Alternativas Alimentares Para Modular a Microbiota Intestinal de Cães e Gatos



XV Congresso CBNA Pet

Dr. Maria R. C. de Godoy
Assistant Professor
Department of Animal Sciences

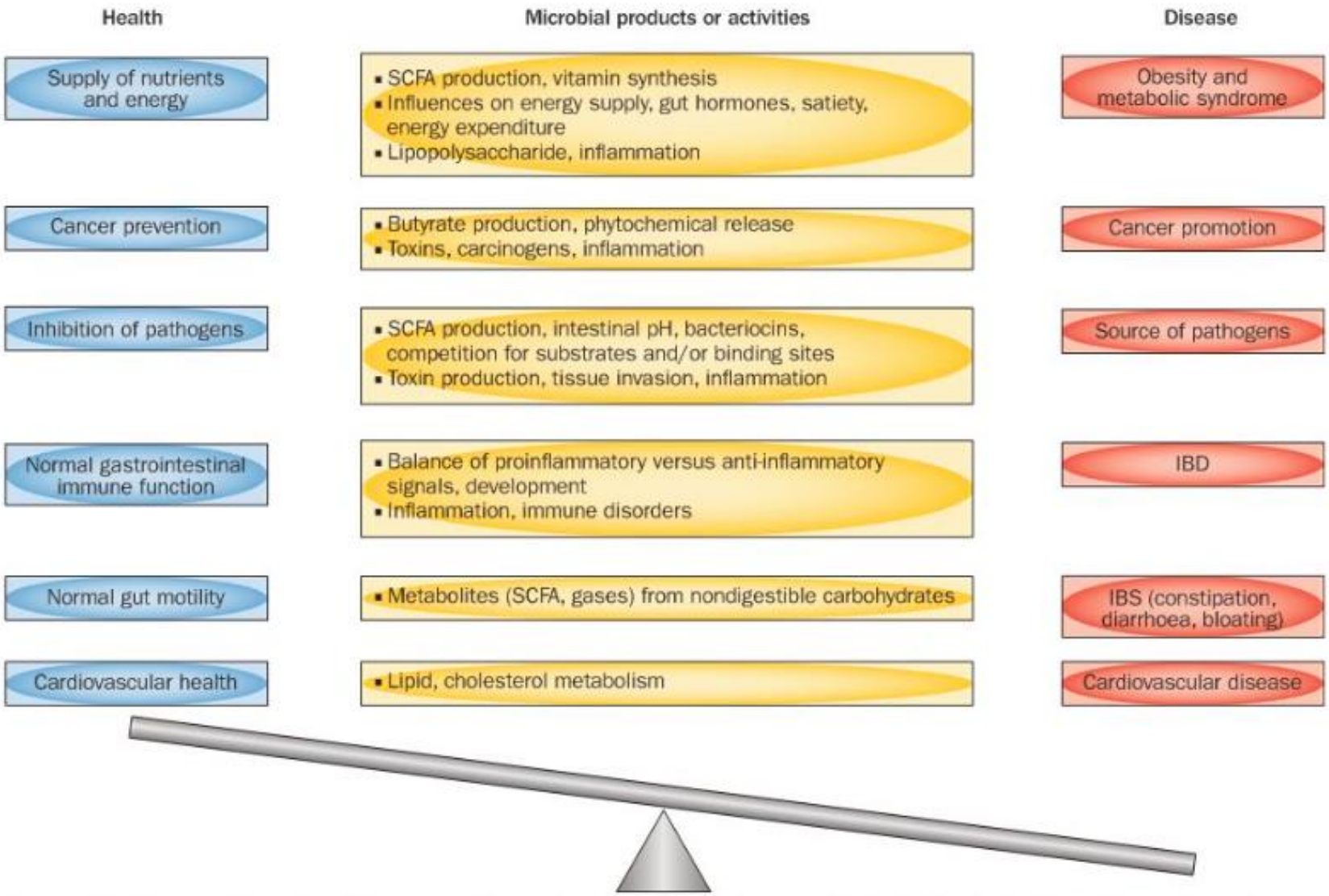
ILLINOIS
UNIVERSITY OF ILLINOIS AT URBANA-CHAMPAIGN

Função da Microbiota Gastrointestinal

- Barreira contra patógenos
- Ajuda em processos digestórios
  - Fermentação de fibras dietéticas
- Fornece nutrientes para enterócitos e colonócitos
- Ajuda no desenvolvimento do sistema imunológico



Função da Microbiota Gastrointestinal



Flint et al., 2012

Função da Microbiota Gastrointestinal

- Pessoas e animais saudáveis
  - Microbiota estável
  - Resistente a alterações
  - Modulação transitória

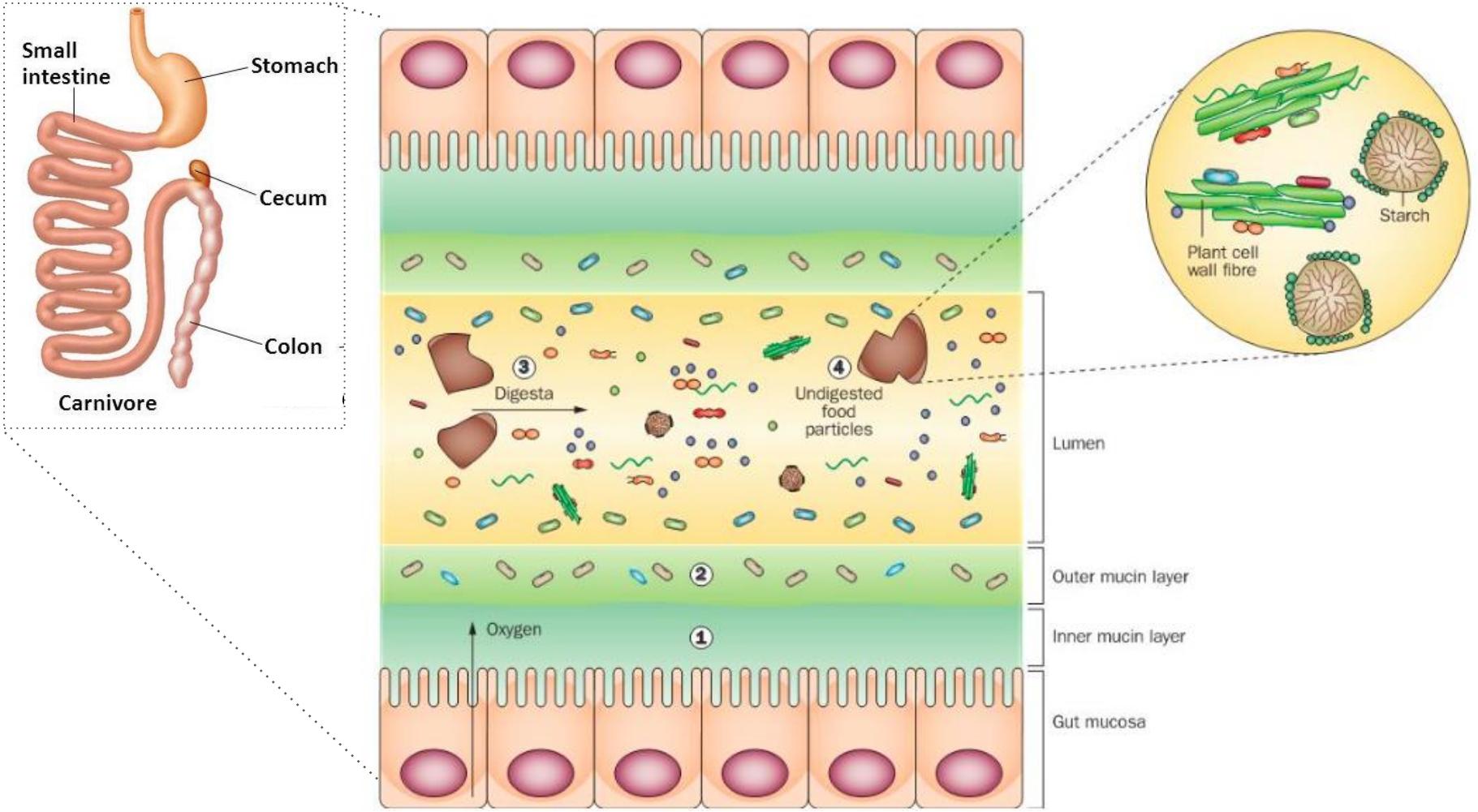


Dieta e a Microbiota Gastrointestinal

- Nutrição
  - Fator que pode alterar a composição microbiana a curto e longo prazo
  - Grupo de animais responsivos e não-responsivos a diferentes tratamentos

