March 2026

Galaxis Frontier:

Technical Fact Sheet

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What is Galaxis Frontier?

How does Galaxis Frontier work?

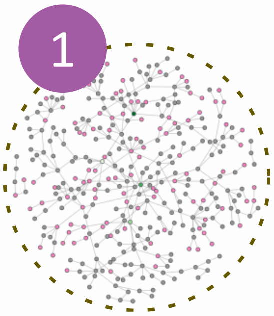
What is the impact of feeding Galaxis Frontier?

Galaxis Frontier:

The only product built from live, rumen-native microbes.

Generating the world's first rumen-native microbial consortia for dairy cows, from dairy cows

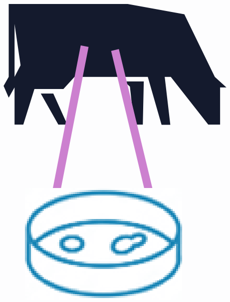
1



Genetically identify keystone rumen microorganisms[1]

Using next-generation sequencing data from more than 6,500 rumen samples across breeds, diets, and regions, we applied patented bioinformatics to identify the microbes most strongly associated with highly efficient, high-producing cows.

2



Isolate key microbes from rumen fluid and ferment at scale[2]

Individual strains were isolated from rumen fluid using defined carbon-source media to recover the top candidates identified in Step 1. From thousands of isolates, we selected organisms that could be reliably propagated at scale and characterized their genomes and metabolic capacities both in vitro and in silico. Because FDA regulations require each strain to be produced axenically, each microbe in Galaxis Frontier is grown independently.

3

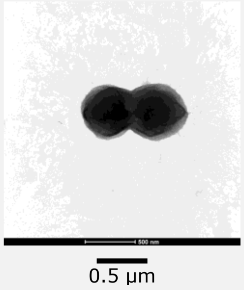
No cold chain;
add directly to TMR

Freeze dry and encapsulate live, rumen-native microbes[3]

Viable microbial biomass is preserved using the patented preservation-by-vaporization process, then coated through a proprietary encapsulation technology that protects each strain during TMR mixing and ensures delivery to the rumen alive. Native Microbials is the first and only company to obtain GRAS status for anaerobic rumen microbes.

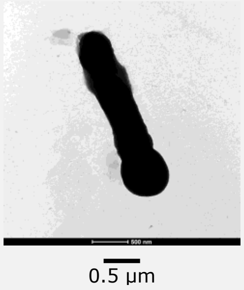
Galaxis Frontier is comprised of four live rumen-native microorganisms

Ruminococcus bovis
DY10, AGRN 68



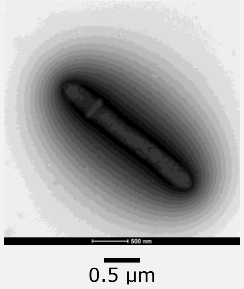
0.5 µm

Clostridium beijerinckii
DY20, AGRN 41



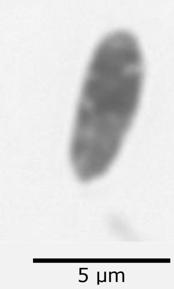
0.5 µm

Butyrivibrio fibrisolvens
DY19, AGRN 42



0.5 µm

Pichia kudriavzevii
DY21, AGRN 38

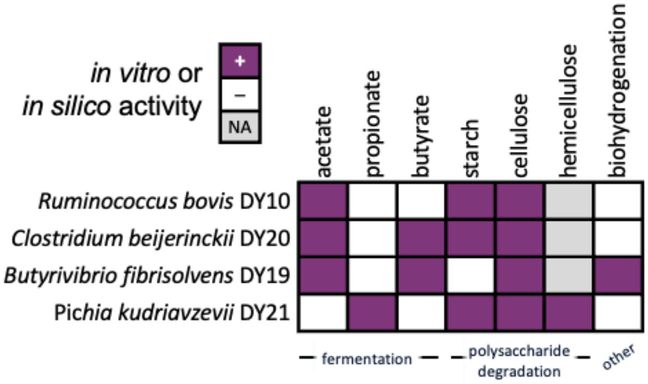


5 µm

DY designations indicate individual strains;
ARGN numbers indicate GRAS notifications.

Microbe-specific metabolic capability

Each of the four-member consortium in Galaxis Frontier contributes discrete metabolic pathways, but their dominant mode of action emerges from community-level interactions that reshape the rumen microbiome.



in vitro or *in silico* activity: + / – / NA

	acetate	propionate	butyrate	starch	cellulose	hemicellulose	biohydrogenation
Ruminococcus bovis DY10	+	–	–	+	+	NA	–
Clostridium beijerinckii DY20	+	–	+	+	+	NA	–
Butyrivibrio fibrisolvens DY19	+	–	+	–	+	NA	+
Pichia kudriavzevii DY21	–	+	–	+	+	+	–

fermentation — polysaccharide degradation — other

CITATIONS

1. Zengler, Karsten, and Mallory Embree. "Methods, apparatuses, and systems for analyzing microorganism strains from complex heterogeneous communities, predicting and identifying functional relationships and interactions thereof, and selecting and synthesizing microbial ensembles based thereon." U.S. Patent No. 9,540,676. 10 Jan. 2017.
2. Gaffney J, Embree J, Gilmore S, Embree M. Ruminococcus bovis sp. nov., a novel species of amylolytic Ruminococcus isolated from the rumen of a dairy cow. International Journal of Systematic and Evolutionary Microbiology. 2021 Aug 11;71(8):004924.
3. Bronshtein V, inventor. Preservation by vaporization. United States patent US 9,469,835. 2016 Oct 18.

