground beef (Catrett et al., 2025) and found that commercial translation may involve blending enriched lean and fat sources rather than marketing only intact steaks, illustrating a growing interest in product format applications.

5.3 Chlorella, Spirulina/Arthrospira and other biomass products

Chlorella and *Arthrospira* products may contribute protein, pigments, minerals and antioxidants (Sarmikasoglou et al., 2025; Gadzama et al., 2025; Malyugina, 2026; Zhao et al., 2026a; Radican et al., 2026) to ruminants, but are not necessarily concentrated sources of EPA or DHA (Sarmikasoglou et al., 2025). Their effects on performance or meat quality may arise through mechanisms other than direct LC n-3 PUFA delivery (Zhao et al., 2026b). Therefore, studies using these products should not be combined uncritically with DHA-rich microalgal studies.

5.4 Antioxidants and other bioactive compounds

Microalgal carotenoids, tocopherols and other antioxidant compounds may offset some pro-oxidative effects of PUFA enrichment (Zhao et al., 2026a). However, antioxidant capacity varies among species, batches and production systems (Mavrommatis et al., 2023). Improved systemic antioxidant biomarkers do not necessarily guarantee greater oxidative stability in post-mortem meat, because antioxidant deposition, muscle metabolism, iron availability and storage conditions also contribute (Čmiková et al., 2025). Livestock feeding trial data incorporating low concentrations (0.25% to 0.50%) of *Chlorella* and *Arthrospira* confirm the direct antioxidant power of microalgae species in beef processing and massive surges in DPPH and ABTS radical scavenging activities, thereby lowering lipid oxidation during storage (Čmiková et al., 2025). Zhao et al. (2026b) demonstrated that the concurrent deposition of *Chlorella* or *Spirulina* carotenoids shields fragile fatty acids from rancidity, while the high pigment concentrations maintain stable muscle pH levels over extended refrigeration, preventing the premature browning of fresh meat cuts (Ongaratto et al., 2024).

5.5 Product stability and quality control

A review of recent research progress on the effects of microalgae on lipid metabolism in ruminants by Zhao et al. (2026a) confirms that while microalgae modulate the gastrointestinal microbiota of ruminants and enhance lipid metabolism - a process associated with improved meat quality, highly unsaturated algal lipids are themselves vulnerable to oxidation during storage (Ongaratto et al., 2024). Feed grade products should therefore be characterised for peroxide value, secondary oxidation products, storage conditions and antioxidant protection for improving meat quality, safety and sustainability (Prates, 2025). Feeding an oxidised lipid source could influence intake, metabolism and product quality independently of its nominal DHA or EPA content. Feed quality metrics dictate that the baseline peroxide value for microalgae and blended oil matrices must be kept under 5 meq/kg to ensure feed viability (Rodrigues, 2025). Studies by Kazemi & Valizadeh (2026) reconfirm that peroxide value solely reflects early stage hydroperoxide formation because hydroperoxides are chemically unstable, Peroxide Value (PV) increases to a peak and then rapidly declines as the molecules break down. Consequently, Rodrigues (2025) in their study on feed and processing effects on meat quality and sensory evaluation warn that a low PV in stored cattle feed can mistakenly mask advanced rancidity. Kop et al. (2019) in their study of the effects of different storage temperatures and durations on PV of feed ingredients, demonstrated that storing polyunsaturated feed ingredients at 4°C drastically suppresses PV spikes and preserves long-term freshness, whereas ambient tropical storage (30°C+) triggers rancidity within 60 days.

5.6 Microalgal species selection for beef production

Studies and comprehensive literature reviews evaluating species selection parameters for beef and livestock systems include those of Wong et al. (2025), Li et al. (2025), McKinley & Ozbay (2026), and Zhao et al. (2026b). Li et al. (2025) investigated 10 distinct freshwater microalgae species (*Auxenochlorella protothecoides*, *Chlamydomonas pulvinata*, *Chlorella luteoviridis*, *Chlorella variabilis*, *Euglena mutabilis*, *Parachlorella kessleri*, *Stichococcus bacillaris*, *Tetradesmus acuminatus*, *Tetradesmus obliquus*, and *Tetraselmis gracilis*) selected explicitly for high unsaturated fatty acid content. While *in vitro* screenings demonstrated that selection criteria prioritising unsaturated fatty acid rich profiles actively inhibited gut methanogens, yielded methane reductions between 9.7% and 17.4% without hindering essential ruminal digestibility, no single species could currently be identified as universally superior for meat quality impact. However, Zhao et al. (2026b) stated that DHA-rich *Schizochytrium*/*Aurantiochytrium* products have the strongest direct beef evidence for increasing DHA and establishing a framework for species selection based on how microalgae interact with the gut-brain axis to modulate immune functions and carcass lipid profiles. Zhao et al. (2026b) also contrasts high protein species (*Spirulina*, *Chlorella*) with high fat alternatives (*Schizochytrium spp*.), noting that excessive fat strains can inadvertently lower dry matter intake. EPA-rich *Nannochloropsis* products may be attractive where EPA is the primary target, but more cattle studies are needed. Species selection should be based on:

- the target fatty acid;
- bioavailability and ruminal stability;
- consistency of composition;
- effects on intake and ruminal fermentation;
- antioxidant content;
- product cost;
- supply security; and
- the intended beef product and regulatory claim.