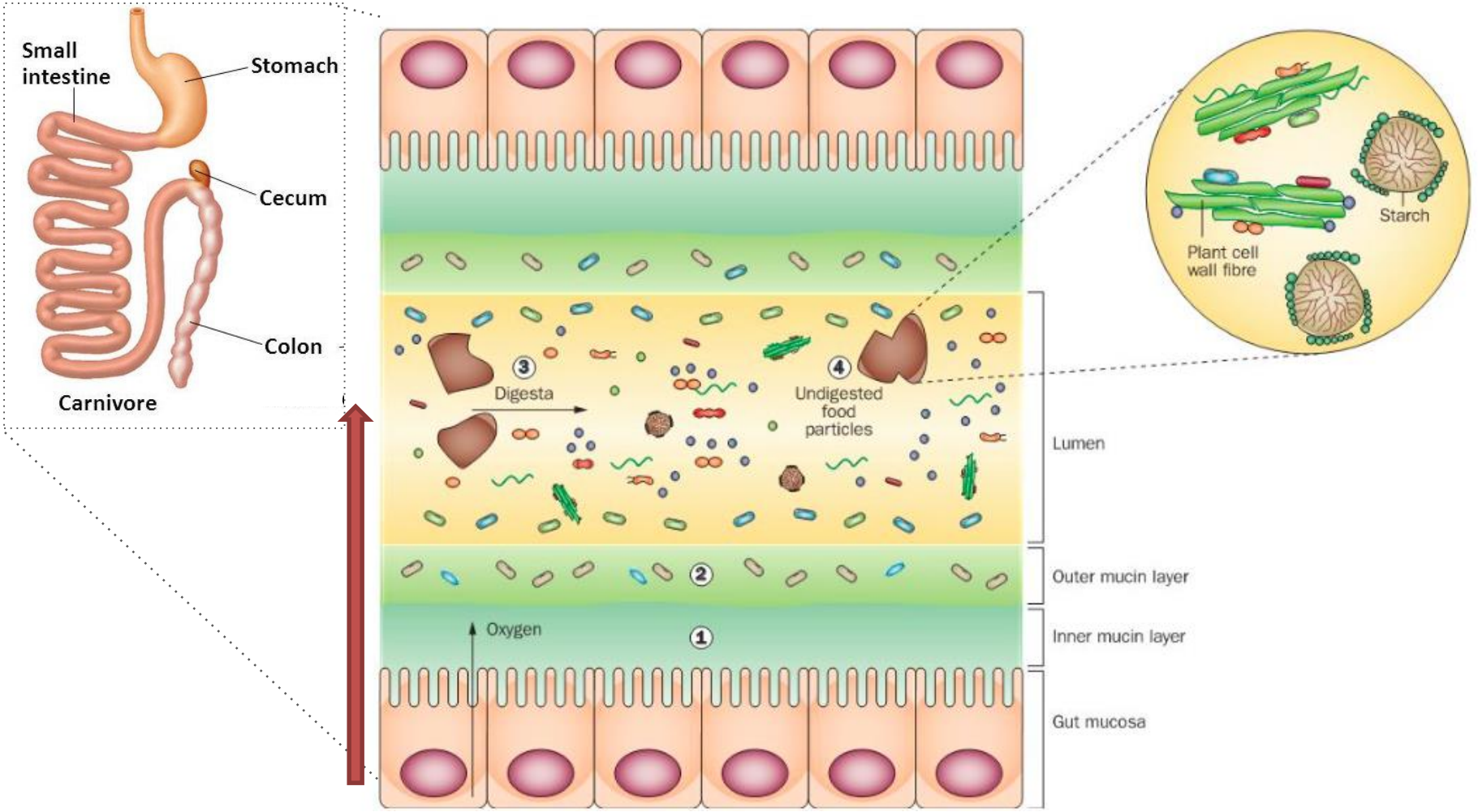


O Ambiente Gastrointestinal



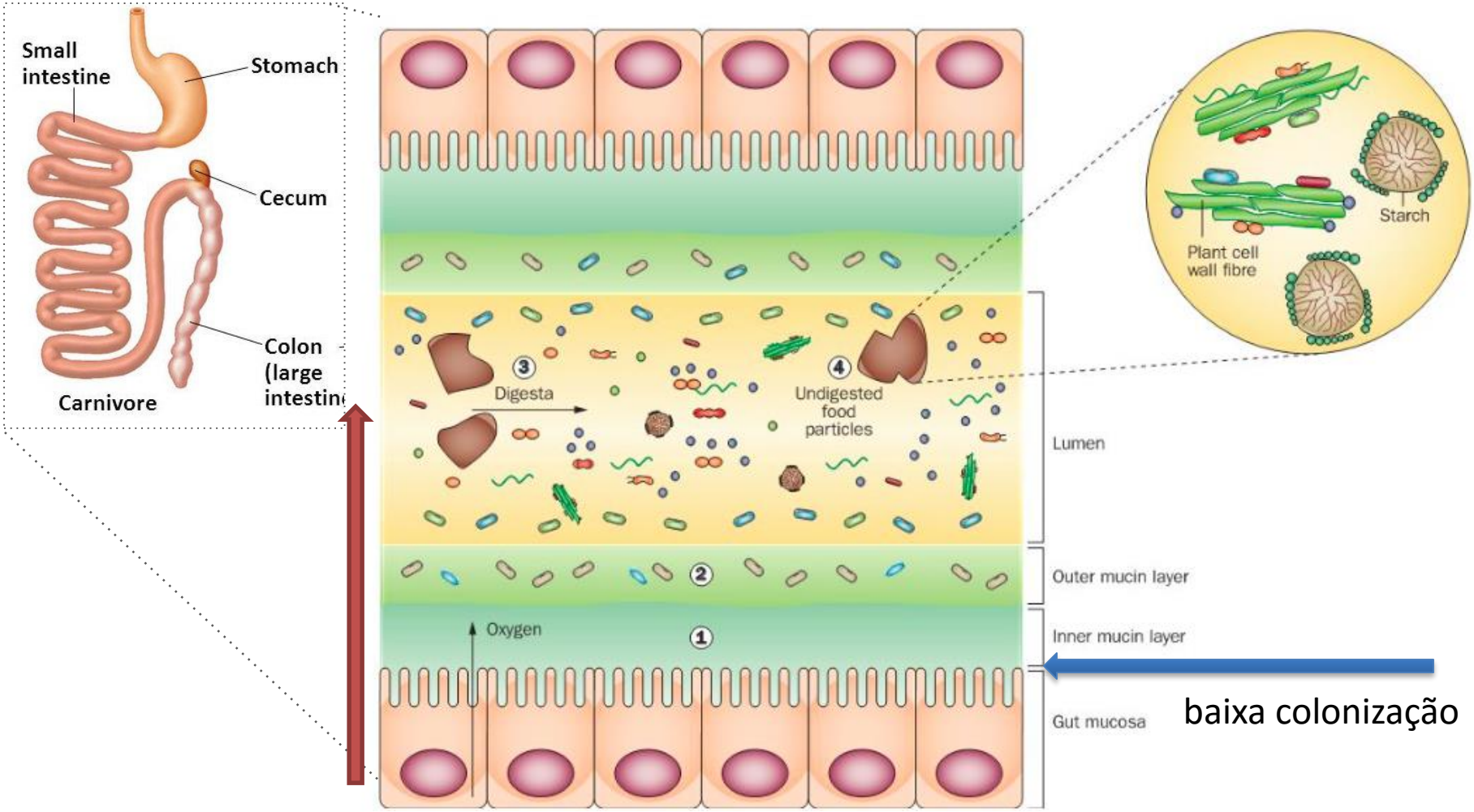
Adapted from Flint et al., 2012

O Ambiente Gastrointestinal



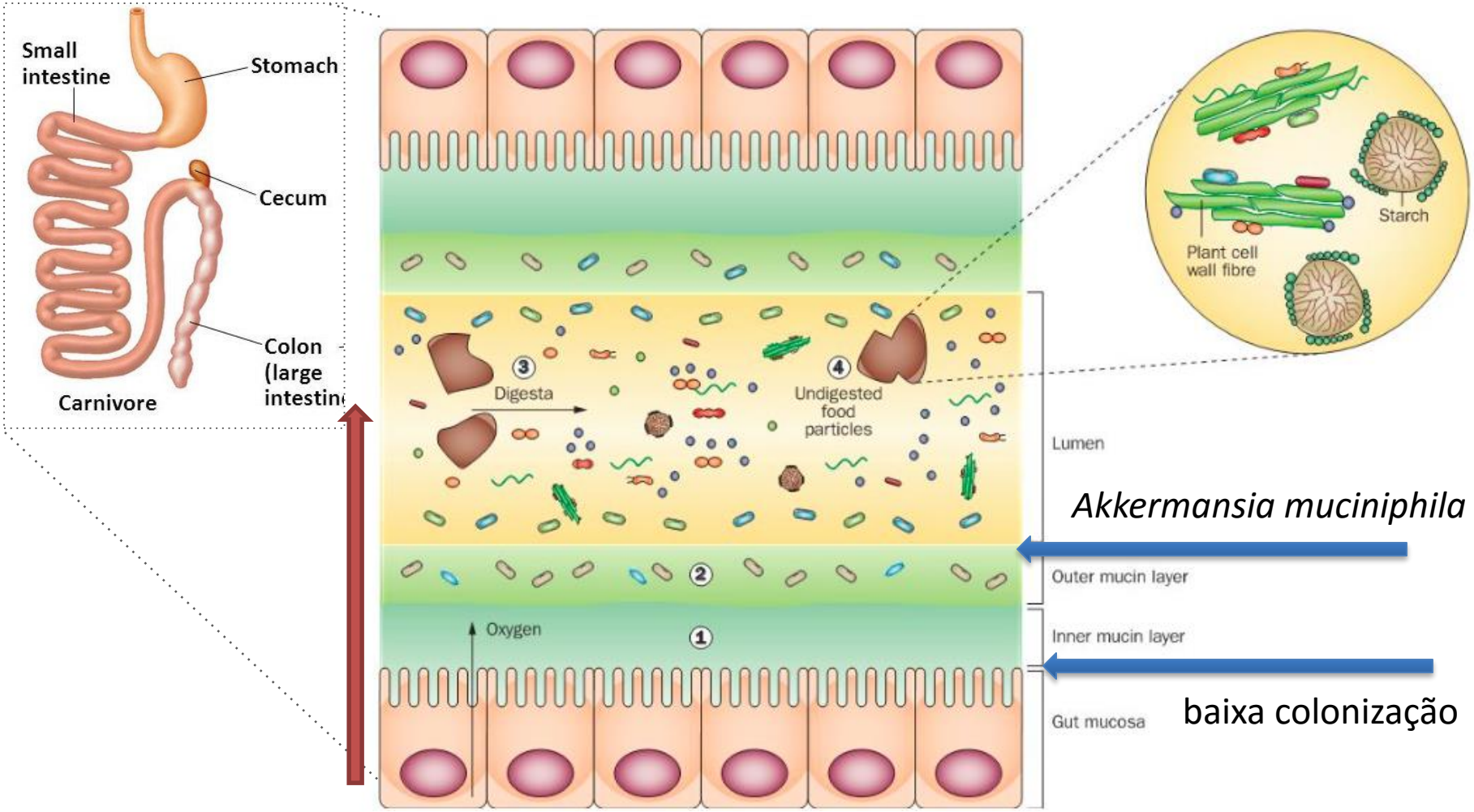
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O Ambiente Gastrointestinal