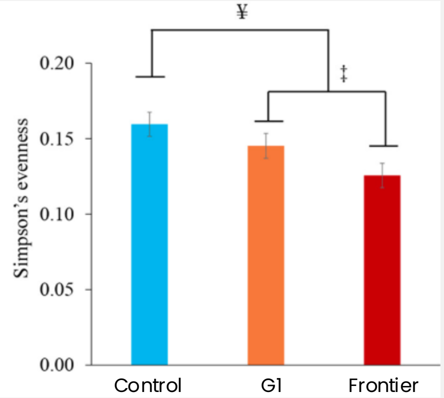
Galaxis Frontier

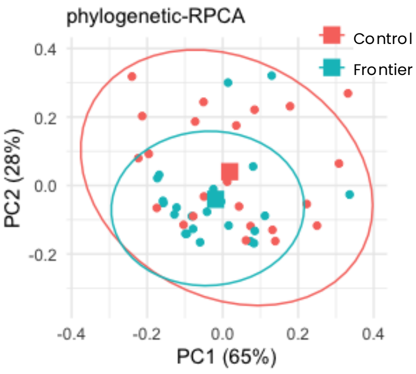
Mechanism of Action: changes to the rumen environment

Daily supplementation streamlines the rumen microbiome

In Marinho 2025[1], **16S rRNA gene amplicon sequencing** revealed that Frontier-fed cows exhibited reduced microbial diversity and greater dominance by select taxa (lower Simpson's evenness) compared with either Control or the G1 treatment (two of Frontier's four native strains). This indicates that the full consortium reshapes the broader rumen ecosystem rather than simply adding additional microbes.

These community shifts were associated with higher ECM and improved feed efficiency, consistent with prior independent studies[2-3]. In addition, one Frontier strain, *Ruminococcus bovis*, was positively correlated with milk yield and total solids.





PERMANOVA p=0.09; beta-dispersion p=0.04

Restructured rumen microbiome with coordinated metabolic function

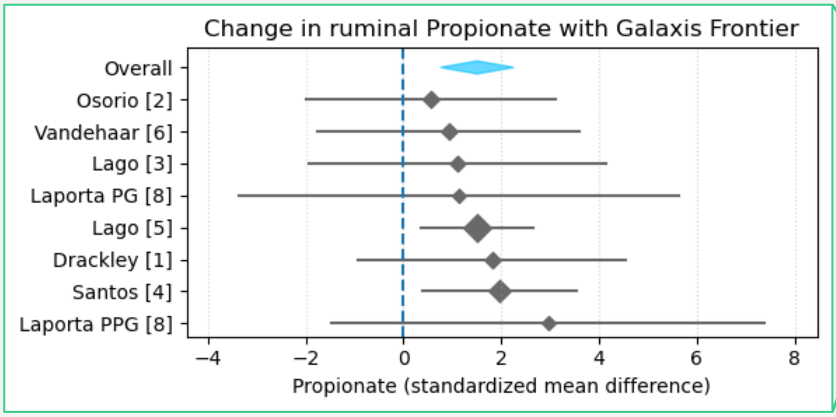
Because 16S rRNA gene amplicon sequencing provides limited information on functional gene content, we also applied **shotgun metagenomic sequencing** to 48 rumen fluid samples from Marinho (2024). Frontier-fed cows showed convergent microbial community structure, clustering more tightly in principal component analysis (left), whereas Control cows had more dispersed and variable microbiomes. This analysis also revealed changes in microbial gene abundances that underlie important metabolic pathways, including TCA cycle intermediates and amino acid metabolism. Notably, enrichment of arginine- and ornithine-related pathways suggests increased microbial capacity for polyamine synthesis, alongside shifts in fermentation end products linked to energy metabolism. We are continuing to analyze this dataset for further insights into the biochemical changes induced by Frontier supplementation.

Altered rumen genetic landscape leads to increased total VFAs

We evaluated the concentration of **ruminal SCFA** across our academic trial datasets using **HPLC** data. A random-effects meta-analysis of the standardized mean difference between Control and Frontier-fed animals revealed consistent increases across all major VFAs, with propionate significantly elevated in Frontier-fed cows. The acetate:propionate ratio was unchanged, indicating that the pattern of fermentation remained stable even as total energy yield increased.

The microbial taxa enriched with Frontier supplementation were also independently correlated with VFA concentrations. Together this suggests that the shift in ruminal chemistry did not arise simply from adding the four Frontier strains, but rather Frontier reshaped the broader microbial community, creating a more efficient metabolic network that generates more usable energy (VFAs) from the same diet.