6. Effects of microalgal supplementation on feed intake, growth performance and animal metabolism

A critical question in the literature is whether microalgal supplementation can improve or at least maintain animal performance while altering muscle fatty acid composition. This is especially important in beef systems because any nutritional intervention that reduces intake, depresses growth, or compromises efficiency may not be economically sustainable. Carvalho et al. (2018) demonstrated that DHA-rich microalgal supplementation in steers not only altered fatty acid profiles in a favourable direction, but also reduced dry matter intake. The steers weighing an average of 438 kg were lot fed and supplemented with 100g of microalgae per steer daily and slaughtered at 621 kg with a clear demonstration that EPA and DHA percentages increased approximately fourfold and 6.25-fold, respectively. Furthermore, there was reduced dry matter intake and greater oxidative susceptibility after prolonged ageing. This finding is significant because it highlights a recurring tension in enrichment research: Improvements in meat composition may not always align with improvements in productive performance. Reduced intake may reflect palatability issues, altered rumen fermentation, or metabolic effects associated with high levels of unsaturated lipids (Carvalho et al., 2018). Microalgal supplementation may also influence systemic metabolic function. Carvalho et al. (2018) further assessed insulin sensitivity and carcass related outcomes, showing that microalgal feeding can interact with broader physiological pathways rather than merely changing muscle lipid composition. This is important because it suggests that animal response to supplementation should be evaluated through a more integrated metabolic lens, incorporating body weight gain, metabolic biomarkers, and possibly rumen fermentation characteristics. In broader terms, the emerging literature suggests that growth responses are likely to be dose dependent and context specific rather than universally beneficial or detrimental. This supports the importance of repeated measurement of liveweight, average daily gain, plasma metabolites, and ruminal indices when assessing the practical value of microalgal supplementation in young cattle.

A nutritional enrichment strategy is unlikely to be adopted if it consistently reduces intake, growth or feed efficiency. Productive outcomes should therefore be regarded as primary endpoints rather than secondary observations. Phelps et al. (2016a, 2016b) studied microalgae meal in finishing heifers and showed that dietary algae could modify fatty acid composition, but adverse flavour and colour responses were observed in some circumstances. These studies reinforce the need to evaluate productive and product quality outcomes together. An intervention that increases tissue PUFA but reduces eating quality may have limited commercial value unless the effect can be controlled through dose, antioxidant supplementation, ageing or product formulation. Xu et al. (2021) compared control cattle with animals receiving *Schizochytrium* supplementation and reported changes in antioxidant status, fatty acid composition and volatile compounds. The study indicates that microalgae can affect metabolic and flavour related pathways in addition to serving as a fatty acid source. However, responses from one breed, diet and production context should not be treated as universal. Across the limited beef literature, productive effects range from negative to neutral. Evidence for consistent improvement in average daily gain or feed efficiency is insufficient. Disagreement among studies can plausibly be explained by:

- different lipid and DHA concentrations of the products;
- low versus high dietary inclusion;
- adaptation period;
- forage to concentrate ratio;
- stage of growth and finishing;
- breed and sex;

- duration of feeding;
- palatability and product freshness; and
- replacement of other energy or protein ingredients.

Microalgal supplementation may also affect insulin sensitivity, circulating metabolites and ruminal fermentation. Such effects could influence lipid partitioning independently of total dietary fatty acid supply. Future experiments should measure dry matter intake, average daily gain, feed conversion, body composition, ruminal pH, volatile fatty acids, ammonia, digestibility, blood metabolites and relevant endocrine indicators. Measurements should be repeated over time to distinguish transient adaptation from persistent effects. The collective evidence does not support describing microalgae as growth promoters in beef cattle. A more defensible conclusion is that appropriately formulated microalgal supplements may maintain acceptable performance while enhancing tissue LC n-3 PUFA, but the tolerable and economically optimal dose depends on the product and production system.

7. Effects of microalgal supplementation on muscle fatty acid composition and omega-3 deposition

The most consistent finding across the literature is that microalgal supplementation can increase the concentration of LC n-3 PUFA in beef. This is the central nutritional rationale for the strategy and forms the basis for most experimental work in this field. In cattle fed a DHA-rich algal supplement, Carvalho et al. (2018) found increased muscle LC n-3 PUFA content and improvements in the n-6:n-3 ratio, indicating that preformed LC n-3 PUFA from microalgae can be incorporated into beef tissue despite ruminal biohydrogenation. Similar findings were reported by Xu et al. (2021), who observed that dietary supplementation with *Schizochytrium* sp. improved the long chain omega-3 fatty acid composition of beef and increased antioxidant status. These data reinforce the conclusion that microalgae are a viable route to nutritional enrichment in cattle (Xu et al., 2021). The significance of this work lies not only in demonstrating enrichment, but in showing that meaningful changes can occur in specific LC n-3 PUFA fractions relevant to human nutrition. However, the literature also makes clear that the extent of enrichment depends on several interacting factors, including the dose and duration of supplementation, the basal diet, rumen metabolism, breed, and tissue characteristics. Therefore, studies seeking to assess efficacy should quantify EPA, DHA, DPA, total LC n-3 PUFA, and derived indices such as the n-6:n-3 ratio, rather than relying on more general measures of total unsaturation.

7.1 General evidence for enrichment

Increasing muscle LC n-3 PUFA is the most consistent biological effect reported in beef microalgal studies. Carvalho et al. (2018) demonstrated marked increases in EPA and DHA despite ruminal biohydrogenation. Rodriguez-Herrera et al. (2018) reported that finishing heifers receiving 15 or 30 g microalgae/kg diet for 95 days produced beef with greater long chain n-3 fatty acid content and relatively modest sensory effects. Xu et al. (2021) also found favourable changes in beef fatty acid composition following *Schizochytrium* supplementation.These findings establish proof of biological incorporation. They do not establish a common transfer efficiency, optimal dose or commercially sufficient concentration. The number of independent beef studies remains small, and interventions differ in product composition and outcome reporting.

7.2 Dose-response relationships

A greater dietary dose can increase LC n-3 PUFA supply, but tissue deposition may not rise linearly. At higher doses, reduced intake, greater ruminal exposure, impaired fibre digestion or metabolic regulation may limit the incremental response. The dose yielding the highest tissue DHA concentration may therefore differ from the dose optimising

intake, growth, oxidation, sensory quality and profitability. Dose-response studies should include at least three well-characterised supplementation levels and an unsupplemented control. The actual daily intake of EPA and DHA should be quantified, and broken line or non-linear models should be considered rather than assuming a linear response.