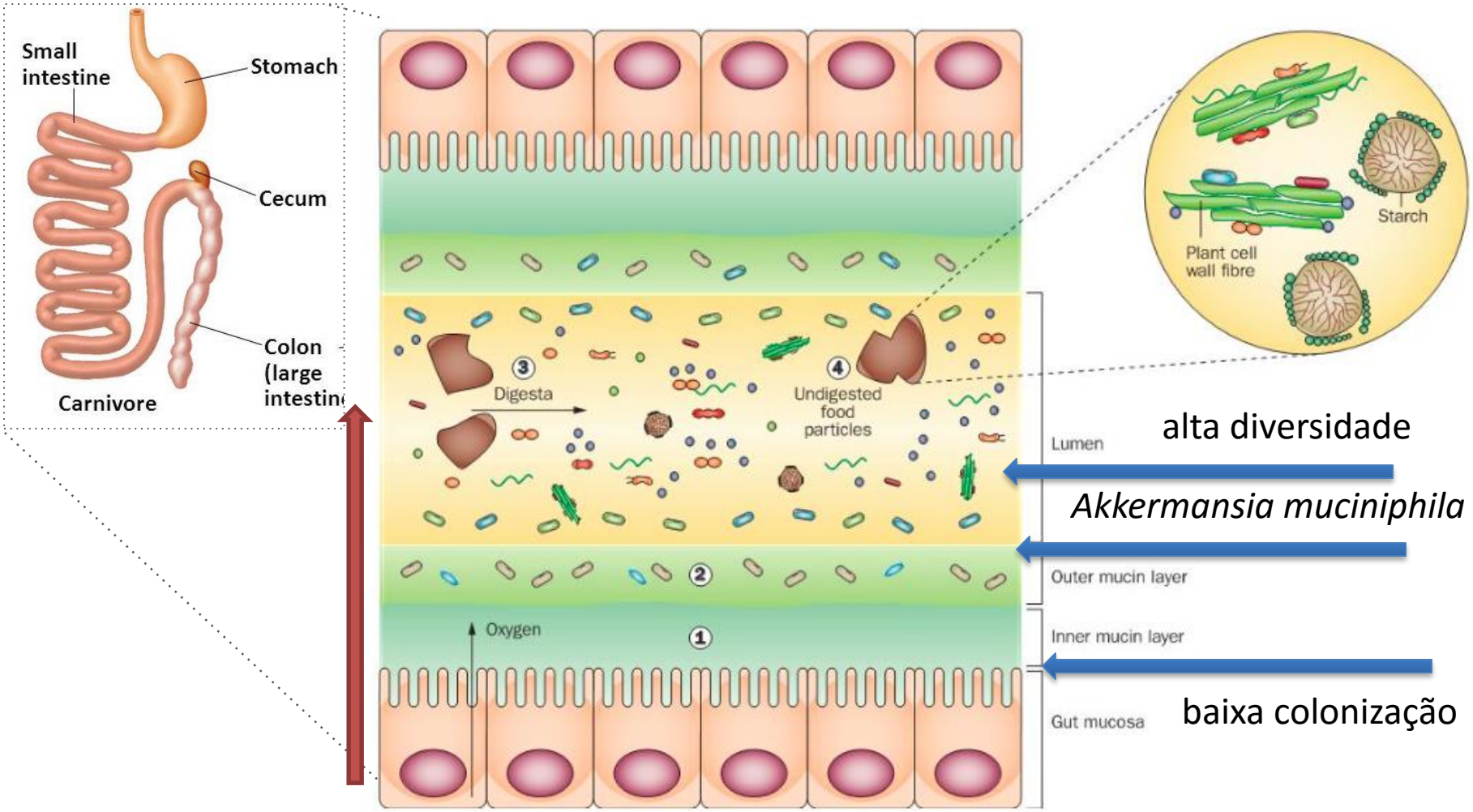
Adapted from Flint et al., 2012

O Ambiente Gastrointestinal



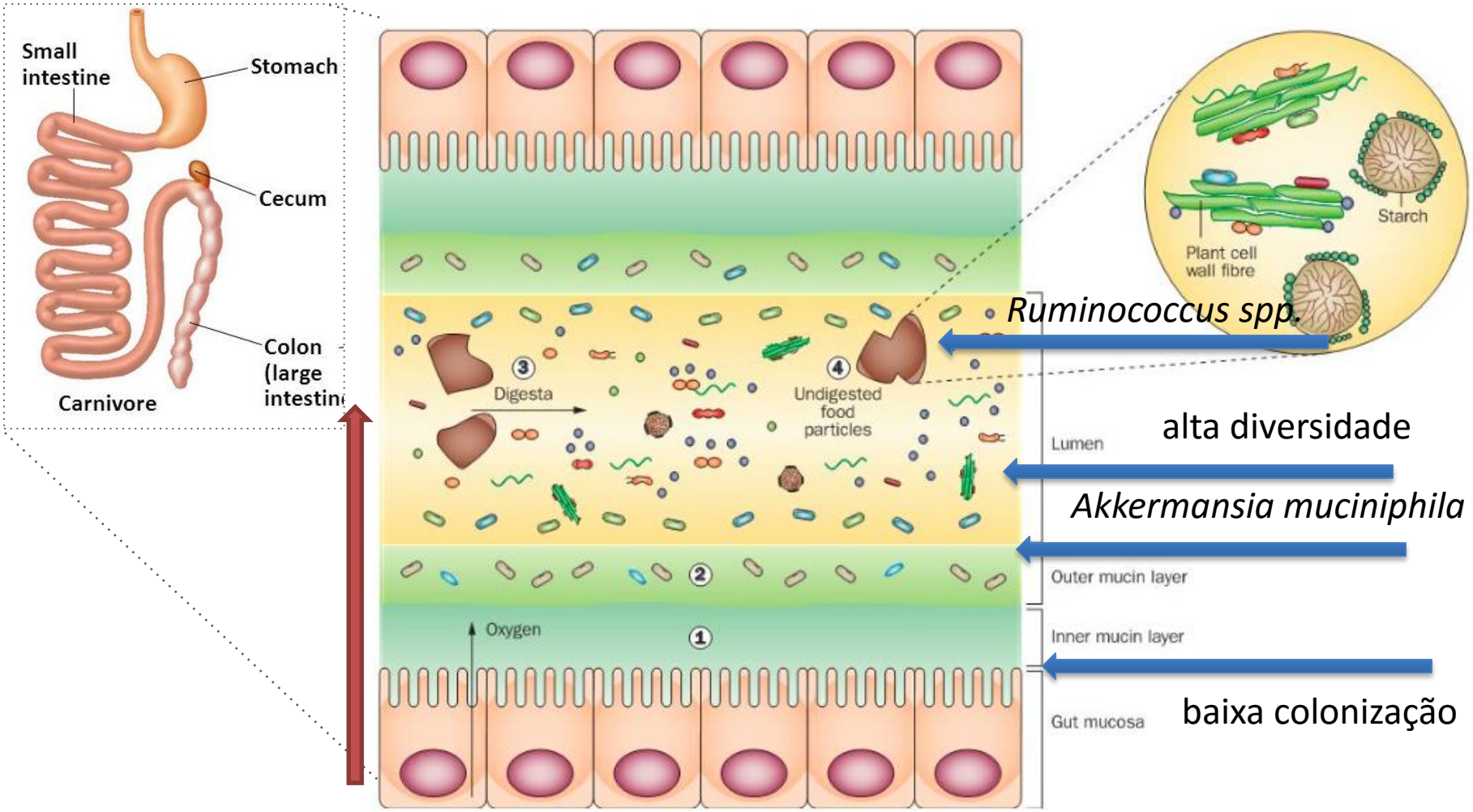
Adapted from Flint et al., 2012

O Ambiente Gastrointestinal



Adapted from Flint et al., 2012

O Ambiente Gastrointestinal



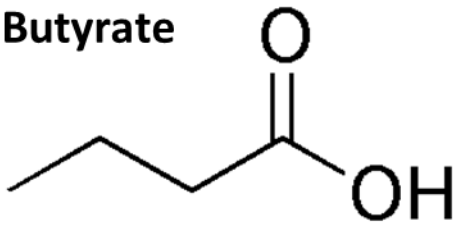
Adapted from Flint et al., 2012

Metabolismo Microbiano

- Substratos
  - Carboidratos
    - Fibras
    - Amidos resistentes
    - Oligossacarídeos
    - Açucares não absorvidos
      - Alcoóis de açucar
  - Proteínas dietéticas
  - Secreções do trato gastrointestinal
    - Muco, células descamadas, etc.

Metabolismo Microbiano

- Produtos da fermentação de carboidratos
  - Ácidos graxos de cadeia curta
  - CO_2, H_2, and CH_4

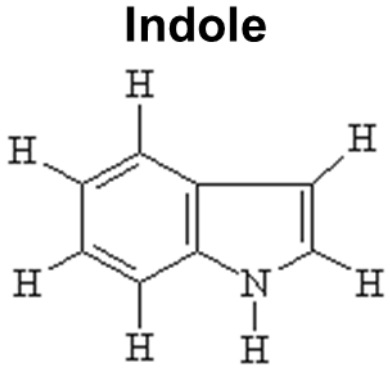


- Importância metabólica
  - Fonte de energia para o hospedeiro
  - ↓ pH luminal
  - Alteração de electrólitos e absorção mineral

Binder, 2010

Metabolismo Microbiano

- Produtos da fermentação de proteína
  - Ácidos graxos de cadeia ramificada
  - Fenóis and indols
  - Amônia
  - Compostos contendo enxofre



- Importância metabólica
  - Odor fecal
  - Associação com doenças TGI

Dieta e Modulação da Microbiota

- Principais estratégias
  - Fibras dietéticas
  - Pré- and probióticos
  - Produtos de levedura
  - Outros ingredientes funcionais

- Principal alvo
  - Saúde do trato gastrointestinal (colon)
  - ↑ fermentação de carboidratos
    - ↓ fermentação proteíca

Efeitos de Fibras Dietéticas e Prebióticos

- Dependente do tipo e dose
- Qualidade fecal
- Produção de ácidos graxos e pH fecal
- Alterações modestas/ médias no microbiome TGI

Dieta-Microbioma em Cães e Gatos

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Phylogenetic Characterization of Fecal Microbial Communities of Dogs Fed Diets with or without Supplemental Dietary Fiber Using 454 Pyrosequencing

Ingmar S. Middelbos[1], Brittany M. Vester Boler[1], Ani Qu[1,3], Bryan A. White[1,2,3], Kelly S. Swanson[1,2,4], George C. Fahey, Jr.[1,2]*

1 Department of Animal Sciences, University of Illinois, Urbana, Illinois, United States of America, 2 Division of Nutritional Sciences, University of Illinois, Urbana, Illinois, United States of America, 3 Institute for Genomic Biology, University of Illinois, Urbana, Illinois, United States of America, 4 Department of Veterinary Clinical Medicine, University of Illinois, Urbana, Illinois, United States of America

Abstract

Background: Dogs suffer from many of the same maladies a… knowledge of the canine microbiome is incomplete. Thi… phylogenetically characterize hindgut microbiome in dogs… community structure.

Principal Findings: Six healthy adult dogs were used in a cros… beet pulp-supplemented (7.5%) diet were fed. Fecal DNA wa… 16S rDNA gene amplified using primers suitable for 454-pyros… sequence subsamples of individual and pooled DNA samples… length of 141 nt. Individual samples contained approximately … – 28% of reads) and *Bacteroidetes* (31 – 34% of reads) being … *Fusobacteria* and increased *Firmicutes*, but these changes we… that structure of the gut microbiome was affected by diet and…

Conclusions: Our data suggest three co-dominant bacterial… amount of dietary fiber changed the structure of the gut… characterize the healthy canine gut microbiome using pyrose… dietary interventions for microbiome-associated diseases.

Citation: Middelbos IS, Vester Boler BM, Qu A, White BA, Swanson KS, et al. (20… Diets with or without Supplemental Dietary Fiber Using 454 Pyrosequencing. PL…

OPEN ACCESS Freely available online — PLOS ONE

Effects of Dietary Cooked Navy Bean on the Fecal Microbiome of Healthy Companion Dogs

Katherine R. Kerr[1], Genevieve Forster[2], Scot E. Dowd[3], Elizabeth P. Ryan[2], Kelly S. Swanson[1]*

1 Division of Nutritional Sciences and Department of Animal Sciences, University of Illinois, Urbana, Illinois, United States of America, 2 Department of Environmental and Radiological Health Sciences, Colorado State University, Fort Collins, Colorado, United States of America, 3 MR DNA (Molecular Research LP), Shallowater, Texas, United States of America

Abstract

Background: Cooked bean powders are a promising novel protein and fiber source for dogs, which have demonstrated potential to alter microbial composition and function for chronic disease control and prevention. This study aimed to determine the impact of cooked navy bean powder fed as a staple food ingredient on the fecal microbiome of healthy adult pet dogs.

Methodology/Principal Findings: Fecal samples from healthy dogs prior to dietary control and after 4 wk of dietary treatment with macro- and micronutrient matched diets containing either 0 or 25% cooked navy beans (n = 11 and n = 10, respectively) were analyzed by 454-pyrosequencing of the 16S rRNA gene. There were few differences between dogs fed the control and navy bean diets after 4 wk of treatment. These data indicate that there were no major effects of navy bean inclusion on microbial populations. However, significant differences due to dietary intervention onto both research diets were observed (i.e., microbial populations at baseline versus 4 wk of intervention with 0 or 25% navy bean diets). After 4 wk of dietary intervention on either control or navy bean diet, the Phylum Firmicutes was increased and the Phyla Actinobacteria and Fusobacteria were decreased compared to baseline.