Random-effects meta-analysis of Propionate (C3) Across Trials



Summary of Meta-analysis Outputs for all SCFAs

	Effect size	SE	p value
Acetate [C2]	0.234	0.115	0.081
Propionate [C3]	**0.422**	**0.116**	**0.008**
Butyrate [C4]	0.224	0.138	0.179
Valerate [C5]	0.347	0.172	0.084
Total VFA	**0.269**	**0.115**	**0.052**
Acetate:Propionate	-0.044	0.149	0.779

CITATIONS

1. Marinho et al., 2025, *J. Dairy Sci.* 2. Monteiro et a., 2024 *Anim Microbiome.* *3 Shabat et al., 2016, ISME* 4. Marinho et al., 2024, *J. Dairy Sci.*

**numbered citations in Propionate meta-analysis correspond to academic meta-analysis page*

Galaxis Frontier

Mechanism of Action: systemic changes that alter physiology

What is the impact on the cow when rumen genetics and chemistry are altered?

Mammary tissue changes

Galaxis Frontier increased mammary milk-producing capacity in Holstein cows, whether feeding began pre-partum or immediately after calving. In a University of Wisconsin–Madison study led by Dr. Jimena Laporta, cows receiving Galaxis Frontier developed 20% more alveoli, 10% more mammary epithelial cells, and showed a 30% reduction in cell apoptosis compared to untreated controls. These changes occurred without differences in alveolar area or cell density, indicating an increase in functional secretory units rather than tissue enlargement.

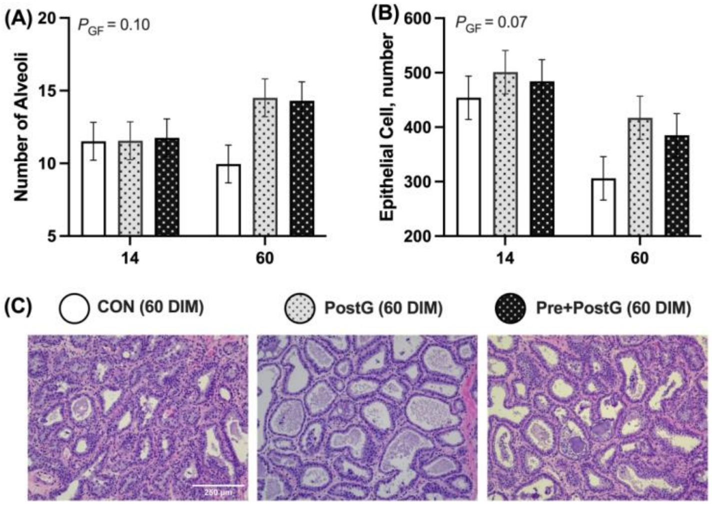


*Figure at right from **Tabor** et al. Journal of Dairy Science (2025).*

Inflammation and Immune Readiness

Galaxis™ Frontier supported greater innate immune activity during the transition period, when immune function is typically suppressed. In the University of Wisconsin–Madison study, cows receiving Galaxis Frontier showed numerically higher neutrophil phagocytic capacity and oxidative burst activity during the first two weeks postpartum compared with controls. Oxidative burst intensity was approximately 30–35% greater in treated cows (≈ +7–8 MFI), with treatment-by-day effects trending toward significance, indicating that differences emerged specifically during the fresh period. This pattern is biologically meaningful, as enhanced neutrophil effector function during early lactation suggests improved immune readiness at a time of heightened metabolic and inflammatory challenge.

Oxidative Stress markers

In a transition cow study at South Dakota State University[1], Frontier-fed cows showed a modest increase in reactive oxygen metabolites (ROM). This pattern fits with a metabolic state characterized by more complete β-oxidation of fatty acids rather than pathological oxidative stress; ROM production is a normal byproduct of mitochondrial fatty-acid oxidation, and elevations during early lactation typically mirror increases in NEFA and incomplete oxidation. In this study, however, Frontier cows maintained similar NEFA and BHB levels to controls, indicating they were not experiencing excessive lipid mobilization or ketotic strain. Importantly, the rise in ROM was transient and returned to values consistent with normal physiological ranges by 30 DIM, rather than exhibiting the sustained elevations reported in ketotic cows. This pattern supports a profile of efficient substrate use rather than oxidative overload.

Table below adapted from metric units in:
***Bulnes** et al. Journal of Dairy Science (2025).*

	Control	Frontier	SEM	p-value
GOT (U/L)	94.8	103.2	2.69	**0.02**
Paraoxonase (U/mL)	85.2	78.9	2.83	0.08
Ceruloplasmin (μmol/L)	2.95	3.21	0.1	**0.01**
Haptoglobin (g/L)	0.14	0.21	0.24	**0.03**
ROM (mg H_2O_2/100 mL)	15.7	17.4	0.47	**0.01**
NEFA (mmol/L)	0.15	0.19	0.18	0.18
BHB (mmol/L)	0.44	0.45	0.10	0.67
Milk (lbs)	78.93	85.32	2.71	0.06
DMI (lbs)	44.8	45.9	0.99	0.43
FE (MY/DMI)	1.71	1.82	0.05	0.10

Importantly, antioxidant capacity remained intact. Paraoxonase (PON), an enzyme inversely associated with oxidative stress and lipid peroxidation, stayed within physiologically normal ranges, supporting adequate antioxidative buffering even with slightly higher ROM output. Together with increased milk yield at comparable dry-matter intake, these data point to a metabolic state in which Frontier cows were more effectively oxidizing fatty acids to meet energy demands, without tipping into oxidative damage or inflammation-driven pathology.

