

US HORSES

Age-dependent modulation
of equine hindgut fermentation by
a Multi-Seaweed Marine Bioactive



EXECUTIVE SUMMARY

The equine hindgut microbiome plays a central role in fibre digestion, energy harvest, and overall gastrointestinal health. As obligate hindgut fermenters, horses rely on a highly specialised microbial ecosystem optimised for the slow degradation of structural carbohydrates and the production of short-chain fatty acids (SCFAs), predominantly acetate. Disruption of this balance—whether through excessive rapid fermentation, lactate accumulation, or increased proteolytic metabolism—can predispose horses to hindgut instability and associated health issues.

Prebiotic interventions targeting the equine microbiome must therefore strike a careful balance: enhancing fibre fermentation efficiency without overstimulating rapid or dysbiotic pathways. Increasingly, there is recognition that effective prebiotics act not by forcing uniform compositional changes, but by **regulating microbial ecosystems in a context-dependent manner**, allowing host physiology and baseline microbial state to shape the outcome.

This exploratory trial investigated the effects of a **blended seaweed intervention** on the equine hindgut microbiome. Particular attention was paid to **functional fermentation pathways, age-dependent responses**, and whether enhanced fibre fermentation occurred **without metabolic trade-offs** elsewhere in the system.

Rather than focusing on isolated taxa or single endpoints, this study employed a functional, systems-based analytical framework tailored to equine hindgut biology. Composition-based proxy indices were used to evaluate fibre fermentation capacity, acetate-linked metabolism, downstream SCFA cross-feeding, and potential risk pathways such as lactate production and proteolytic fermentation. This approach was designed to assess whether microbiome modulation occurred in a biologically coherent manner, without evidence of destabilisation or metabolic trade-offs.

As an exploratory study based on faecal microbiome composition, findings should be interpreted as indicative of directional biological tendencies rather than direct measurements of hindgut fermentation metabolites.



TRIAL OBJECTIVES

The primary objective was **not** to demonstrate clinical efficacy or statistical significance, but to evaluate whether a multi-seaweed formulation produces consistent, biologically coherent microbiome patterns across multiple analytical perspectives within a diverse population of horses of different ages and breeds.

This exploratory trial investigated the effects of a **blended seaweed intervention** on the equine hindgut microbiome. Particular attention was paid to **functional fermentation pathways, age-dependent responses**, and whether enhanced fibre fermentation occurred **without metabolic trade-offs** elsewhere in the system.

TRIAL DESIGN

Animal population

- 10 horses within 2 stables in Florida
- Mixed breeds (Warmbloods, Thoroughbred, Gypsy Vanner),
- 1 horse was 2yo, 1 horse 3yo, 4 horses 6yo, 3 horses 22yo, 1 horse 23yo

Dietary groups

All horses had 1.6oz/45g of **OceanFeed™** Equine added to their normal diet:

Inclusion rate and design rationale

45g/day is our standard recommended inclusion for an adult horse. The horses consumed the additive for 60 days.