Conclusions: No negative alterations of microbial populations occurred following cooked navy bean intake in dogs, indicating that bean powders may be a viable protein and fiber source for commercial pet foods. The highly variable microbial populations observed in these healthy adult pet dogs at baseline is one potential reason for the difficulty to detect alterations in microbial populations following dietary changes. Given the potential physiological benefits of bean intake in humans and dogs, further evaluation of the impacts of cooked navy bean intake on fecal microbial populations with higher power or more sensitive methods are warranted.

Citation: Kerr KR, Forster G, Dowd SE, Ryan EP, Swanson KS (2013) Effects of Dietary Cooked Navy Bean on the Fecal Microbiome of Healthy Companion Dogs. PLoS ONE 8(9): e74998. doi:10.1371/journal.pone.0074998

RESEARCH ARTICLE — FEMS

Faecal microbiota in lean and obese dogs

Stefanie Handl[1,2], Alexander J. German[3], Shelley L. Holden[3], Scot E. Dowd[4], Jörg M. Steiner[2], Romy M. Heilmann[2], Ryan W. Grant[5], Kelly S. Swanson[5,6] & Jan S. Suchodolski[2]

[1]Institute of Animal Nutrition and Functional Plant Compounds, University of Veterinary Medicine Vienna, Vienna, Austria; [2]Gastrointestinal Laboratory, Texas A&M University, College Station, TX, USA; [3]Department of Obesity and Endocrinology, Institute of Ageing and Chronic Disease, University of Liverpool, Liverpool, UK; [4]MR DNA (Molecular Research), Shallowater, TX, USA; [5]Division of Nutritional Sciences, University of Illinois, Urbana, IL, USA; and [6]Department of Animal Sciences, University of Illinois, Urbana, IL, USA

…shown obesity to be associated with changes in intestinal …besity is common in dogs, limited information is available …intestinal microbiota. The aim of this study was to inves… …tions in the intestinal microbiota may be associated with …g 16S rRNA gene pyrosequencing and quantitative real… …ated the composition of the faecal microbiota in 22 lean …gs, as well as in five research dogs fed *ad libitum* and four …g as lean controls. *Firmicutes*, *Fusobacteria* and *Actinobacte*… …hinant bacterial phyla. The phylum *Actinobacteria* and the …re significantly more abundant in the obese pet dogs. …les significantly increased under *ad libitum* feeding in the …e intestinal microbiota is highly diverse and shows consid… …al variation. In the pet dogs, influence on the intestinal …ody condition, like age, breed, diet or lifestyle, might have …obesity. The study population of research dogs was small, …required before the role of the intestinal microbiota in …ified.

MicrobiologyOpen — Open Access

ORIGINAL RESEARCH

Dietary format alters fecal bacterial populations in the domestic cat (*Felis catus*)

Emma N. Bermingham[1], Wayne Young[1], Sandra Kittelmann[2], Katherine R. Kerr[3], Kelly S. Swanson[3,4], Nicole C. Roy[1,5] & David G. Thomas[6]

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Keywords: Feline, feca… throughput…

Correspon… Emma N. B… Grasslands… 11008, Pal… Zealand. Tel… +64 6 351… bermingha…

Funding by… No funding…

Received: 1… 2012; Acce…

Microbiol…

doi: 10.100…

British Journal of Nutrition (2013), **109**, 1637–1646 — doi:10.1017/S0007114512003479
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The gut microbiome of kittens is affected by dietary protein:carbohydrate ratio and associated with blood metabolite and hormone concentrations

Seema Hooda[1], Brittany M. Vester Boler[1], Katherine R. Kerr[1], Scot E. Dowd[2] and Kelly S. Swanson[1]*

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(*Submitted 24 February 2012 – Final revision received 28 May 2012 – Accepted 5 July 2012 – First published online 31 August 2012*)

Abstract

High-protein, low-carbohydrate (HPLC) diets are common in cats, but their effect on the gut microbiome has been ignored. The present study was conducted to test the effects of dietary protein:carbohydrate ratio on the gut microbiota of growing kittens. Male domestic short-hair kittens were raised by mothers fed moderate-protein, moderate-carbohydrate (MPMC; *n* 7) or HPLC (*n* 7) diets, and then weaned at 8 weeks onto the same diet. Fresh faeces were collected at 8, 12 and 16 weeks; DNA was extracted, followed by amplification of the V4–V6 region of the 16S rRNA gene using 454 pyrosequencing. A total of 384 588 sequences (average of 9374 per sample) were generated. Dual hierarchical clustering indicated distinct clustering based on the protein:carbohydrate ratio regardless of age. The protein:carbohydrate ratio affected faecal bacteria. Faecal Actinobacteria were greater ($P<0·05$) and Fusobacteria were lower ($P<0·05$) in MPMC-fed kittens. …terns, while …incipal com… …he clustering …ghrelin with …obacillaceae. …ons between

ORIGINAL ARTICLE

Phylogenetic and gene-cent… canine intestinal microbiome reveals similarities with humans and mice

Kelly S Swanson[1,2,3], Scot E Dowd[4], Jan S Suchodolski[5], Ingmar S Middelbos[1], Brittany M Vester[1], Kathleen A Barry[1], Karen E Nelson[6], Manolito Torralba[6], Bernard Henrissat[7], Pedro M Coutinho[7], Isaac KO Cann[1,8], Bryan A White[1,2,8] and George C Fahey Jr[1,2]

[1]*Department of Animal Sciences, University of Illinois, Urbana, IL, USA;* [2]*Division of Nutritional Sciences, University of Illinois, Urbana, IL, USA;* [3]*Department of Veterinary Clinical Medicine, University of Illinois, Urbana, IL, USA;* [4]*Research and Testing Laboratory and Medical Biofilm Research Institute, Lubbock, TX, USA;* [5]*Gastrointestinal Laboratory, Texas A&M University, College Station, TX, USA;* [6]*J. Craig Venter Institute, Rockville, MD, USA;* [7]*Architecture et Fonction des Macromolecules Biologiques, Universites Aix-Marseille I and II, Marseille, France and* [8]*The Institute for Genomic Biology, University of Illinois, Urbana, IL, USA*

This study is the first to use a metagenomics approach to characterize the phylogeny and functional capacity of the canine gastrointestinal microbiome. Six healthy adult dogs were used in a crossover design and fed a low-fiber control diet (K9C) or one containing 7.5% beet pulp (K9BP). Pooled fecal DNA samples from each treatment were subjected to 454 pyrosequencing, generating 503 280 (K9C) and 505 061 (K9BP) sequences. Dominant bacterial phyla included the Bacteroidetes/Chlorobi group and Firmicutes, both of which comprised ~35% of all sequences, followed by Proteobacteria (13–15%) and Fusobacteria (7–8%). K9C had a greater percentage of Bacteroidetes, Fusobacteria and Proteobacteria, whereas K9BP had greater proportions of the Bacteroidetes/Chlorobi group and Firmicutes. Archaea were not altered by diet and represented ~1% of all sequences. All archaea were members of Crenarchaeota and Euryarchaeota, with methanogens being the most abundant and diverse. Three fungi phylotypes were present in K9C, but none in K9BP. Less than 0.4% of sequences were of viral origin, with >99% of them associated with bacteriophages. Primary functional categories were not significantly affected by diet and were associated with carbohydrates; protein metabolism; DNA metabolism; cofactors, vitamins, prosthetic groups and pigments; amino acids and derivatives; cell wall and capsule; and virulence. Hierarchical clustering of several gastrointestinal metagenomes demonstrated phylogenetic and metabolic similarity between dogs, humans and mice. More research is required to provide deeper coverage of the canine microbiome, evaluate effects of age, genetics or environment on its composition and activity, and identify its role in gastrointestinal disease.

The ISME Journal (2011) 5, 639–649; doi:10.1038/ismej.2010.162; published online 21 October 2010
Subject Category: microbe–microbe and microbe–host interactions
Keywords: canine gut; gastrointestinal bacteria; metagenomics; pyrosequencing

FEMS

…healthy adult dogs fed raw …t inulin or yeast cell wall extracts as assessed by 454 pyrosequencing

Alison N. Beloshapka[1], Scot E. Dowd[2], Jan S. Suchodolski[3], Jörg M. Steiner[3], Laura Duclos[4] & Kelly S. Swanson[1,5,6]

[1]Department of Animal Sciences, University of Illinois, Urbana, IL, USA; [2]Research and Testing Laboratory, Lubbock, TX, USA; [3]Gastrointestinal Laboratory, Department of Small Animal Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA; [4]Nature's Variety, Inc., Lincoln, NE, USA; [5]Department of Veterinary Clinical Medicine, University of Illinois, Urbana, IL, USA; and [6]Division of Nutritional Sciences, University of Illinois, Urbana, IL, USA

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DOI: 10.1111/1574-6941.12081

Editor: Julian Marchesi

Keywords
raw diets; pyrosequencing; canine; microbiota; prebiotics; yeast cell wall.

Abstract

Our objective was to determine the effects of feeding raw meat–based diets with or without inulin or yeast cell wall extract (YCW) on fecal microbial communities of dogs using 454 pyrosequencing. Six healthy female adult beagles (5.5 ± 0.5 years; 8.5 ± 0.5 kg) were randomly assigned to six test diets using a Latin square design: (1) beef control; (2) beef + 1.4% inulin; (3) beef + 1.4% YCW; (4) chicken control; (5) chicken + 1.4% inulin; and (6) chicken + 1.4% YCW. Following 14 days of adaptation, fresh fecal samples were collected on day 15 or day 16 of each period. Fecal genomic DNA was extracted and used to create 16S rRNA gene amplicons, which were subjected to 454 pyrosequencing and qPCR. Predominant fecal bacterial phyla included Bacteroidetes, Firmicutes, Bacteroidetes, and Proteobacteria. Beef-based diets increased ($P < 0.05$) *Escherichia*, but decreased ($P < 0.05$) *Anaerobiospirillum* vs. chicken-based diets. Inulin decreased ($P < 0.05$) *Enterobacteriaceae*. Inulin increased ($P < 0.05$) *Megamonas* vs. control. Inulin also decreased ($P < 0.05$) *Escherichia* vs. YCW. qPCR data showed that YCW increased ($P < 0.05$) *Bifidobacterium* vs. inulin and control and inulin increased ($P < 0.05$) *Lactobacillus* vs. YCW. Although a few changes in fecal microbiota were observed with inulin or YCW consumption, a strong prebiotic effect was not observed.