CITATIONS

1. Tabor et al., 2025 *J. Dairy Sci.*
2. Bulnes et al., 2025, *J. Dairy Sci.*

Galaxis Frontier

Mechanism of Action: summary of evidence

Galaxis Frontier improves efficiency by coordinating rumen fermentation with host metabolism

1 – Keystone rumen microbes streamline rumen genetics

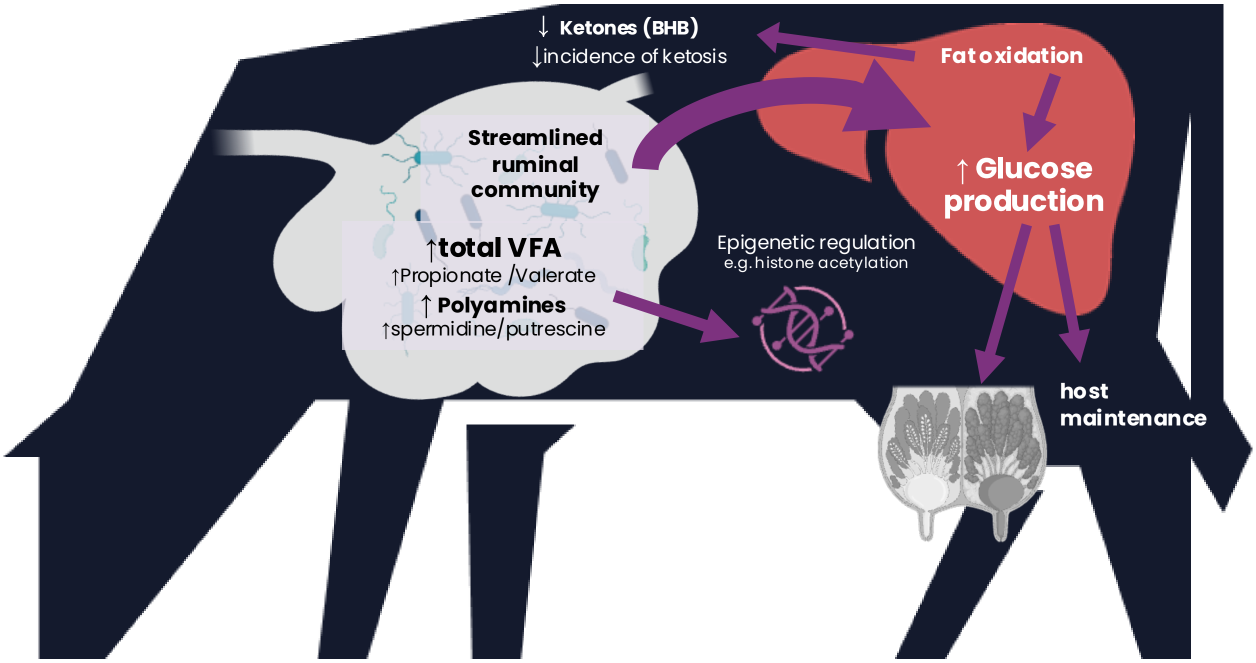
Daily inclusion of live, rumen-native microorganisms shifts rumen genetics towards profiles consistently observed in more feed-efficient cattle. Rather than adding transient organisms, Galaxis Frontier reinforces core microbial functions that stabilize fermentation and improve the efficiency of substrate use across diets.

2 - Streamlined rumen genetics increase energetically favorable metabolites.

This refined microbial network increases propionate and total VFAs—key metabolites in energy metabolism—without altering total-tract digestibility or destabilizing fermentation. The result is greater usable energy availability from the same ration.

3 – Metabolic signals drive systemic efficiency and resilience

Higher propionate supply increases hepatic gluconeogenesis, improving glucose availability during periods of high demand. At the same time, microbial-derived metabolites such as polyamines act as signaling molecules that support cellular function and epigenetic regulation, influencing how tissues allocate energy, manage oxidative load, and maintain function under stress.



Summarized Conceptual Model

Galaxis Frontier supports a streamlined rumen microbial community that shifts fermentation toward greater total VFAs, increased propionate, and polyamine production without altering total-tract digestibility. These metabolites function as both energetic substrates and signaling molecules linking rumen metabolism to host physiology. Increased propionate supports hepatic glucose production and reduces reliance on ketone production during early lactation, while SCFAs and polyamines participate in pathways involved in epigenetic regulation and immune function. Together, these coordinated metabolic signals support improved fatty acid oxidation, host maintenance, and immune readiness—contributing to greater feed efficiency and resilience across the lactation curve.