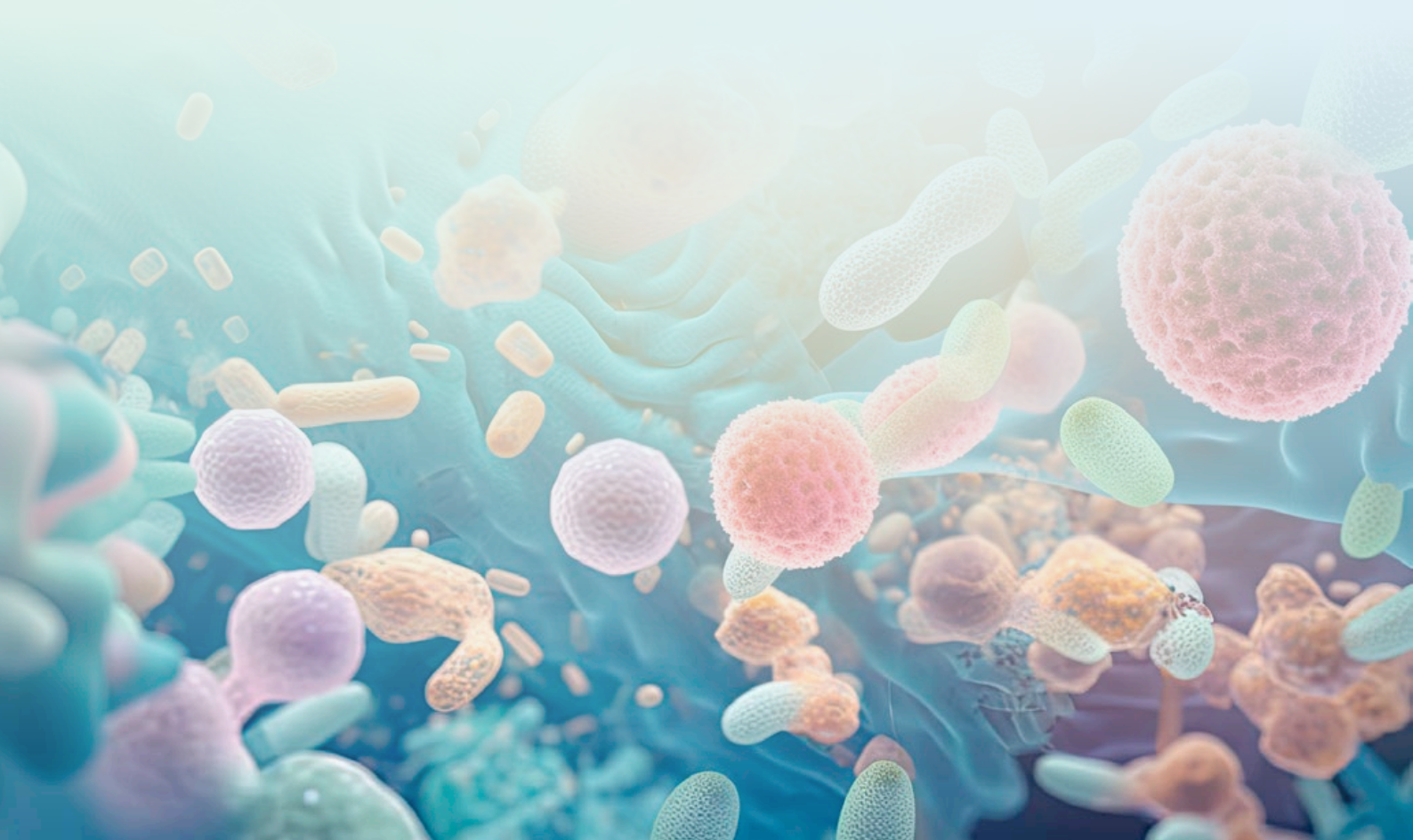


MICROBIOME METHODS AND LIMITATIONS

- Faecal samples collected before and after dietary exposure;
- Microbiome profiling via 16S rRNA sequencing;
- Raw read counts normalised to total reads per sample and expressed as **relative abundance (%)**;
- Analyses conducted at family and genus level, depending on metric

Given the exploratory nature and small sample size, no formal hypothesis testing or p-values are reported. Emphasis is placed on **directional patterns, consistency, and biological plausibility**.

The Functional Indices used within this analysis are composition-based proxies derived from faecal 16S rRNA profiles, and the study did not directly measure short-chain fatty acids (SCFAs), pH, lactate, or other fermentation metabolites. Relative abundance in microbiome data may shift due to compositional effects and does not necessarily imply an increase or decrease in absolute bacterial abundance. Given the lack of a control group in this trial, causality cannot be established, and larger, controlled studies would be required to confirm these findings.



ANALYTICAL FRAMEWORK

Given the functional specialisation of the equine hindgut, analysis focused on biologically defined functional indices, rather than isolated taxa. To that end, we defined 5 separate functional indices, with some bacteria appearing in more than one index.