Journal of proteome research — Article — pubs.acs.org/jpr

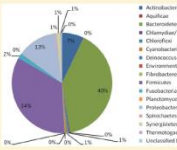
Effects of Dietary Fiber on the Feline Gastrointestinal Metagenome

Kathleen A. Barry,[†,‡] Ingmar S. Middelbos,[†,§] Brittany M. Vester Boler,[†] Scot E. Dowd,[∥] Jan S. Suchodolski,[⊥] Bernard Henrissat,[#] Pedro M. Coutinho,[#] Bryan A. White,[†,¶,○] George C. Fahey, Jr.,[†,¶] and Kelly S. Swanson*[,†,¶,▲]

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Supporting Information

ABSTRACT: Four healthy adult cats were used in a crossover design to determine phylogeny and metabolic functional capacity of the cat's gastrointestinal microbiota using a metagenomic approach. Healthy adult cats (1.7 years old) were fed diets containing 4% cellulose, fructooligosaccharides (FOS), or pectin for 30 d, at which time fresh fecal samples were collected. Fecal DNA samples from each cat consuming each diet were subjected to 454 pyrosequencing. Dominant phyla determined using two independent databases (MG-RAST and IMG/M) included Firmicutes (mean = 36.3 and 49.8%, respectively), Bacteroidetes (mean = 36.1 and 24.1%, respectively), and Proteobacteria (mean = 12.4 and 11.1%, respectively). Primary functional categories as determined by KEGG were associated with carbohydrates, clustering-based subsystems, protein metabolism, and amino acids and derivatives. Primary functional categories as determined by COG were associated with amino acid metabolism and transport, general function prediction only, and carbohydrate transport and metabolism. Analysis of carbohydrate-active enzymes revealed modifications in several glycoside hydrolases, glycosyl transferases, and carbohydrate-binding molecules with FOS and pectin consumption. While the cat is an obligate carnivore, its gut microbiome is similar regarding microbial phylogeny and gene content to omnivores.



KEYWORDS: *feline gut, gastrointestinal bacteria, microbiome, metagenomics, pyrosequencing*

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PLoS one

Phylogenetic Characterization of Fecal Microbial Communities of Dogs Fed Diets with or without Supplemental Dietary Fiber Using 454 Pyrosequencing

Ingmar S. Middelbos[1], Brittany M. Vester Boler[1], Ani Qu[1,3], Bryan A. White[1,2,3], Kelly S. Swanson[1,2,4], George C. Fahey, Jr.[1,2]*

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Abstract

Background: Dogs suffer from many of the same maladies as humans that may be affected by the gut microbiome, but knowledge of the canine microbiome is incomplete. This work aimed to use 16S rDNA tag pyrosequencing to phylogenetically characterize hindgut microbiome in dogs and determine how consumption of dietary fiber affects community structure.

Principal Findings: Six healthy adult dogs were used in a crossover design. A control diet without supplemental fiber and a beet pulp-supplemented (7.5%) diet were fed. Fecal DNA was extracted and the V3 hypervariable region of the microbial 16S rDNA gene amplified using primers suitable for 454-pyrosequencing. Microbial diversity was assessed on random 2000-sequence subsamples of individual and pooled DNA samples by diet. Our dataset comprised 77,771 reads with an average length of 141 nt. Individual samples contained approximately 129 OTU, with *Fusobacteria* (23 – 40% of reads), *Firmicutes* (14 – 28% of reads) and *Bacteroidetes* (31 – 34% of reads) being co-dominant phyla. Feeding dietary fiber generally decreased *Fusobacteria* and increased *Firmicutes*, but these changes were not equally apparent in all dogs. UniFrac analysis revealed that structure of the gut microbiome was affected by diet and *Firmicutes* appeared to play a strong role in by-diet clustering.

Conclusions: Our data suggest three co-dominant bacterial phyla in the canine hindgut. Furthermore, a relatively small amount of dietary fiber changed the structure of the gut microbiome detectably. Our data are among the first to characterize the healthy canine gut microbiome using pyrosequencing and provide a basis for studies focused on devising dietary interventions for microbiome-associated diseases.

Citation: Middelbos IS, Vester Boler BM, Qu A, White BA, Swanson KS, et al. (2010) Phylogenetic Characterization of Fecal Microbial Communities of Dogs Fed Diets with or without Supplemental Dietary Fiber Using 454 Pyrosequencing. PLoS ONE 5(3): e9768. doi:10.1371/journal.pone.0009768

Middelbos et al., 2010

Fibra Dietética – Microbiota Canina

- Dietas
  - Controle
  - 7.5% polpa de beterraba
    - Ingredientes principais
      - Farinha de frango
      - Quirera de arroz
- Animais
  - 6 cães adultos (< 2anos)



OPEN ACCESS Freely available online PLoS one

Phylogenetic Characterization of Fecal Microbial Communities of Dogs Fed Diets with or without Supplemental Dietary Fiber Using 454 Pyrosequencing

Ingmar S. Middelbos[1], Brittany M. Vester Boler[1], Ani Qu[1,3], Bryan A. White[1,2,3], Kelly S. Swanson[1,2,4], George C. Fahey, Jr.[1,2]*

1 Department of Animal Sciences, University of Illinois, Urbana, Illinois, United States of America, 2 Division of Nutritional Sciences, University of Illinois, Urbana, Illinois, United States of America, 3 Institute for Genomic Biology, University of Illinois, Urbana, Illinois, United States of America, 4 Department of Veterinary Clinical Medicine, University of Illinois, Urbana, Illinois, United States of America

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Middelbos et al., 2010

Fibra Dietética – Microbiota Canina



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Phylogenetic Characterization of Fecal Microbial Communities of Dogs Fed Diets with or without Supplemental Dietary Fiber Using 454 Pyrosequencing

Ingmar S. Middelbos[1], Brittany M. Vester Boler[1], Ani Qu[1,3], Bryan A. White[1,2,3], Kelly S. Swanson[1,2,4], George C. Fahey, Jr.[1,2]*

1 Department of Animal Sciences, University of Illinois, Urbana, Illinois, United States of America, 2 Division of Nutritional Sciences, University of Illinois, Urbana, Illinois, United States of America, 3 Institute for Genomic Biology, University of Illinois, Urbana, Illinois, United States of America, 4 Department of Veterinary Clinical Medicine, University of Illinois, Urbana, Illinois, United States of America

Abstract

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Principal Findings: Six healthy adult dogs were used in a crossover design. A control diet without supplemental fiber and a beet pulp-supplemented (7.5%) diet were fed. Fecal DNA was extracted and the V3 hypervariable region of the microbial 16S rDNA gene amplified using primers suitable for 454-pyrosequencing. Microbial diversity was assessed on random 2000-sequence subsamples of individual and pooled DNA samples by diet. Our dataset comprised 77,771 reads with an average length of 141 nt. Individual samples contained approximately 129 OTU, with *Fusobacteria* (23 – 40% of reads), *Firmicutes* (14 – 28% of reads) and *Bacteroidetes* (31 – 34% of reads) being co-dominant phyla. Feeding dietary fiber generally decreased *Fusobacteria* and increased *Firmicutes*, but these changes were not equally apparent in all dogs. UniFrac analysis revealed that structure of the gut microbiome was affected by diet and *Firmicutes* appeared to play a strong role in by-diet clustering.

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- Período experimental e design
  - 14 dias (10 d adaptação; 4 d coleta)
  - Cross-over

- Sequencimento DNA
  - Região V3 – 16S rRNA gene
  - Pirosequenciamento 454
    - Primers 341F and 534R

Middelbos et al., 2010

Fibra Dietética

- 3 filos principais:
  - Fusobacteria (23-40%)
  - Firmicutes (14-28%)
  - Bacteroidetes (31-34%)

- Fibra dietética
  - ⬇Fusobacteria
  - ⬆Firmicutes



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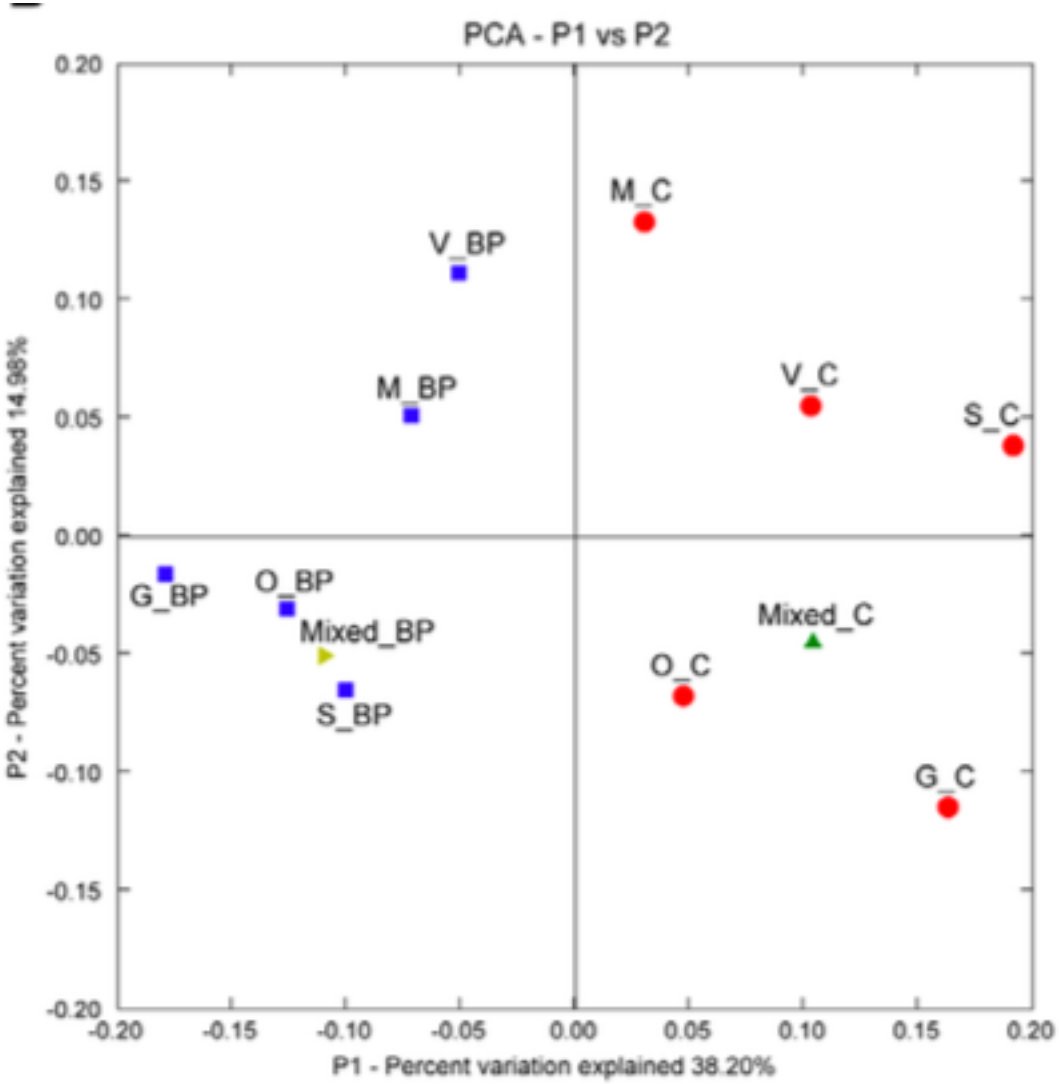
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Middelbos et al., 2010