GF Consistently Improves Feed Efficiency Across 8 independent Academic Trials

Eight independent academic studies were included in the meta-analysis: seven published in peer-reviewed journals and one completed but not yet drafted. All were randomized controlled trials using a covariate-based block design, with milk yield, components, DMI, and feed efficiency measured at the cow level (except Cornell, where intake was measured at the pen level). One of the eight studies evaluated two distinct treatment groups initiated at different stages of lactation; these were analyzed as separate study arms, resulting in nine total comparisons in the meta-analysis. Across trials, treatment duration averaged 20 weeks (range: 16–39), and while one study evaluated Jerseys, all others were conducted in Holsteins.

Feed efficiency improved by an average +0.05 points (range of true effect size = 0.03-0.08, p < 0.01)

Feed efficiency was measured as ECM/DMI in all studies except SDSU, which reported in units of milk/DMI. A leave-one-out sensitivity analysis confirmed the result is consistent across trials – pooled effect sizes from any eight of the nine studies ranged from 0.05 to 0.06 (p < 0.01).

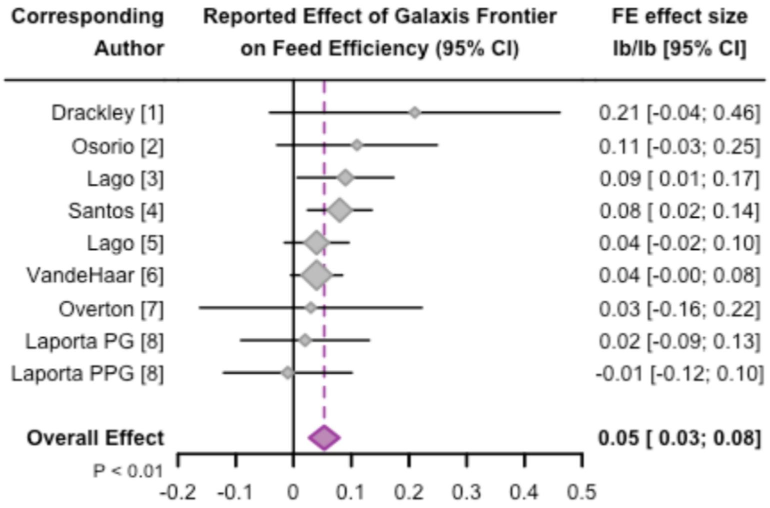


Figure 1. Average of reported effect sizes from studies that measured changes in feed efficiency (milk or ECM / DMI). Diamond size shows weight (inverse of variance).

response	covariate factor	FDR-adj. *p*-value
milk, fat, protein, or ECM yield (lbs)	DIM at enrollment	**<0.01**
	parity; time fed GF; milk covariate (standardized)	>0.19
dry matter intake (lbs)	DIM at enrollment	**<0.05**
	parity; time fed GF; milk covariate (standardized)	>0.64
feed efficiency (ECM/DMI)	DIM at enrollment, parity; time fed GF; milk covariate (standardized)	>0.58

Milk and components yield are greater when Galaxis Frontier is started early in lactation

This analysis tells us that stage of lactation at the start of supplementation—not baseline production, parity, or duration on Galaxis Frontier—**drives much of the variation in response.**

Mixed effect models showed that days in milk (DIM) when Frontier was started explains differences in milk, fat, protein, and energy-corrected milk (ECM) yield, as well as dry matter intake (p < 0.01).

No significant treatment-interaction effects were found for parity, production level, or time on product (all p > 0.05).

Studies enrolling animals <70 DIM showed improvements in production and efficiency[2,3,4,5,8]

- Milk +4.8 lbs (p=0.043)
- Fat +0.22 lbs (p=0.037)
- Protein not significant (p=0.120)
- ECM +5.0 lbs (p=0.049)
- DMI not significant (p=0.211)
- FE (ECM/DMI) +0.06 pts (p<0.01)

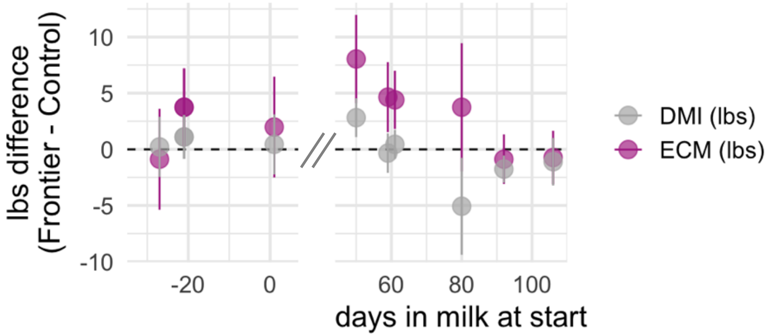


Figure 2. Production (energy-corrected milk) and intake results (dry matter intake) according to DIM at enrollment.