FUNCTIONAL INDICES

Five functional groupings were defined a priori based on known microbial ecology:

1. **Equine Fibrolytic Proxy Index (EFI)** – composed of core hindgut fibre degraders
2. **Acetate Potential Proxy Index (API)** – composed of broad polysaccharide degraders contributing to acetate-based fermentation
3. **SCFA/Butyrogenic Quality Proxy Index (SBI)** – composed of taxa associated with downstream SCFA conversion and cross-feeding
4. **Lactate-Producing Guild Index (LPI)** – composed of bacteria acting as a proxy for rapid fermentation and acidosis risk
5. **Proteolytic Guild Index (PRI)** – composed of bacteria acting as a proxy for inefficient or potentially harmful protein fermentation



There were no direct measurements of short-chain fatty acids (SCFAs), pH, lactate, or other fermentation metabolites in this study. Accordingly, the functional indices presented here are composition-based proxy measures derived from fecal 16S rRNA profiles and should be interpreted as indicators of directional biological tendencies rather than direct measurements of hindgut fermentation or metabolic flux.

These indices were analysed before and after intervention based on relative abundance %, and stratified between a young horse (n=6) and old horse (n=4) groups as well as across the full cohort. The bacteria used for each index are set out in [Table 1](#) below.

Table 1: Bacterial genus/family in each functional index

Equine Fibrolytic	Acetate potential	SCFA/butyrogenic quality	Lactate-producing	Proteolytic
Fibrobacter	Fibrobacter	Butyricoccaceae	Ligilactobacillus	Clostridium senso stricto 1
Kiritimatiellae	Lachnospiraceae	Butyricoccus	Lactobacillus equigenerosi	Desulfovibrio
Lachnospiraceae	Monoglobus	Butyrivibrio	Lactobacillus hayakitensis	Terrisporobacter
Marvinbryantia	Ruminococcaceae	Coprococcus	Selenomonadaceae	
Ruminococcaceae	Ruminococcus	Eubacterium hallii	Streptococcus	
Ruminococcus	Treponema*	Faecalibacterium	Streptococcus equinus	
Treponema*		Phascolarctobacterium		
		Roseburia		
		Saccharofermentans		

→ The Equine Fibrolytic and Acetate Potential indices were analysed with and without Treponema. Directionally this made no difference to the conclusions.

Functional Index membership reflects typical tendencies reported in equine/gut literature and should be interpreted as directional proxies, not definitive functional assignments.

OVERALL MICROBIOME RESPONSE: A COORDINATED FERMENTATIVE SHIFT

Across the full cohort, the blended seaweed intervention produced **directionally coherent changes across multiple fermentation-relevant axes** rather than isolated or opposing signals.

- Fibre-associated and acetate-linked fermentation pathways increased or stabilised.
- Lactate-producing and proteolytic pathways declined.
- No obvious bloom-like patterns were observed in these faecal 16S profiles

Table 2 below is intended to give an overall sense of the impact on the different functional indices before the results are explored in more detail.

Table 2: Illustrative scorecard indicating aggregate direction of change

	Young horses	Old horses	Full cohort
Equine Fibrolytic	++	+	++
Acetate potential	+++	--	+
SCFA/butyrogenic quality	+	--	-
Lactate-producing	--	-	--
Proteolytic	---	--	---

→ Note: Symbols indicate direction and relative magnitude of change (+: increase, -: decrease; additional symbols denote greater magnitude)

This pattern indicates a re-routing of microbial metabolism toward slow, fibre-first fermentation rather than a general increase in fermentative activity.

AGE-DEPENDENT RESPONSES REVEAL CONTEXT-AWARE MODULATION

YOUNGER HORSES: AMPLIFICATION OF FERMENTATIVE CAPACITY

In younger horses, the response was characterised by **marked enhancement of fibre fermentation capacity**:

- The EFI increased substantially in younger horses (mean 19.1% to 25.7%; similar magnitude when *Treponema* is included).
- The API rose very strongly and the SBI increased slightly in parallel.
- These increases were **consistent across individuals**, rather than driven by outliers – all 6 horses saw increased EFI, all 6 horses saw increased API, in both cases whether you included *Treponema* or not. For the SBI, 3 increased and 3 decline, albeit the magnitude of moves was small – averages of +1.8% and -0.5% respectively.

Figure 1.