7.3 Feeding duration

Tissue enrichment requires sufficient exposure, but the time course may differ between plasma, liver, adipose tissue and muscle phospholipids. Short studies may capture circulating changes without achieving stable muscle deposition. Conversely, prolonged supplementation may add cost after tissue concentrations approach a plateau. Repeated liveanimal biopsy could help establish the minimum effective duration and whether a strategic finishing period intervention is sufficient. Withdrawal studies would also determine how rapidly enrichment declines when supplementation ceases.

7.4 Basal diet and production system

Forage based diets commonly provide more α-linolenic acid and can produce a more favourable n-6:n-3 ratio than grain heavy diets. A microalgal supplement may therefore produce a different absolute and relative response in pasture finished cattle than in feedlot cattle. High concentrate diets can alter ruminal pH and microbial ecology, which may affect lipolysis and biohydrogenation. Basal diet also influences vitamin E and other antioxidants. Consequently, a similar increase in tissue PUFA may have different oxidative consequences in pasture-fed and concentrate-fed animals.

7.5 Breed, sex and adiposity

Breed differences in IMF, fat melting point and fatty acid composition can affect both baseline values and apparent supplementation response. Wagyu cattle, for example, generally have greater IMF and distinct lipid characteristics compared with leaner breeds. Otto et al. (2024) demonstrated breed and sex related differences in biopsy derived LC n-3 PUFA, IMF and fat melting point in pasture-based Angus, Hereford and Wagyu cattle. Greater IMF may dilute the proportional contribution of membrane phospholipids while increasing total fatty acids per unit of tissue. Therefore, an animal may have a lower LC n-3 PUFA percentage but a similar or greater absolute amount per 100 g meat. Both metrics are required.

7.6 Tissue and analytical variability

Fatty acid composition differs among muscles and between muscles, subcutaneous fat and perirenal fat. Studies that sample different anatomical sites cannot be compared directly. Sample trimming, ageing and whether results are reported on a wet tissue, total lipid or total fatty acid basis also influence interpretation.

Recommended reporting includes:

- EPA, DPA and DHA individually;
- total LC n-3 PUFA;
- α-linolenic acid and total n-3 PUFA;
- total n-6 PUFA;
- n-6:n-3 ratio;
- saturated and monounsaturated fatty acids;
- IMF or total lipid;
- mg fatty acid/100 g edible tissue;

- percentage of total identified fatty acids;
- lipid extraction and methylation method;
- chromatographic conditions and standards; and
- technical and biological replication.

7.7 Nutritional relevance

An increase in tissue DHA should be interpreted in relation to a realistic serving of beef. Serving level data permit comparison with dietary recommendations and competing omega-3 sources. Without such data, terms such as "healthier beef" or "nutritionally significant enrichment" may overstate the evidence. The most defensible conclusion is that microalgae can increase muscle LC n-3 PUFA, but the nutritional importance of the increase varies. Demonstrating statistical enrichment is a necessary but insufficient basis for a functional food claim.

8. Consequences for oxidative stability, colour and sensory quality of microalgae and conventional meat

In beef production, nutritional enhancement must be understood alongside conventional meat quality indicators. Among these, intramuscular fat and fat melting point are especially important because they influence marbling, flavour, mouthfeel, and eating quality. Any intervention that changes fat composition may also affect these traits. Recent Australian research (Otto et al., 2024) has shown that IMF and FMP vary substantially by breed and sex in pasture-based cattle. Otto et al. (2024) also reported that Wagyu cattle displayed the highest IMF and lowest FMP, while also exhibiting comparatively favourable LC n-3 PUFA composition. These results confirm that baseline lipid characteristics differ markedly among Angus, Hereford, and Wagyu animals and that such differences must be considered when evaluating supplementation effects (Otto et al., 2024). This is especially relevant in the context of microalgal supplementation because enhancement of tissue LC n-3 PUFA content should ideally occur without loss of desirable IMF characteristics or undesirable hardening of fat. The capacity to measure IMF and FMP *in vivo* through biopsy also means that these relationships can be explored longitudinally. A major concern in the enrichment literature is that increasing unsaturated fatty acids may make beef more susceptible to oxidation. Higher concentrations of PUFA can accelerate lipid oxidation, leading to rancidity, colour deterioration, and reduced shelf life if antioxidant protection is insufficient. This issue was clearly illustrated by Carvalho et al. (2018), who found increased oxidation in aged steaks from steers receiving DHA-rich microalgae. Likewise, Phelps et al. (2020) reported that supplementation with DHA-rich microalgae affected steak colour stability and sensory attributes, demonstrating that nutritional enrichment may come at the cost of some retail quality characteristics if oxidative balance is not well managed. By contrast, Xu et al. (2021) observed improved antioxidant status in association with *Schizochytrium* supplementation, suggesting that the relationship between omega-3 enrichment and oxidation is not inevitably negative and may depend on the antioxidant environment of the supplement and the muscle system under investigation. These apparently differing findings highlight the need to assess product stability empirically rather than assume a single direction of effect. Ultimately, the success of nutritionally enhanced beef depends on whether consumers find it acceptable. Sensory quality therefore remains a critical outcome even in studies primarily motivated by nutritional goals. Phelps et al. (2020) demonstrated that DHA-rich microalgae influenced sensory characteristics of beef *longissimus lumborum*, reinforcing the view that flavour and palatability must be evaluated alongside LC n-3 PUFA enrichment. More recent work on ground beef by Catrett et al. (2025) adds an important dimension to the literature. In that study, incorporation of flaxseed and microalgae improved LC n-3 PUFA content while maintaining, and in some respects improving, colour stability and palatability in patties.