CITATIONS

1. Dickerson et al., 2022, *J. Dairy Sci.* 2. Bulnes et al., 2025, *J. Dairy Sci.* 3. Valldecabres et al., 2025 *J. Dairy Sci.* 4. Marinho et al., 2024, *J. Dairy Sci.*
5. Valldecabres et al., 2022, *J. Dairy Sci.* 6. Goldsmith et al., 2023, *J. Dairy Sci.* 7. *Ferro et al, 2022 ADSA poster.* 8. Tabor et al., 2025 *J. Dairy Sci.*

GF Improves Colostrum Quantity and Quality in Two Independent Controlled Studies

University of Wisconsin-Madison

The study took place from August to December 2023, and utilized 60 dry, pregnant multiparous Holstein dairy cows to evaluate the effects Frontier administered prepartum. The experimental design combined two control groups (CON and PostG, total n=40) into a single "Control" group that did not receive the supplement before calving, which was then compared to the "Frontier" group (Pre+PostG n=20) that did receive the prepartum treatment. Continuous outcome variables related to colostrum quality and calf weight were analyzed using generalized linear mixed models in R software. The models included fixed effects for treatment and block, and random effects for individual cows, adjusting for parity and initial milk yield as covariates. Reported SEM values represent the overall pooled standard error of the mean for the treatment comparisons derived from the mixed model, accounting for all fixed and random effects. Fat % was analyzed and was higher in the treatment group (2.96% vs 3.72%), but was excluded from the manuscript because the colostrum samples were frozen before analysis.

Dr. Jimena Laporta

Table below adapted from metric units in:
***Tabor** et al. Journal of Dairy Science (2025).*

	Control	Frontier	SEM	diff	p-value
# cows	40	20			
parity	2.61	2.67	0.49		
Colostrum (lbs)	11.90	16.40	1.91	4.49	0.06
IgG (g/L)	100	108	6.7	8	0.34
IgG (g)	530.0	788.4	-	258.4	-
Protein (%)	16.50	17.20	0.80	0.70	0.47
Protein (lbs)	1.72	2.71	0.26	0.99	0.03
Calf weight (lbs)	87.30	93.26	2.29	5.95	0.03
NEFA (mM)	0.15	0.09	0.02	-0.06	0.02
BHB (mg/dL)	8.69	6.99	0.72	-1.70	0.05

Fresno State University & Producer's Dairy

This trial was conducted on a commercial 6,500-cow Holstein dairy in California using eight close-up groups from December 2021 through May 2022. Cows entered the close-up pen 21 days before calving due date and were assigned to treatment or control pens based on ear-tag ID (odd = treatment, even = control), with four pens per treatment. Treatment pens received the standard close-up ration with Galaxis Frontier added; control pens received the same ration without supplementation. Colostrum outcomes were assessed from a random subset of approximately 100 mature animals (2nd lactation or greater) per group. Generalized linear models were applied to compare the treatment groups using the least square means ± standard error. Brix was analyzed separately using chi-square and Fisher's exact tests. The standard errors presented in the table are specific to the least squares means (LSM ± SE) for each treatment group comparison, calculated within the linear model framework.

Dr. Kyle Thompson

Table below adapted from metric units in:
***Real**, Logan. MS thesis. Cali State, Fresno, 2022.*

	Control	Frontier	diff	p-value
# cows	111	94		
parity	2.53 ± 73	2.35 ± 48		
Colostrum (lbs)	15.59 ± 1.19	18.01 ± 1.34	2.43	0.03
Fat %	5.08 ± 0.52	6.13 ± 0.45	1.05	0.007
Fat (lbs)	0.79 ± 0.09	1.12 ± 0.13	0.33	0.0013
Protein %	14.34 ± 0.28	14.68 ± 0.3	0.34	0.56
Protein (lbs)	2.47 ± 0.4	2.8 ± 2.14	0.33	0.28
IgG (g/L)	85.88 ± 3.82	84.8 ± 3.08	-1.1	0.88
IgG (g)	611 ± 39	665 ± 44	54	0.35
Brix (refractometer)	22.49 ± 0.29	23.21 ± 0.30	0.72	0.23

Galaxis Frontier

Commercial validation of production response

COMMERCIAL TRIALS. 64,867 Trial Cows on 31 Dairies (182,700 Total Head)

At each commercial trial site, matched pens were selected based on parity distribution, days in milk (DIM), and baseline milk production. Pens were then randomly assigned to either the control group (farm's standard TMR) or the treatment group (standard TMR plus 5 g/cow/day of Galaxis® Frontier). Pens remained open throughout the study, allowing continuous enrollment as new cows entered; individual cow–level data were tracked through daily automated exports, enabling assignment of time on product for each animal.

To estimate the effect of Frontier on milk and component production, we fit linear mixed-effects models of the form:

$$\text{response}_{ij} = \text{time\_on\_product}_i + \text{treatment}_i + (\text{treatment} \times \text{time})_i + \text{lactation group}_i + \text{starting DIM}_i + \text{baseline production}_i + \text{random}(\text{cow}_j)$$

where i denotes cows and j denotes repeated records. The random cow intercept accounted for within-cow correlation over time.