Relative Abundance of Functional Indices for the Young Horse cohort (n=6)



VERY OLD HORSES: REBALANCING RATHER THAN AMPLIFICATION

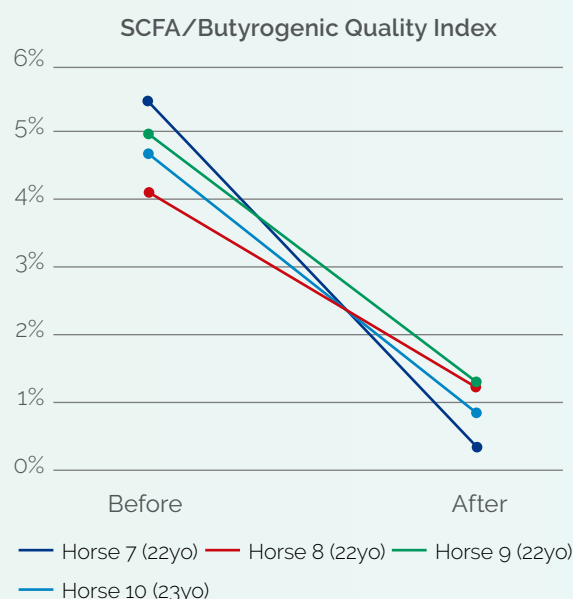
In contrast, very old horses exhibited a different—but biologically coherent—response:

- The EFI declined modestly or stabilised.
- API and SBI were maintained or slightly reduced.
- Importantly, LPI and PRI **still declined**.

Figure 2.

Relative Abundance of Functional Indices for the Old Horse cohort (n=4)





Given that aged horses often exhibit highly specialised, dominance-driven fermentative communities at baseline, these patterns are consistent with **rebalancing of an already saturated system**, rather than loss of fermentative function.

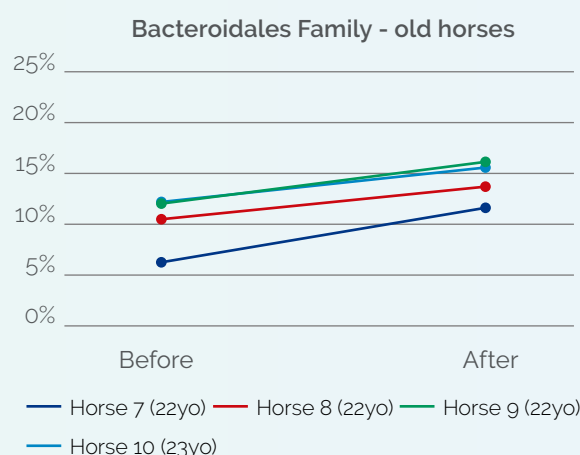
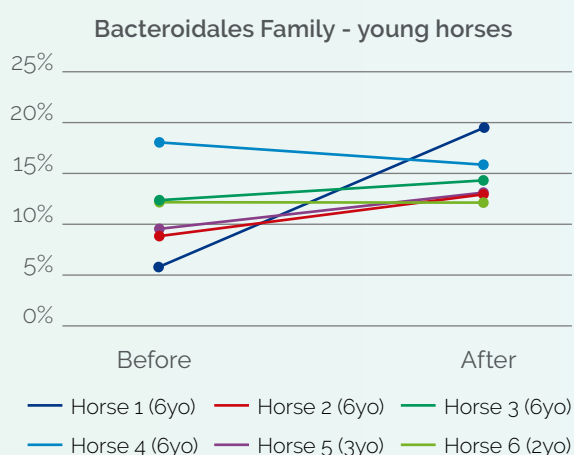
COORDINATED EXPANSION OF BACTEROIDALES ACROSS AGE GROUPS

Notably, Bacteroidales **increased** in both younger and very old horses:

- Younger horses: ~10.8% → ~14.4%
- Very old horses: ~9.8% → ~14.0%

Figure 3.

Change in Relative Abundance of Bacteroidales family



Bacteroidales are broad polysaccharide degraders capable of utilising a wide range of complex and soluble carbohydrates. Their coordinated expansion across age groups suggests **increased substrate accessibility** driven by the blended seaweed intervention.

Crucially, this expansion occurred:

- alongside enhanced fibrolytic capacity in younger horses, and
- alongside rebalancing (not destabilisation) in very old horses.

This hierarchical response supports a **substrate-driven, ecosystem-aware mechanism**, rather than indiscriminate stimulation of a single fermentative guild.