This suggests that product format may mediate the sensory consequences of enrichment, and that ground beef systems may provide a particularly useful pathway for commercial translation (Catrett et al., 2025).

8.1 Lipid oxidation

PUFA are more susceptible to peroxidation than saturated or monounsaturated fatty acids. Increased EPA and DHA may therefore raise the oxidative potential of beef. Oxidation produces aldehydes, ketones and other volatiles that can alter aroma and flavour. It can also interact with protein oxidation and pigment chemistry. Carvalho et al. (2018) found no difference in thiobarbituric acid-reactive substances after short ageing but reported a tendency towards greater oxidation in steaks aged for 21 days. This result should not be interpreted as showing that correctly controlled vacuum ageing inevitably causes extensive oxidation. Oxidative expression depends on oxygen availability, packaging integrity, temperature and subsequent exposure during display or cooking. Precise reporting of post-mortem conditions is essential.

8.2 Colour stability

Beef colour is a critical purchase cue. Lipid oxidation can promote metmyoglobin formation, while pigment oxidation can accelerate lipid oxidation. Phelps et al. (2016b, 2020) showed that DHA-rich microalgae could adversely affect retail colour stability, although antioxidant strategies modified some responses. Colour should be measured instrumentally and visually across a defined retail-display period. Studies should report illuminant, observer angle, packaging atmosphere, display temperature and time. Single-time-point colour measurements are insufficient to characterise commercial shelf life.

8.3 Antioxidant protection

Dietary vitamin E and naturally occurring microalgal antioxidants may protect enriched beef. The effectiveness of antioxidant supplementation depends on dose, duration, tissue deposition and interaction with the basal diet. Increasing systemic antioxidant enzyme activity does not necessarily prevent oxidation in stored meat. Both live-animal biomarkers and post-mortem product assays are needed. A factorial design comparing microalgae with and without antioxidant supplementation would help determine whether oxidative damage is attributable to LC n-3 PUFA enrichment and whether it can be mitigated economically.

8.4 Flavour and sensory acceptance

Marine, fishy, grassy, oxidised or atypical flavours may occur when highly unsaturated lipids or their oxidation products accumulate. Phelps et al. (2016b) reported adverse flavour effects associated with algae meal, whereas Rodriguez-Herrera et al. (2018) found only small sensory changes despite enrichment. Differences may reflect dose, product, diet, ageing, oxidation and sensory methodology. Xu et al. (2021) demonstrated changes in volatile compounds, suggesting that supplementation can affect flavour chemistry even when panel scores are not uniformly negative. Volatile profiles should not be interpreted as consumer acceptance without sensory validation.

8.5 Product format

Ground beef may provide a different route to commercialisation than whole-muscle steaks. Grinding distributes lean and fat, increases oxygen exposure and can accelerate oxidation, but it also allows formulation and blending. Catrett et al. (2025) evaluated enriched ground-beef patties and found that product source and formulation influenced fatty-acid composition, colour and palatability. Whole-muscle and ground-beef applications should therefore be evaluated

separately. A supplementation strategy unsuitable for long retail display of premium steaks may still have value in frozen, vacuum-packed or antioxidant-formulated ground products.

8.6 Tenderness and fat quality

Changes in fatty acid composition can alter fat firmness and melting point. Greater unsaturation generally lowers melting point, which may influence mouthfeel and processing. However, tenderness is primarily affected by connective tissue, sarcomere shortening, proteolysis, cooking and IMF rather than fatty-acid composition alone. Claims that microalgae improve tenderness require direct instrumental and sensory evidence. Overall, microalgal enrichment creates a quality-management problem rather than an inevitable quality penalty. Oxidative and sensory effects can potentially be managed, but they must be measured under commercially relevant conditions.

9. Live animal phenotyping and non-terminal meat quality assessment

Carcass and fatty acid phenotypes are expensive to measure and traditionally require slaughter. This limits the availability of records from elite breeding animals. Muscle biopsy provides a non-terminal method for assessing IMF, fat melting point and fatty acid composition. Otto et al. (2024) demonstrated the use of Longissimus dorsi biopsy to quantify LC n-3 PUFA, IMF and fat melting point in live pasture-based cattle. Such measurements can support longitudinal supplementation studies by allowing each animal to serve partly as its own baseline. They may also improve estimates of individual response by separating pretreatment differences from dietary effects. However, biopsy measurements have limitations. A small sample may not represent the entire muscle or carcass, particularly for heterogeneous IMF. Sampling location, depth, handling and tissue composition must be standardised. Repeat biopsies may introduce local injury or scar tissue and should be spatially separated. Validation against corresponding carcass measurements is required. Emerging non-invasive technologies including ultrasound, near-infrared spectroscopy, hyperspectral imaging and metabolomic biomarkers may eventually reduce phenotyping costs. Their prediction equations must be externally validated across breeds, diets and production systems. High-throughput phenotyping is essential if fatty-acid traits are to be incorporated into genomic selection.

One of the most important methodological advances in this research area is the increasing use of live animal muscle biopsy to assess meat quality traits in valuable breeding animals. This is especially important for stud breeders, who need information on IMF, FMP, and fatty acid composition without sacrificing high-value stock. Otto et al. (2024) showed that *Longissimus dorsi* biopsy can be used effectively to quantify LC n-3 PUFA, IMF, and FMP in live beef cattle. Their findings demonstrated marked breed and sex differences and established biopsy as a practical and scientifically robust tool for non-terminal meat-quality phenotyping. The significance of this work extends beyond breeding management. Longitudinal biopsy permits researchers to examine within-animal changes before and after nutritional intervention, making it possible to link supplementation directly to changes in muscle composition. It also creates an important bridge between phenotypic assessment and genomic analysis, allowing candidate marker data to be interpreted alongside repeated tissue measures.