For each farm, we report the baseline-corrected least squares mean (LSM) difference between treatment and control cows for milk yield, ECM, and fat %, restricted to **animals enrolled before peak milk** and evaluated during the **final weeks on product**. Only time windows with sufficient sample size to detect a ≥3 lb treatment difference (typically ≥100 cows per group) were included.

These farm-level estimates provide the input values for the meta-analysis summarized in the first row of the table below.

Farm Code	Weeks on product	State	Breed	Milk Improvement (lbs)	ECM Improvement (lbs)*	Fat % Improvement*	Avg group size
Meta Analysis	**23 weeks**			**4.01** **($p < 0.001$)**	**4.82** **($p < 0.001$)**	**0.08%** **($p = 0.002$)**	**825**
CAJ03	25	CA	Jersey	1.28	3.64	0.29%	910
CAH02	12	CA	Holstein	1.80	-	-	300
CAJ01	20	CA	Jersey	1.80	2.80	0.00%	320
WIH05	24	WI	Holstein	1.90	6.50	0.07%	1540
CAJ04	25	CA	Jersey	2.00	4.00	0.15%	970
CAH03	13	CA	Holstein	2.20	-	-	745
CAH01	20	CA	Holstein	2.42	4.89	0.22%	1630
CAH04	25	CA	Holstein	2.80	-	-	150
CAJ02	17	CA	Jersey	2.82	5.51	0.18%	910
IDH02	24	ID	Holstein	2.92	3.55	0.17%	1045
SDX01	29	SD	J/X	3.10	-	-	1640
CAJ05	20	CA	Jersey	3.10	6.20	0.08	525
CAH09	22	CA	Holstein	3.33	3.86	-0.10%	515
MIH02	25	MI	Holstein	3.50	-	-	530
WAH02	20	WA	Holstein	3.82	4.69	0.10%	2050
CAH07	22	CA	Holstein	4.00	5.00	0.01%	400
OHH01	20	OH	Holstein	4.10	4.75	0.04%	445
WIH04	23	WI	Holstein	4.30	7.75	0.12%	365
IDH01	26	ID	Holstein	4.67	-0.22	-0.03%	1135
IDJ01	26	ID	Jersey	4.88	-	-	3500
CAH05	25	CA	Holstein	5.00	-	-	680
CAX01	29	CA	H/J/X	5.00	-	-	650
WIH02	28	WI	Holstein	5.00	3.80	-0.04	540
MNH01	21	MN	Holstein	5.20	-	-	525
CAH06	24	CA	Holstein	5.50	5.6	0.13%	680
CAH11	24	CA	Holstein	5.50	-	-	700
WAH01	21	WA	Holstein	5.75	4.00	0.05%	600
CAH10	23	CA	Holstein	5.79	-	-	180
CAX02	27	CA	Crosses	5.80	6.55	0.06	460
MIH01	25	MI	Holstein	6.25	-	-	550
IDH03	29	ID	Holstein	9.70	8.80	0.03	400

**Component data (ECM and fat) available only at sites with cow-level test-day records*

Galaxis Frontier

Effects on culling risk and survivability

Summary: Supplementing cows with a live consortium of rumen-native microbes (Galaxis® Frontier) improved health and survivability across 21 controlled commercial trials.

Supplemented cows were less likely to be culled, regardless of geographical region or breed.

Commercial Dairy Trial	Weeks on product	State	Breeds	Avg DIM at enroll	Avg DIM at cull	Avg LACT at enroll	Avg LACT at cull	Hazard Ratio [95% CI]
WAH01	24	WA	Holstein	125	305	1.97	2.44	0.71 [0.42; 1.19]
SDX01	34	SD	J/X	118	222	2.75	3.26	0.74 [0.58; 0.94]
MIH02	22	MI	Holstein	159	282	2.77	3.23	0.75 [0.51; 1.12]
CAX01	29	CA	H/J/X	97	232	2.71	3.14	0.79 [0.54; 1.16]
OHH01	28	OH	Holstein	101	238	3.48	4.26	0.80 [0.50; 1.30]
CAJ04	34	CA	Jersey	65	202	3.41	3.73	0.81 [0.64; 1.04]
WIH02	36	WI	Holstein	61	260	3.29	3.73	0.82 [0.61; 1.11]
CAH07	32	CA	Holstein	93	219	2.23	2.52	0.86 [0.52; 1.41]
CAJ02	21	CA	Jersey	72	212	2.56	3.34	0.88 [0.59; 1.32]
WIH05	27	WI	Holstein	120	202	2.21	2.81	0.90 [0.68; 1.19]
MNH01	24	MN	Holstein	140	236	3.16	3.85	0.90 [0.59; 1.38]
OHH02	28	OH	Holstein	89	250	3.23	3.74	0.91 [0.69; 1.21]
MIH01	29	MI	Holstein	123	260	4.08	4.58	0.91 [0.69; 1.21]
CAJ05	28	CA	Jersey	101	228	3.74	4.27	0.92 [0.61; 1.38]
WIH04	43	WI	Holstein	99	210	2.63	3.06	0.93 [0.58; 1.49]
WAH02	26	WA	Holstein	123	201	2.94	3.47	0.97 [0.72; 1.31]
CAH01	26	CA	Holstein	64	162	1.90	2.34	0.98 [0.70; 1.37]
CAH11	36	CA	Holstein	40	221	2.94	3.28	1.00 [0.82; 1.23]
IDH02	26	ID	Holstein	116	220	2.83	3.62	1.08 [0.83; 1.41]
CAX02	34	CA	Tricrosses	91	222	3.13	3.76	1.09 [0.80; 1.50]
IDH01	26	ID	Holstein	116	240	2.92	3.27	1.20 [0.94; 1.54]
Overall Effect								**0.92 [0.86; 0.98]**
Prediction interval								[0.85; 0.99]
P = 0.01								