A CLOSER LOOK AT THE OLDER HORSE COHORT AND THE SCFA/BUTYROGENIC QUALITY INDEX

The changes in the older horse cohort were notably different vs. the younger horse cohort which is consistent with equine biology and differing needs. Particularly with very old horses, a relative abundance decline in this proxy index is consistent with other changes seen and should not be a cause for concern.

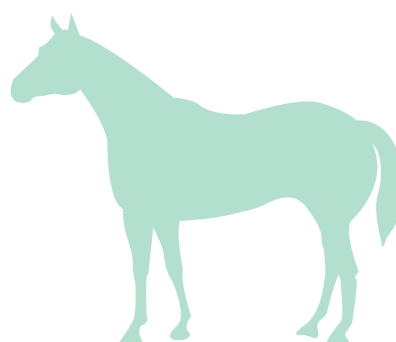
Fermentative strategy needs to be age-appropriate and for very old horses, a reduction in butyrogenic taxa may reflect a shift away from energetically expensive, niche-specialised fermentation toward a broader, stabilised fermentative strategy dominated by acetate and polysaccharide generalists, rather than loss of hindgut function.

With very old horses it is common to see reduced chewing efficiency, altered digesta flow, reduced microbial plasticity and dominance of a narrow set of specialist taxa. In this context, butyrogenic taxa may already be over-represented or inefficient (their starting point was 2.5x the relative abundance of the same bacteria in the young horse cohort for example). Maintaining complex cross-feeding networks may be less sustainable in old age and a favourable regulatory intervention could easily be to simplify and stabilise rather than amplify.

The key signals that this decline is not a cause for concern are that Bacteroidales levels increased meaningfully (see [Figure 3](#) above) on a relative basis whilst LPI and PRI taxa declined (see [Figure 4](#) below). There were also no obvious signs of bloom-like patterns or destabilising taxa emerging either.

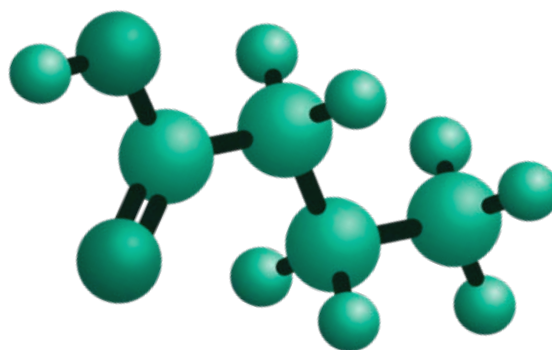
This combination is suggestive that:

- Fermentation is not becoming harsher;
- Acid stress risk is lower, not higher;
- Protein putrefaction is reduced;
- Polysaccharide utilisation remains active.



If Butyrate potential were falling because the system was deteriorating, you would expect to see the opposite.

In very old horses, the relative abundance of SBI declined following intervention. This occurred alongside relative abundance reductions in LPI and PRI taxa, and a coordinated relative abundance increase in Bacteroidales. The pattern observed in the oldest horses, where SBI declined while certain other indices remained stable or improved, may indicate a rebalancing of microbial community structure rather than a loss of fermentative capacity.



Given the central role of acetate as the dominant SCFA in horses, this could reflect a system favouring primary fibre fermentation over secondary cross-feeding pathways. However, as SBI represents a composition-based proxy and absolute metabolite levels were not measured, this interpretation should be considered indicative rather than conclusive.

Given the primacy of acetate as the dominant energy substrate in equine hindgut metabolism, and the tendency for aged microbiomes to operate near functional saturation, this pattern likely reflects a streamlining of fermentative networks toward stable, lower-risk pathways rather than loss of fermentative capacity. Importantly, no markers of dysbiosis or metabolic trade-off were observed.

In light of the magnitude of the compositional shifts observed, it was important to assess whether these changes occurred at an apparent metabolic cost elsewhere in the hindgut ecosystem.



“COST” ANALYSIS: ENHANCED FERMENTATION WITHOUT TRADE-OFFS

To assess whether increased fibre fermentation occurred at a biological cost, changes in lactate-producing and proteolytic guilds were examined.