10. Candidate genes, SNP molecular markers, genome-wide associations and genomic selection

10.1 Molecular genetics of beef quality

Beef quality traits are influenced by a complex combination of genetic, nutritional, physiological, and environmental factors. Nonetheless, a substantial body of evidence now supports the use of candidate genes and molecular markers to explain part of the variation in marbling, IMF, fat quality, tenderness, and fatty-acid composition. Nutritional

intervention alone, however, is unlikely to maximise LC n-3 PUFA deposition efficiently across diverse cattle populations. This is where single nucleotide polymorphism (SNP) markers become highly relevant. Fatty acid composition is now recognised as a complex polygenic trait affected by both genotype and environment. Reviews of beef genetics consistently identify genes involved in lipogenesis, desaturation, transport, and adipogenesis as important determinants of fatty acid composition and related meat quality traits. Romero et al. (2024) reviewed the literature on genetic markers associated with beef quality and concluded that genes such as *FASN*, *SCD*, *CAST*, *CAPN*, *LEP*, and *FABP4* have recurring importance across cattle populations and meat-quality traits. Their review also underscored the polygenic nature of beef quality, while arguing that biologically plausible markers remain highly valuable for breeding and research applications (Romero et al., 2024). Among the most frequently implicated genes are *FASN*, *SCD*, *FABP4*, *THRSP*, and members of the *FADS* family, which influence the synthesis, desaturation, storage, and partitioning of fatty acids in muscle and adipose tissue (Pećina & Ivanković, 2021; Romero et al., 2024). Genome-wide and candidate gene studies support the practical use of these loci. In American Angus cattle, Dawood et al. (2021) identified genomic regions associated with multiple fatty acid traits and highlighted candidate genes such as *FASN*, *SCD*, *THRSP*, *FADS2*, and *FADS3*, confirming that fatty acid composition can be improved through genomic selection as well as through feeding. Functional genomics reviews now place these genes within wider regulatory networks affecting marbling, intramuscular fat deposition, and fatty acid balance, suggesting that future selection strategies will likely move beyond single markers to more integrated genomic prediction models (Dawood et al., 2021; Tian et al., 2024). In terms of LC n-3 PUFA enriched beef, the work of Mwangi et al. (2022) is especially relevant because it directly links SNPs in lipogenic genes to health-beneficial lipid traits in tropical crossbred beef cattle. Their 2022 study reported significant associations between SNP loci in *FABP4*, *SCD*, and *FASN* and fatty acid composition in the loin eye muscle, including links between *SCD* and LC n-3 PUFA, and between *FASN* and intramuscular fat and other lipid classes. The authors argued that these polymorphisms could be used in marker-assisted selection to support breeding for healthier beef lipid profiles in northern Australian crossbred systems (Mwangi et al. 2022). The same research group also showed that polymorphisms in *FABP4*, *FASN*, and *SCD* influence carcass characteristics in tropical crossbred beef steers, indicating that these markers may have dual relevance for carcass grading and lipid quality. This duality matters because industry adoption is more likely when molecular markers can improve both economic traits and nutritional traits simultaneously. From a breeding perspective, such markers are valuable not because they act in isolation, but because they help identify animals more likely to respond favourably to targeted nutritional strategies such as microalgal supplementation (Mwangi et al., 2022; Pećina et al., 2023). This literature provides a strong rationale for using selected SNP markers as part of a targeted, trait-informed genomic strategy, particularly when the focus is on lipid related beef quality outcomes. Taken together, the literature suggests that the strongest future strategy is an integrated one: Use microalgae to provide the nutritional substrate for LC n-3 PUFA enrichment and use SNP or genomic markers to identify cattle with superior capacity to deposit, retain, and express favourable lipid profiles without unacceptable trade-offs in carcass or sensory quality. In practice, this could mean selecting animals carrying advantageous alleles in *FASN*, *SCD*, *FABP4*, THRSP, or related pathways, then finishing them on diets containing carefully titrated, possibly rumen protected microalgal products plus antioxidant support. Such a precision livestock approach aligns with current trends in sustainable meat production, where nutritional enhancement, product differentiation, and genetic improvement are pursued simultaneously rather than separately (Romero et al., 2024; Ponnampalam et al., 2025).

10.2 FABP4, SCD, and FASN as candidate markers

Among the many genes associated with fat biology, *FABP4*, *SCD*, and *FASN* have particular relevance to the topic of LC n-3 PUFA enrichment and meat quality. These genes act at different points in lipid metabolism and together provide a biologically coherent framework for examining variation in IMF, FMP, and fatty acid composition. Mwangi et al. (2022) showed that SNP in these lipogenic genes influenced carcass traits in tropical crossbred beef steers, including characteristics linked to fat deposition and muscle development. In a related study, Otto et al. (2022) reported associations between these same marker systems and IMF, FMP, and health-beneficial LC n-3 PUFA in Australian pasture-based Angus, Hereford, and Wagyu cattle. These findings are especially important because they indicate that the relevant markers may influence not only conventional carcass traits, but also nutritionally desirable lipid composition (Otto et al., 2022). Thus, these three genes are not merely convenient markers; they are biologically meaningful candidates for linking genotype with both meat quality and nutritional value.

10.3 Nutritional intervention and genotype responsiveness

A particularly promising implication of the marker literature is that cattle may differ genetically in their response to dietary enrichment strategies. In other words, not all animals may respond equally to microalgal supplementation. Some may show greater increases in LC n-3 PUFA, more favourable FMP shifts, or better preservation of meat quality traits. Although the literature has not yet fully characterised genotype by supplementation interactions in cattle fed microalgae, the convergence of evidence from nutritional and molecular studies suggests that this is a highly plausible and important area for future research. A combined nutrition-genomics approach may therefore offer greater precision than either strategy alone.