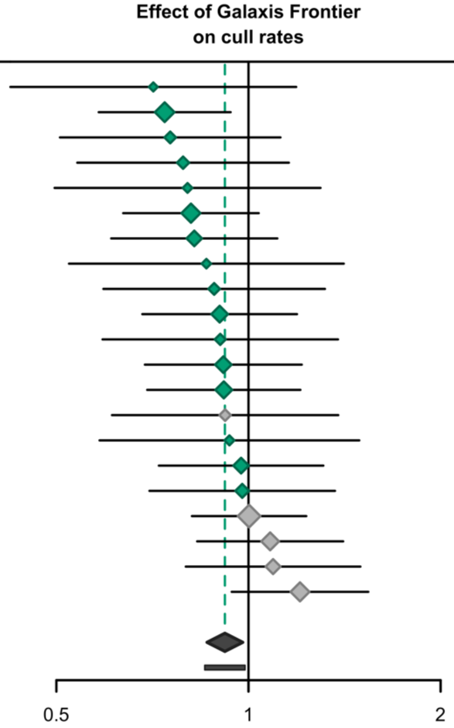


Figure 1. **Hazard ratios for culling across 21 commercial dairy trials.** Values less than 1 indicate a lower daily risk of culling in the Galaxis® Frontier-treated group compared to control. Percent cull rate reduction is calculated as *(1 – HR) × 100%*. HPAI (bird flu) outbreaks occurred in 5 trials (gray diamonds) and increased non-specific culling; those trials not affected by disease outbreak (green diamonds) observed a **14.6% reduction in culls (p<0.001) in cows fed Galaxis Frontier**.

At a single trial site with appropriate record tracking, we observed significantly lower transition-related health events, including ketosis and metritis, indicating improved metabolism & health.

	1-HR (% reduction)	treatment p-value	total cow counts Control	total cow counts Frontier	event counts Control	event counts Frontier
All Transition Events	**28.4% (9.9–43.1%)**	**0.004**	**2193**	**2043**	**192**	**120**
Metritis	25.8% (2.8–43.3%)	0.029	2193	2043	130	90
Ketosis	48.0% (5.7–71.3%)	0.025	2193	2043	41	15
Milk Fever	31.7% (-17.5–60.3%)	0.161	2193	2043	38	20
All Non-Transition Events	**3.0% (-8.3–13.2%)**	**0.584**	**3221**	**3084**	**668**	**624**
Mastitis	5.7% (-7.7–17.5%)	0.386	3221	3084	466	424
Lame	7.4% (-12.9–24.0%)	0.447	3221	3084	222	187
Diarrhea	59.4% (-30.2–87.3%)	0.111	3221	3084	10	4
Blood in milk	-10.0% (-104.3–40.7%)	0.762	3221	3084	20	22
Infection	-16.6% (-93.9–29.9%)	0.553	3221	3084	29	32

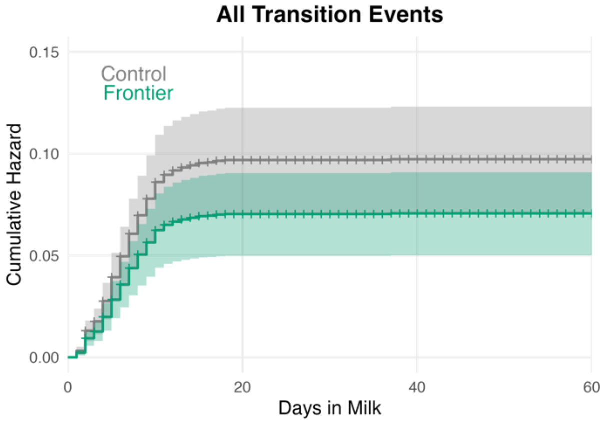


Figure 2. **Incidence rate of common events tracked at CAH01.** Cox proportional hazards models adjusted for parity (lactation group). Hazard ratios (HR) compare the risk of an event occurring in Galaxis Frontier-treated groups to the risk in the control group; HR < 1 indicates reduced risk in the Frontier group. Cows fed Galaxis Frontier had a **28.4% lower risk (p=0.004) of metabolic disease** in the first 60 days in milk.