Lactate producers

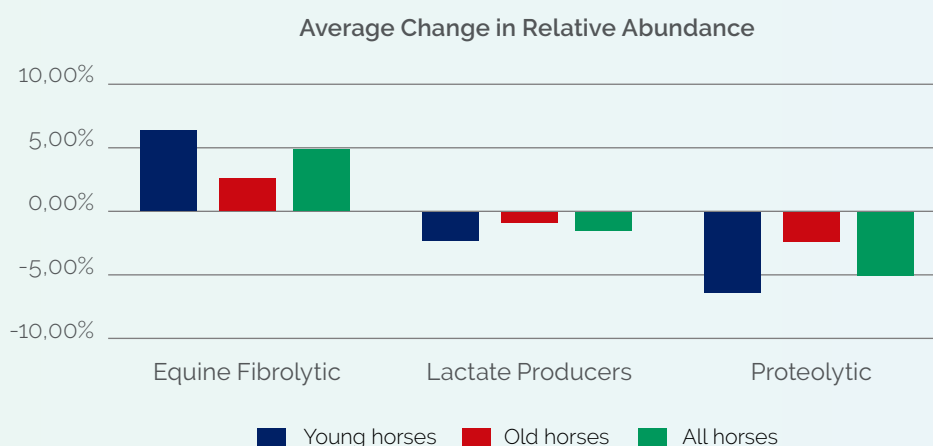
- Relative abundance declined sharply in younger horses.
- Relative abundance declined or remained suppressed in very old horses.
- Relative abundance declined at the whole-cohort level.

Proteolytic bacteria

- Relative abundance declined markedly in younger horses.
- Relative abundance declined or remained stable in very old horses.
- Relative abundance declined across the full cohort.

Figure 4.

Coordinated re-routing of hindgut fermentation toward fibre-first metabolism



Together, these results demonstrate that increased fibre fermentation was **not achieved via rapid lactate-heavy pathways nor via increased protein fermentation**, but through improved routing of microbial metabolism toward efficient, stable fibrolytic processes.



INTEGRATED INTERPRETATION: REGULATION, NOT STIMULATION

When considered together, the data support a clear interpretation:

- The blended seaweed does **not impose a uniform microbiome outcome**.
- Instead, it increases **substrate diversity and accessibility**, allowing the hindgut ecosystem to respond according to **age-dependent capacity and constraints**.
- Where fermentative headroom exists (younger horses), fibre fermentation is amplified.
- Where systems are saturated (very old horses), dominance is reduced and balance restored.
- In all cases, potentially destabilising pathways are suppressed.

This is consistent with a **regulatory prebiotic mechanism**, rather than a stimulant effect.

ANECDOTAL OBSERVATIONS DURING THE TRIAL

In addition to microbiome sampling, informal observations were recorded by an Equine Osteopath overseeing the trial as well as comments from owners and trainers. These observations were not systematically collected, scored or blinded and are therefore presented for contextual purposes only.

- ✓ **Coat:** Shinier, healthier, even during winter coat changes. Positive effects on rain scabs
- ✓ **Hooves:** stronger growth, notably reduced farrier interval for one horse
- ✓ **Behaviour:** calmer, less anxious, easier to manage
- ✓ **Appetite:** more balanced
- ✓ **Respiratory:** reduced nasal discharge
- ✓ **Digestive:** more solid manure, less gas
- ✓ **Performance & Recovery:** improved sweat response, faster muscle rehabilitation

These observations are consistent with what would be expected per independent science, to occur downstream as a result of positive upstream effects on the gut ecosystem as discussed at length in our Equine White Paper. They are also consistent with previous comments from established riders that have previously trialled the product.

CONCLUSIONS

This exploratory trial indicates that a blended seaweed intervention can modulate the equine hindgut microbiome in a **biologically coherent and age-dependent manner**. Enhanced fibre fermentation in younger horses occurred alongside reductions in lactate-producing and proteolytic bacteria, indicating improved fermentative efficiency without metabolic trade-off. In very old horses, responses reflected rebalancing and stabilisation rather than overstimulation and a shift towards simpler, safer energy routing.

Taken together, these findings support the concept that **effective prebiotic interventions operate by regulating microbial ecosystems**, amplifying host-appropriate functions while preserving stability across life stages.

As an exploratory study with a limited sample size, these findings warrant confirmation in larger, controlled trials. However, the consistency across multiple functional indices strengthens confidence in the observed patterns and changes are aligned with equine biology and published seaweed science.