10.4 Polygenic architecture of beef lipid traits

Fatty acid composition is influenced by many genes of small to moderate effect, together with diet, age, sex, adiposity and environment. Candidate gene studies have identified biologically plausible associations, but the contribution of any single locus is unlikely to determine the phenotype across cattle populations.

Relevant pathways include:

- *de novo* fatty acid synthesis;
- desaturation and elongation;
- intracellular fatty acid transport;
- adipocyte differentiation;
- lipid oxidation;
- phospholipid remodelling; and
- lipoprotein uptake and storage.

FASN encodes a multifunctional enzyme responsible for *de novo* synthesis of long chain fatty acids. Variants have been associated with IMF, marbling and proportions of saturated and monounsaturated fatty acids. In northern Australian tropical crossbred cattle, *FASN* variants were associated with carcass and lipid traits, including IMF and selected fatty acids (Mwangi et al., 2022a, 2022b). Since *FASN* primarily influences endogenous synthesis rather than direct incorporation of dietary DHA, an association with LC n-3 PUFA may reflect broader lipid partitioning, linkage with another functional variant or dilution by total fat. Functional interpretation should therefore remain cautious.

SCD encodes stearoyl-CoA desaturase, which introduces a *cis* double bond into saturated fatty-acyl substrates and influences the balance between saturated and monounsaturated fatty acids. *SCD* variants have been associated with fat

melting point, marbling and fatty acid composition. Associations with LC n-3 PUFA may arise indirectly through changes in overall lipid metabolism or tissue lipid fractions. Otto et al. (2022) reported associations between *SCD*, *FASN* and *FABP4* polymorphisms and IMF, fat melting point and LC n-3 PUFA in Australian Angus, Hereford and Wagyu cattle. Replication in independent populations remains necessary before these variants are used for selection.

FABP4 encodes an intracellular fatty acid binding protein expressed predominantly in adipocytes and involved in fatty acid transport and lipid metabolism. Variants have been associated with marbling, fat deposition and fatty acid composition. In northern Australian crossbred cattle, *FABP4* SNPs were associated with selected carcass or lipid traits (Mwangi et al., 2022a, 2022b). Associations may vary among breeds because of allele frequency, linkage disequilibrium and population structure. A marker that is informative in one population may have little predictive value in another.
Other candidate genes include *THRSP* which participates in lipogenic regulation and has been associated with marbling and fatty acid traits. *FADS2* and *FADS3* are involved in desaturation pathways and are plausible candidates for variation in PUFA metabolism. *SREBF1* regulates lipogenic gene expression, while *LEP* influences appetite and adiposity. Tenderness related genes such as *CAPN1* and *CAST* are relevant to broader meat quality but should not be presented as direct determinants of LC n-3 PUFA deposition.

10.5 Genome-wide association studies and genomic selection

Genome-wide association studies avoid restricting analysis to previously selected genes and can identify genomic regions associated with complex traits. Dawood et al. (2021) identified genomic regions and candidate genes associated with fatty acid composition in American Angus cattle, including regions containing *FASN*, *SCD*, *THRSP*, *FADS2* and *FADS3*. GWAS findings are valuable for biological discovery but can be affected by sample size, population structure, phenotype quality, marker density and multiple testing. Significant associations may explain only a small proportion of total genetic variance. Independent validation and fine mapping are required. Modern genomic selection uses genome-wide marker information to predict genomic breeding values. It is better suited to polygenic traits than selection based on a few candidate SNPs. Its success depends on:

- sufficient numbers of accurately phenotyped and genotyped animals;
- genetic connectedness between training and target populations;
- appropriate statistical models;
- regular recalibration;
- economic weighting of the trait; and
- monitoring of correlated responses.

Fatty acid phenotyping is expensive, which limits reference population size. Lower cost proxy traits or validated spectroscopy and metabolomic measures may expand training populations. Candidate genes remain useful for mechanistic interpretation and targeted research. They should complement rather than replace genome-wide prediction.

11. Market relevance: Domestic and export perspectives

The value of enhanced beef must ultimately be considered in relation to its intended markets. In Australia, domestic beef quality is strongly shaped by systems such as Meat Standards Australia, which emphasise pH, tenderness, colour, and consistency of eating quality. MLA guidance indicates that ultimate pH above 5.70 is detrimental to eating quality, colour, texture, and shelf life, making pH a particularly important parameter in meat quality assessment (Meat &

Livestock Australia [MLA], 2025). These domestic market requirements are highly relevant to LC n-3 PUFA enrichment because any intervention that improves nutritional value but compromises pH related quality, colour stability, or tenderness may struggle to achieve commercial acceptance. Therefore, domestic market suitability requires a careful balance between compositional improvement and established quality benchmarks. Export markets are also highly relevant, especially the United States, where imported beef continues to play an important role in supplying processing and ground beef sectors. USDA Economic Research Service data confirm the ongoing significance of the U.S. beef sector and its relevance to imported beef flows (USDA Economic Research Service, 2025). This makes ground beef and patties strategically important product formats for evaluating nutritionally enhanced beef, particularly when considering how enrichment affects palatability, oxidative stability, and consumer acceptance in processed products.

11.1 Biological rationale for genotype x nutrition interactions

A genotype x nutrition interaction occurs when genotypes differ in the magnitude or direction of response to a dietary intervention. Such interactions are biologically plausible for microalgal supplementation because animals may differ in:

- feed intake and ruminal passage;
- rumen microbial ecology;
- intestinal lipid absorption;
- lipoprotein metabolism;
- tissue uptake;
- fatty acid oxidation;
- IMF deposition;
- phospholipid remodelling; and
- antioxidant capacity.

Cattle with similar dietary DHA intake may therefore deposit different amounts in muscle or experience different oxidative consequences.