Fibra Dietética – Microbiota Canina



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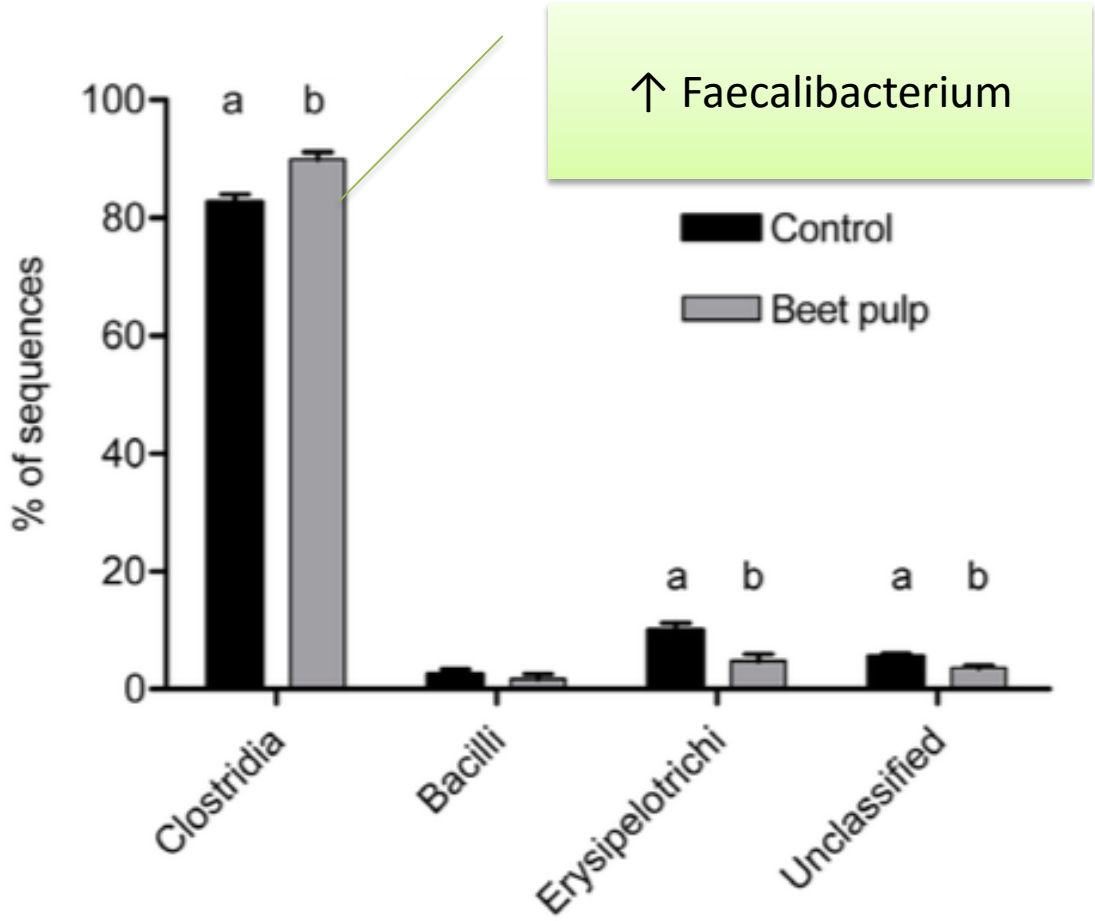
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Middelbos et al., 2010

Classes Afetadas pela Dieta – Filo Firmicutes





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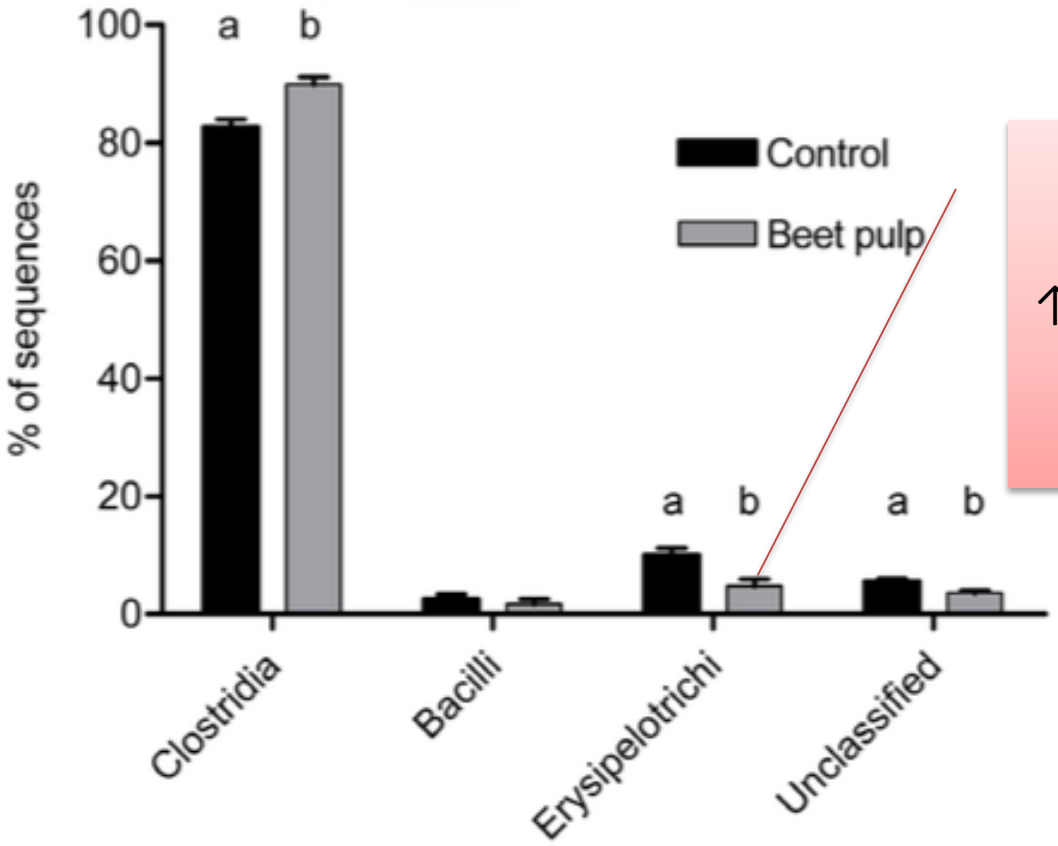
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Associado a obesidade
↑*Clostridium ramosum*
↑Transportadores de Glicose e ácidos graxos

Middelbos et al., 2010

Fibra de Batata – Microbiota Canina

Potato fiber as a dietary fiber source in dog foods

M. R. Panasevich,* M. C. Rossoni Serao,* M. R. C. de Godoy,*
K. S. Swanson,* L. Guérin-Deremaux,† G. L. Lynch,‡ D. Wils,† G. C. Fahey, Jr.,* and R. N. Dilger*[1]

*Department of Animal Sciences, University of Illinois, Urbana 61801; †Roquette Frères, Biology and Nutrition Department, 62136 Lestrem, France; and ‡Roquette America, Inc., Geneva, IL 60134

ABSTRACT: Potato fiber (PF), a coproduct of potato starch manufacture, was evaluated as a potential novel fiber source in dog food. Potato fiber contained 55% total dietary fiber, 29% starch, 4% crude protein, and 2% acid-hydrolyzed fat. The PF substrate was evaluated for chemical composition, in vitro digestion and fermentation characteristics, and in vivo responses. For the in vitro hydrolytic-enzymatic digestion and fermentation experiment, raw and cooked PF substrates were first subjected to hydrolytic-enzymatic digestion to determine OM disappearance and then fermented using dog fecal inoculum. Fermentation characteristics were then measured at 0, 3, 6, 9, and 12 h. For the in vivo experiment, 10 female mixed-breed dogs (6.13 ± 0.17 yr; 22 ± 2.1 kg) were provided 5 diets with graded concentrations (0%, 1.5%, 3%, 4.5%, or 6%) of PF in a replicated 5 × 5 Latin square design. Dogs were acclimated to the test diet for 10 d, followed by 4 d of total fecal collection. Fresh fecal samples were collected to measure fecal pH and fermentation end products. In vitro digestion revealed that raw and cooked PF were 32.3% and 27.9% menta 9 h. R and to at the in viv total t digest of PF. a linea tratio were conco increa tratio of spe increa ed tha charac digest could

Key words: canine, fermentative end products, in vitro fer

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British Journal of Nutrition (2015), **113**, 125–133
doi:10.1017/S0007114514003274
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Modulation of the faecal microbiome of healthy adult dogs by inclusion of potato fibre in the diet

Matthew R. Panasevich[1], Katherine R. Kerr[1], Ryan N. Dilger[1], George C. Fahey Jr[1], Laetitia Guérin-Deremaux[2], Gary L. Lynch[3], Daniel Wils[2], Jan S. Suchodolski[4], Jörg M. Steiner[4], Scot E. Dowd[5] and Kelly S. Swanson[1]*

[1]*Department of Animal Sciences, University of Illinois, 1207 West Gregory Drive, Urbana, IL 61801, USA*
[2]*Roquette Frères, Biology and Nutrition Department, Rue de la Haute Loge, Lestrem 62080, France*
[3]*Roquette America, Inc., 2211 Innovation Drive, Geneva, IL 60134, USA*
[4]*Gastrointestinal Laboratory, Texas A&M University, College Station, TX 77843, USA*
[5]*MR DNA Molecular Research LP, 503 Clovis Road, Shallowater, TX 79363, USA*

(Submitted 3 March 2014 – Final revision received 21 August 2014 – Accepted 10 September 2014 – First published online 24 November 2014)

Abstract

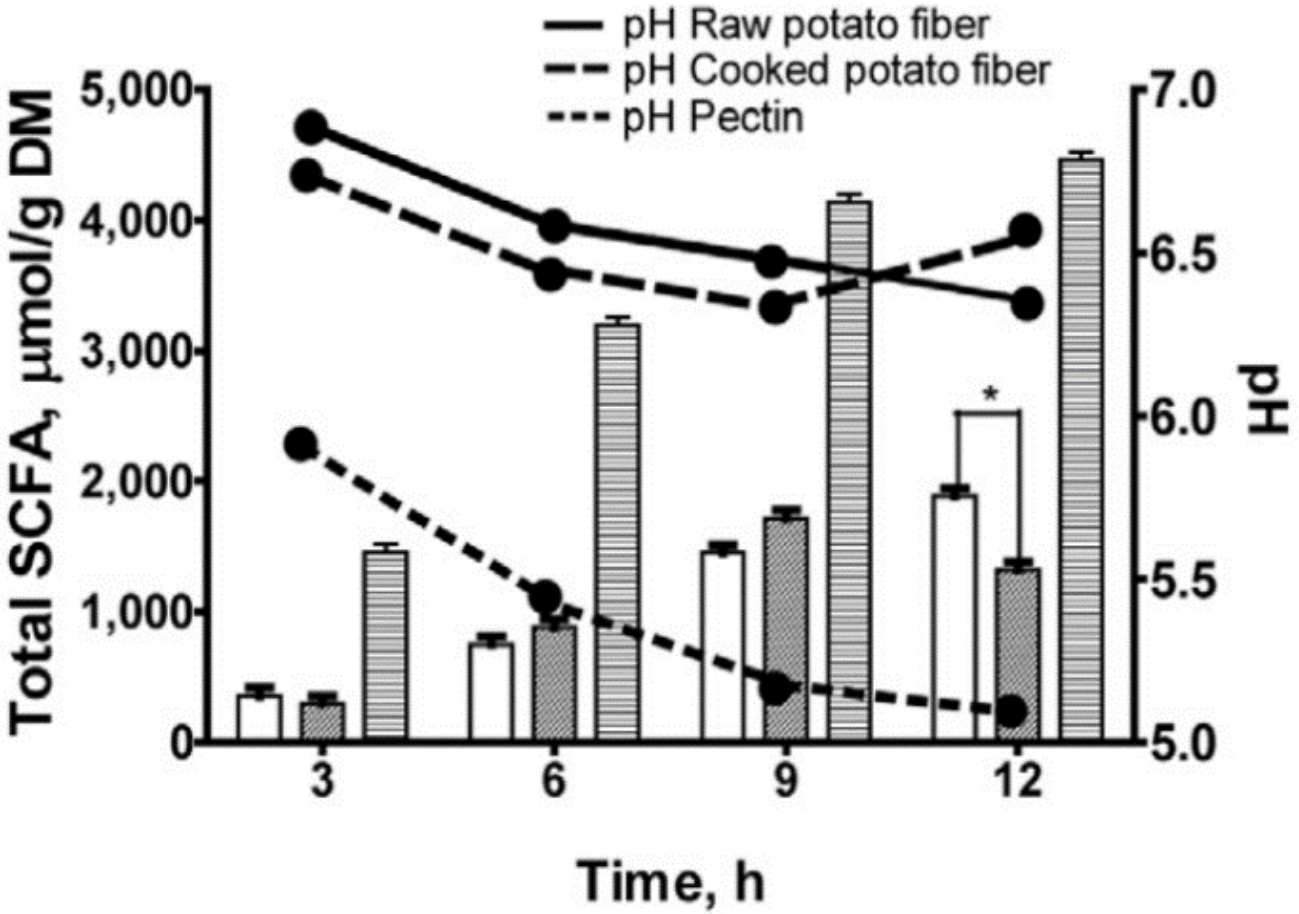
Inclusion of fermentable fibres in the diet can have an impact on the hindgut microbiome and provide numerous health benefits to the host. Potato fibre (PF), a co-product of potato starch isolation, has a favourable chemical composition of pectins, resistant and digestible starch, cellulose, and hemicelluloses. The objective of the present study was to evaluate the effect of increasing dietary PF concentrations on the faecal microbiome of healthy adult dogs. Fresh faecal samples were collected from ten female dogs with hound bloodlines (6·13 (SEM 0·17) years; 22·0 (SEM 2·1) kg) fed five test diets containing graded concentrations of PF (0, 1·5, 3, 4·5 or 6% as-fed; Roquette Frères) in a replicated 5×5 Latin square design. Extraction of DNA was followed by amplification of the V4–V6 variable region of the 16S rRNA gene using barcoded primers. Sequences were classified into taxonomic levels using Basic Local Alignment Search Tool (BLASTn) against a curated GreenGenes database. Inclusion of PF increased ($P<0·05$) the faecal proportions of Firmicutes, while those of Fusobacteria decreased ($P<0·05$). Similar shifts were observed at the genus level and were confirmed by quantitative PCR (qPCR) analysis. With increasing concentrations of PF, faecal proportions of *Faecalibacterium* increased ($P<0·05$). *Post hoc* Pearson's correlation analysis showed positive ($P<0·05$) correlations with *Bifidobacterium* spp. and butyrate production and *Lactobacillus* spp. concentrations. Overall, increases in the proportion of *Faecalibacterium* (not *Lactobacillus*/*Bifidobacterium*, as confirmed by qPCR analysis) and faecal SCFA concentrations with increasing dietary PF concentrations suggest that PF is a possible prebiotic fibre.

Key words: Potato fibre; Faecal microbiome; Dogs

British Journal of Nutrition

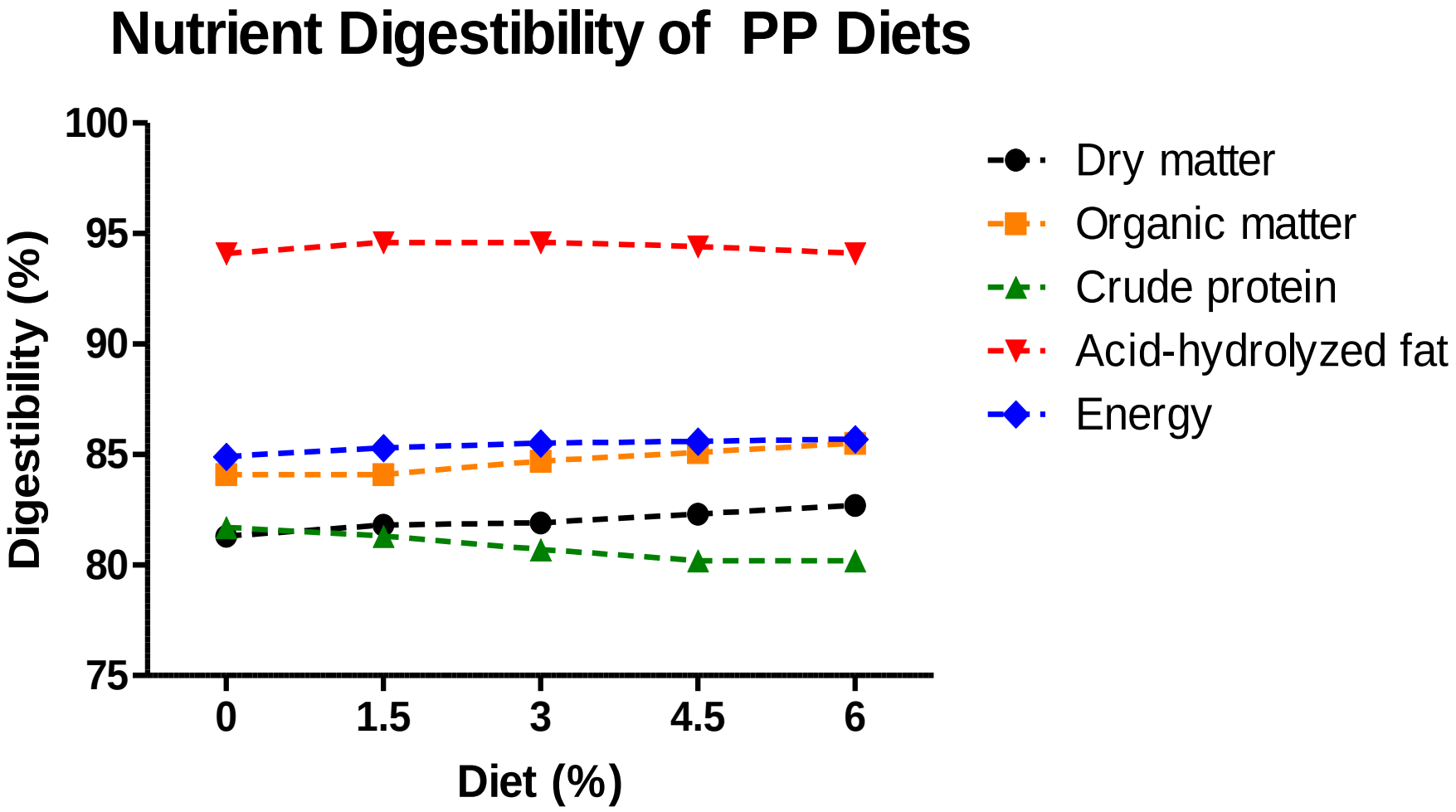
Panasevich et al., 2013; 2015

Perfil Fermentativo – Fibra de Batata



Panasevich et al., 2013

Fibra da Batata – Digestibilidade



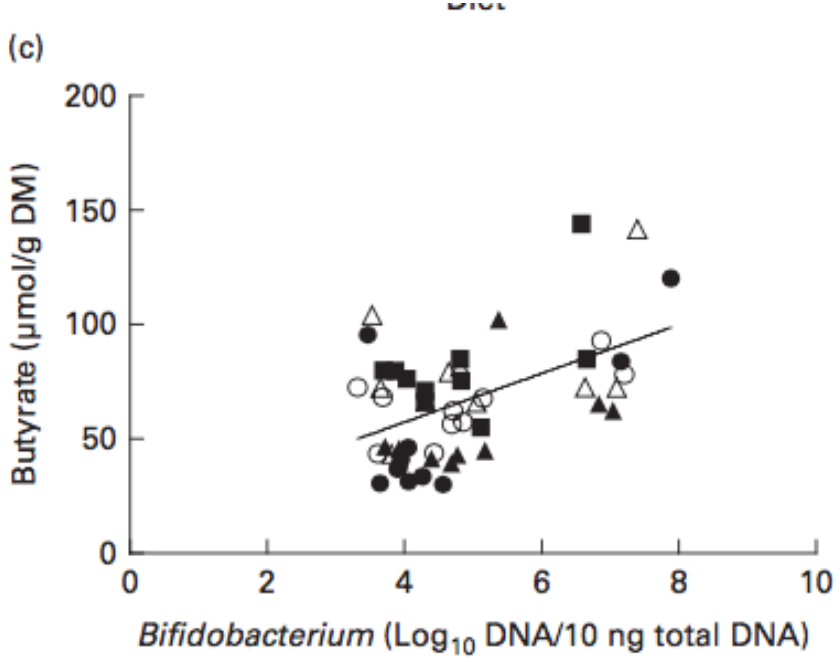
Panasevich et al., 2013

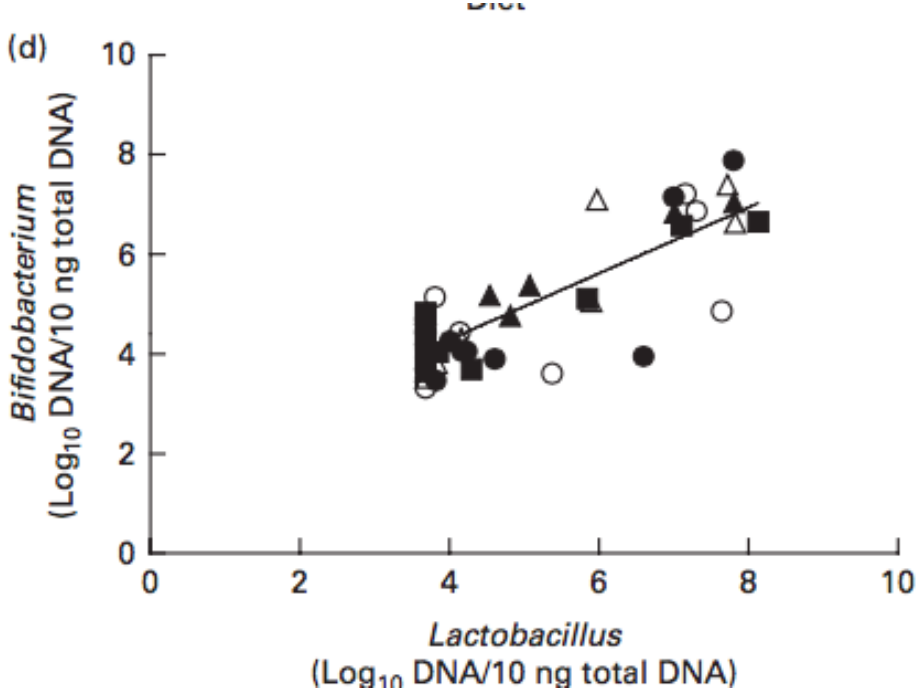
Fibra de Batata – Microbiota Canina

- Efeito benéfico na microbiota canina
  - Aumento de Faecalibacterium and Blautia
    - *F. prausnitzii*
  - Declínio de Fusobacteria
  - Correlação positiva
    - Bifidobacteria and concentração de butirato
    - Bifidobacteria e Lactobacillus
- Potencial efeito prebiótico?