11.2 Current evidence is indirect

Evidence currently consists mainly of two parallel observations: Microalgae can alter beef fatty acid composition, and genetic markers are associated with lipid traits. Few studies have jointly randomised cattle of known genotype to multiple microalgal diets and formally tested interaction terms. It is therefore premature to claim that particular alleles identify "microalgae responsive" cattle.

11.3 Appropriate experimental designs

Future studies should use factorial designs incorporating genotype or genomic breeding value and at least two dietary treatments. Large samples are required because interaction effects are generally smaller and less precisely estimated than main effects. Animals should be balanced by breed, sex, age, initial weight and baseline phenotype. Repeated biopsy can quantify individual trajectories. Statistical models should include diet, genotype, time, relevant interactions and random animal effects. Genome wide reaction norm models may be more informative than testing only a few candidate SNPs.

11.4 Nutrigenomics and multi-omics

Transcriptomics could identify diet induced changes in lipid synthesis, transport, oxidation and antioxidant pathways. Metabolomics and lipidomics could characterise intermediate phenotypes that connect dietary exposure with muscle deposition. Rumen microbiome analysis may identify microbial communities associated with greater LC n-3 PUFA escape. Multi-omics studies should be adequately powered and prospectively designed. Small exploratory datasets can generate hypotheses but are vulnerable to false discovery and overfitting. Findings require validation in independent cattle populations.

11.5 Precision feeding

Precision feeding could eventually allocate supplementation according to predicted biological response, production stage, market endpoint and economic value. In practice, implementation would require:

- rapid genotyping or existing genomic profiles;
- validated prediction equations;
- individual or group specific feed delivery;
- reliable product composition;
- real time intake or growth information;
- traceability; and
- a price signal sufficient to offset added complexity.

Given these requirements, genotype guided microalgal feeding remains a future research strategy rather than a currently validated commercial practice.

12. Commercial implementation and market translation

12.1 Cost and availability

Microalgal biomass is generally more expensive than conventional energy or protein ingredients. Feed grade prices vary with strain, production method, lipid concentration, processing and scale. Economic analysis should use cost per gram of delivered and deposited EPA or DHA rather than cost per kilogramme of product. The relevant question is not simply whether supplementation increases tissue LC n-3 PUFA, but how much saleable nutrient enrichment is obtained per unit of added cost.

12.2 Feedlot logistics

Large scale implementation requires products that can be stored, transported and mixed consistently. Fine powders or lipid rich biomass may create handling, dust, rancidity or segregation problems. Palatability must remain acceptable, and the product must be compatible with total mixed rations, supplements or pellets. Variation among product batches could compromise both biological response and regulatory compliance. Supplier quality assurance and routine compositional testing are therefore necessary.

12.3 Regulatory approval and claims

Feed ingredients must satisfy relevant animal feed and residue requirements. The final beef product must independently meet food labelling criteria. A feeding claim cannot substitute for analytical verification of the meat. Nutrition content claims may require regular product testing and management of biological variation. If only a proportion of carcasses reach the threshold, identity preservation or carcass level testing may be needed. These requirements add cost.

12.4 Producer adoption

Producers are unlikely to adopt supplementation solely for a theoretical nutritional benefit. Adoption depends on:

- no substantial penalty to intake or growth;
- predictable carcass performance;
- an enforceable premium or supply contract;
- manageable feeding logistics;
- confidence in product consistency; and
- limited additional production risk.

The value proposition may be stronger in branded programs than in undifferentiated commodity markets.

12.5 Processor and supply chain requirements

Nutritionally enriched cattle or carcasses may need segregation, traceability and separate labelling. Processors must determine which cuts or product streams maximise value. Ground beef may permit blending to a defined nutrient specification, whereas whole muscle products may show greater carcass to carcass variability. Cold chain, packaging and antioxidant strategies may need modification because PUFA enriched products can be more oxidation sensitive.

12.6 Consumer acceptance

Consumer interest in omega-3 enriched beef does not guarantee willingness to pay. Acceptance will depend on price, taste, trust in claims, attitudes towards feed technologies and perceived naturalness. Terms such as "algae-fed" may be viewed positively as sustainable by some consumers and negatively by others. Market research should test alternative communication strategies without implying health outcomes unsupported by evidence.

12.7 Premium markets and return on investment

Potential markets include health oriented branded beef, premium retail products, food service products and formulated ground beef. Economic assessment should include:

- supplement purchase;
- transport and storage;
- diet reformulation;
- feed conversion effects;
- antioxidant supplementation;
- genotyping and phenotyping;
- carcass or product testing;
- segregation and certification;
- packaging and shelf-life management; and
- marketing.

Partial budget analysis, sensitivity analysis and willingness to pay studies are needed. Commercial feasibility cannot be inferred from biological enrichment alone.

12.8 Sustainability

Microalgae may reduce dependence on wild caught fish oils and can potentially use none arable land or alternative substrates. However, cultivation, aeration, harvesting, drying and extraction can be energy intensive. Comparative life

cycle assessments should evaluate greenhouse gas emissions, land use, water use and energy demand per unit of LC n-3 PUFA delivered in edible beef.

13. Evidence gaps in the literature and future research perspectives and priorities

13.1 Limited and heterogeneous beef evidence

Beef specific intervention studies remain few, and many involve modest sample sizes. Products, doses, breeds, diets, durations and analytical methods differ. The field requires coordinated multi site trials using common outcome definitions.

13.2 Inadequate product characterisation

Studies should report full microalgal composition, including total lipid, EPA, DPA, DHA, antioxidant content, carrier ingredients, processing method and oxidation status. Nominal product inclusion is not an adequate exposure measure.

13.3 Lack of standardised long chain omega-3 fatty acids reporting

EPA, DPA and DHA should be reported individually and in absolute edible tissue units. Reporting only percentages can obscure differences in total lipid and serving level value.

13.4 Incomplete productive and metabolic assessment

Fatty acid outcomes should be integrated with intake, growth, feed efficiency, ruminal fermentation, digestibility, blood metabolites and carcass value. Studies that measure only tissue lipids cannot establish production feasibility.

13.5 Limited dose and duration studies

Multi dose trials are required to identify the point at which additional enrichment is outweighed by reduced intake, oxidation, sensory change or cost. Time course studies should determine the minimum feeding duration and persistence after withdrawal.

13.6 Rumen-protection technologies

Direct comparisons of intact, processed and encapsulated microalgae are needed at equivalent EPA and DHA intakes. Protection should be evaluated through ruminal metabolism, intestinal flow, digestibility and tissue deposition.

13.7 Oxidative and sensory assessment

Studies should use commercially relevant ageing, packaging, retail display and cooking conditions. Antioxidant strategies should be evaluated factorially. Both trained panel and consumer outcomes are needed.

13.8 Genomic validation

Candidatebgene associations require independent validation across breeds and environments. Larger reference populations with standardised fatty acid phenotypes are needed for genomic prediction. Genomic models should be assessed for prediction accuracy, bias and stability over time.

13.9 Direct genotype x diet studies

Formal interaction studies are a central priority. They should be sufficiently powered, preregistered where possible and supported by repeated phenotyping. Candidate gene tests may be included, but genome wide and reaction norm approaches are preferable.

13.10 Microbiome and multi-omics integration

Rumen metagenomics, transcriptomics, metabolomics and lipidomics may explain why animals differ in deposition efficiency. Their value will depend on a robust design, replication and integration with conventional production traits.

13.11 Commercial scale validation

Feedlot scale studies are required to establish mixing feasibility, product consistency, growth performance, carcass variation and supply chain costs. Research herds may not reproduce commercial logistics or economic constraints.

13.12 Consumer and economic research

Willingness to pay, claim comprehension, sensory acceptance and producer return should be investigated alongside biological outcomes. Without a credible premium and supply chain pathway, even biologically effective enrichment may remain commercially marginal.

It is evident therefore, that beef specific studies are still relatively few compared with the broader ruminant or monogastric literature.There is substantial heterogeneity in microalgal species, dose, processing method, duration of feeding, and analytical endpoints. More work is needed on rumen protection technologies, shelf-life stability, retail colour, consumer acceptability, and cost effectiveness under commercial feedlot conditions. Although candidate gene associations are promising, many findings still require validation across breeds, production systems, and environments before routine deployment in breeding programs. Finally, the most important frontier is gene by nutrition interaction: Identifying which genotypes respond most efficiently to specific microalgal formulations could transform LC n-3 PUFA enriched beef production from a generic feeding strategy into a targeted precision system (Tian et al., 2024; Zhao et al., 2025).

Therefore, despite substantial progress, several important knowledge gaps remain, and research is needed to fill these as summarised below:

Firstly, much of the literature considers either dietary supplementation or molecular markers in isolation. Integrated studies examining both microalgal supplementation and SNP based responsiveness in multiple cattle breeds under the same management conditions remain limited. Second, many studies assess only a narrow range of outcomes, such as fatty acid composition or carcass measures, without connecting these to growth performance, metabolic indicators, rumen biology, sensory quality, and product stability. Third, there is a relative shortage of longitudinal studies in young cattle that incorporate repeated live animal phenotyping, especially biopsy based monitoring of IMF, FMP, and LC n-3 PUFA. Fourth, while the potential of microalgae is widely acknowledged, practical challenges remain around cost, consistency, dosage, palatability, and scalability. Ponnampalam et al. (2024) emphasised that future enrichment strategies must integrate antioxidants and quality preservation measures if nutritionally enhanced ruminant meat is to achieve broader success. Finally, more research is needed on product format differences, particularly the distinction between whole muscle cuts and ground beef applications, as these may respond differently to LC n-3 PUFA enrichment.

14. Summary and conclusion

Microalgae provide a direct source of preformed EPA or DHA and can increase LC n-3 PUFA concentrations in beef. The evidence is strongest for DHA-rich *Schizochytrium*/*Aurantiochytrium* type products, although the magnitude of enrichment varies with product composition, inclusion level, feeding duration, basal diet and animal phenotype. Available evidence does not support a universal optimal dose. Higher supplementation may increase tissue deposition but may also reduce feed intake or increase oxidative and sensory risks. Enrichment should not be evaluated using tissue fatty acid percentages alone. EPA, DPA and DHA should be reported in absolute amounts per edible portion (mg/100g of tissue) and interpreted against regulatory claim thresholds. Growth performance, ruminal function, IMF, fat melting point, oxidation, colour, tenderness, flavour, shelf life and production cost are equally important. Associations involving *FASN*, *SCD*, *FABP4*, *THRSP*, *FADS2* and related genes support a genetic contribution to beef lipid composition. However, beef fatty acid traits are polygenic, and candidate gene associations may not transfer across populations. Genome-wide prediction supported by accurate, scalable phenotyping may offer a more robust breeding pathway. Combining microalgal supplementation with genomic information and repeated phenotyping appears promising, but direct genotype x microalgae evidence is currently insufficient. Before precision feeding can be recommended, multi-breed factorial studies must demonstrate reproducible interactions, economic benefit and no unacceptable trade-offs in production or meat quality. Commercial adoption will ultimately depend on delivering a consistent, claim eligible and sensory acceptable product at a cost supported by market premiums. Progress therefore requires coordinated nutrition, rumen biology, quantitative genetics, meat science, consumer research and supply chain economics rather than optimisation of tissue LC n-3 PUFA in isolation. Growth performance, oxidative stability, colour, tenderness, sensory quality, and market suitability are equally important. The most compelling future direction is therefore an integrated approach that combines nutrition, genomics, and live animal phenotyping. Such a framework offers the greatest potential to produce beef that is nutritionally enhanced, commercially acceptable, and genetically optimised for both domestic and export markets.

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