Panasevich et al., 2015

Fibra de Batata – Microbiota Canina





Panasevich et al., 2015

RESEARCH ARTICLE

Fecal microbial communities of healthy adult dogs fed raw meat-based diets with or without inulin or yeast cell wall extracts as assessed by 454 pyrosequencing

Alison N. Beloshapka[1], Scot E. Dowd[2], Jan S. Suchodolski[3], Jörg M. Steiner[3], Laura Duclos[4] & Kelly S. Swanson[1,5,6]

[1]Department of Animal Sciences, University of Illinois, Urbana, IL, USA; [2]Research and Testing Laboratory, Lubbock, TX, USA; [3]Gastrointestinal Laboratory, Department of Small Animal Clinical Sciences, College of Veterinary Medicine and Biomedical Sciences, Texas A&M University, College Station, TX, USA; [4]Nature's Variety, Inc., Lincoln, NE, USA; [5]Department of Veterinary Clinical Medicine, University of Illinois, Urbana, IL, USA; and [6]Division of Nutritional Sciences, University of Illinois, Urbana, IL, USA

Correspondence: Kelly S. Swanson, Department of Animal Sciences, University of Illinois, 1207 W. Gregory Drive, Urbana, IL 61801. Tel: 00+1+217 333 4189; fax: 00+1+217 333 7861; e-mail: kswanso@illinois.edu

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DOI: 10.1111/1574-6941.12081

Editor: Julian Marchesi

Keywords
raw diets; pyrosequencing; canine; microbiota; prebiotics; yeast cell wall

Abstract

Our objective was to determine the effects of feeding raw meat-based diets with or without inulin or yeast cell wall extract (YCW) on fecal microbial communities of dogs using 454 pyrosequencing. Six healthy female adult beagles (5.5 ± 0.5 years; 8.5 ± 0.5 kg) were randomly assigned to six test diets using a Latin square design: (1) beef control; (2) beef + 1.4% inulin; (3) beef + 1.4% YCW; (4) chicken control; (5) chicken + 1.4% inulin; and (6) chicken + 1.4% YCW. Following 14 days of adaptation, fresh fecal samples were collected on day 15 or day 16 of each period. Fecal genomic DNA was extracted and used to create 16S rRNA gene amplicons, which were subjected to 454 pyrosequencing and qPCR. Predominant fecal bacterial phyla included Fusobacteria, Firmicutes, Bacteroidetes, and Proteobacteria. Beef-based diets increased ($P < 0.05$) *Escherichia*, but decreased ($P < 0.05$) *Anaerobiospirillum* vs. chicken-based diets. Inulin decreased ($P < 0.05$) *Enterobacteriaceae*. Inulin increased ($P < 0.05$) *Megamonas* vs. control. Inulin also decreased ($P < 0.05$) *Escherichia* vs. YCW. qPCR data showed that YCW increased ($P < 0.05$) *Bifidobacterium* vs. inulin and control and inulin increased ($P < 0.05$) *Lactobacillus* vs. YCW. Although a few changes in fecal microbiota were observed with inulin or YCW consumption, a strong prebiotic effect was not observed.

Beloshapka et al., 2013

Carne Crua + Inulina/Levedura - Cães

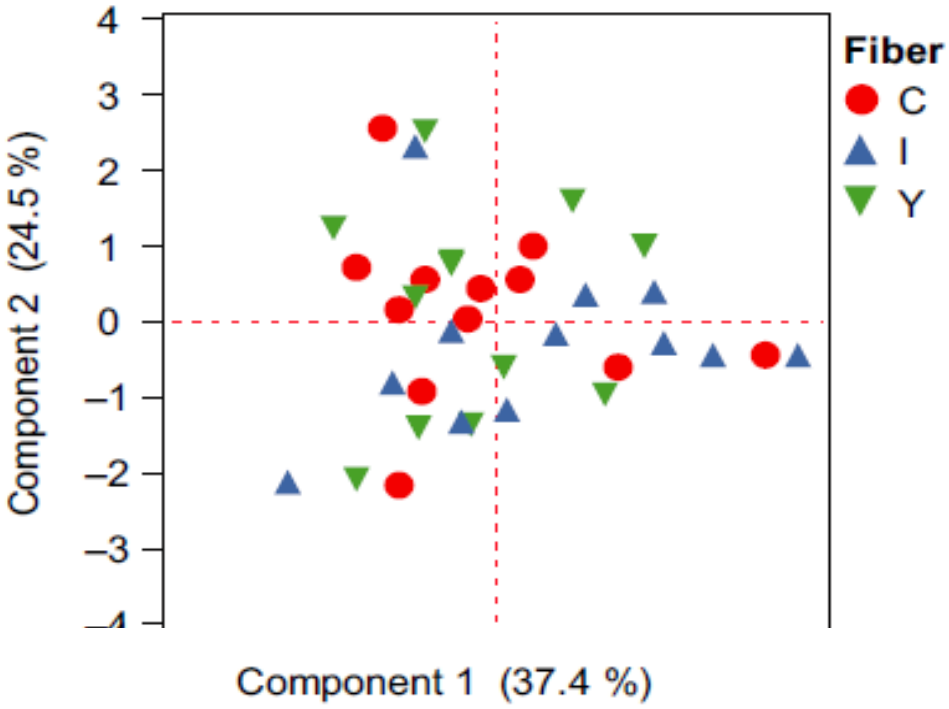
- Animais, dietas e design experimental
  - Beagles
  - Arranjo fatorial 2 x 3
    - Tipo de carne
      - Frango
      - Carne bovina
    - Tipo de prebiótico
      - 1.4% inulina
      - 1.4 % extrato de levedura
      - Controle



Beloshapka et al., 2013

Carne Crua + Inulina/Levedura - Cães

- Alta digestibilidade de nutrientes
- ↑ ácidos graxos cadeia curta;↓ indols and fenóis
- Algumas alterações microbiota fecal



Beloshapka et al., 2012; 2013

Carne Crua + Inulina/Levedura - Cães

- Principais filos
  - Fusobacteria (29-51%)
  - Bacteroidetes (27-34%)
  - Firmicutes (18-6%)
  - Proteobacteria (4-6%)
  - Actinobacteria (1-2.5%)

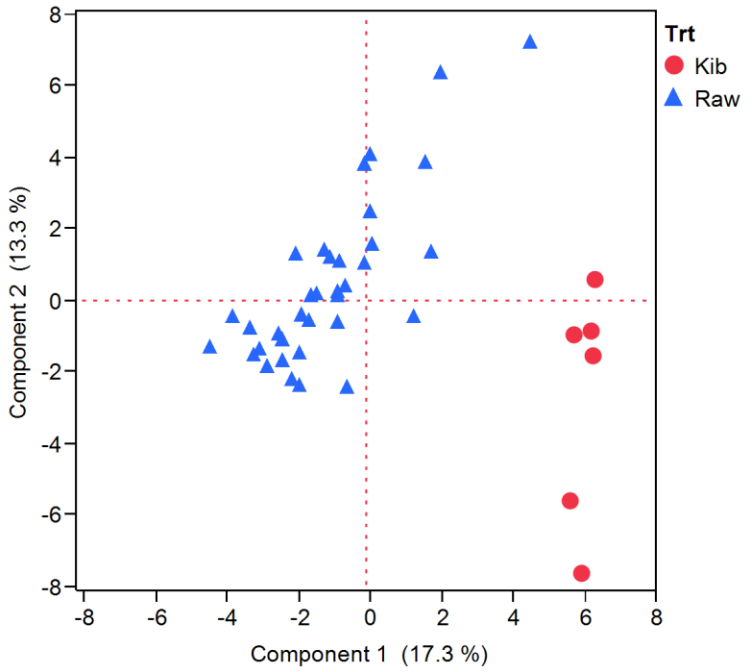
- Inulina
  - ↓ Enterobacteriaceae
    - ↓ Escherichia
  - ↑Lactobacillus
  - ↑Veillonellaceae
    - Megamonas (FOS fermenters)

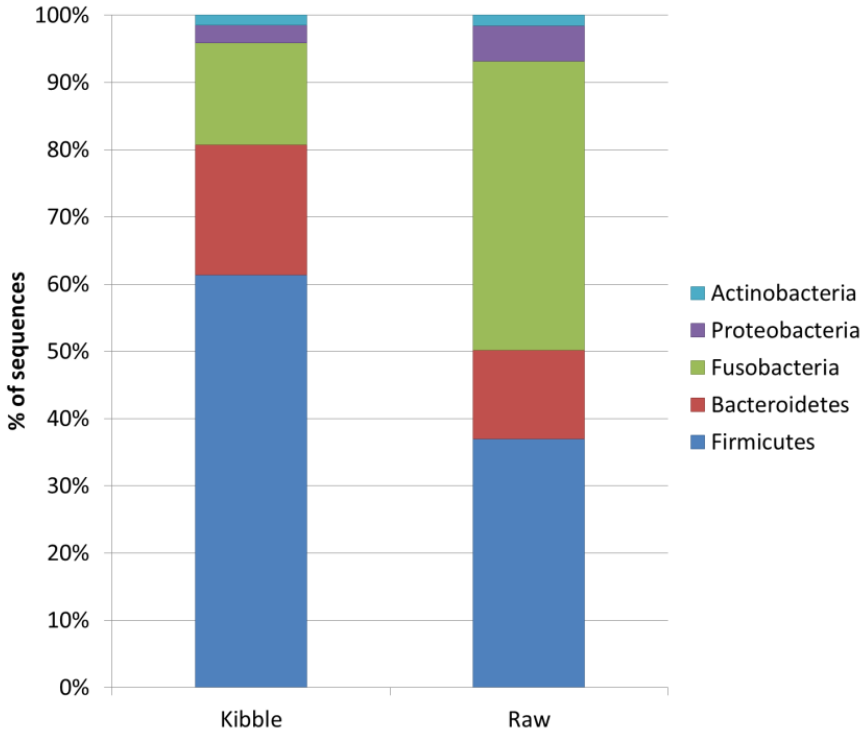
- Levedura
  - ↑Bifidobacteria
  - ↓ *Clostridium celerecrescens* (cluster XIVa)

Beloshapka et al., 2012; 2013

Dietas: Carne Crua vs. Extrusadas

- Composição nutricional distinta
  - Extrusada: 24% proteina; 12% lipídio; 12% TDF
  - Carne Crua: 24-32% proteina; 50-60% lípido; 1-5% fibra

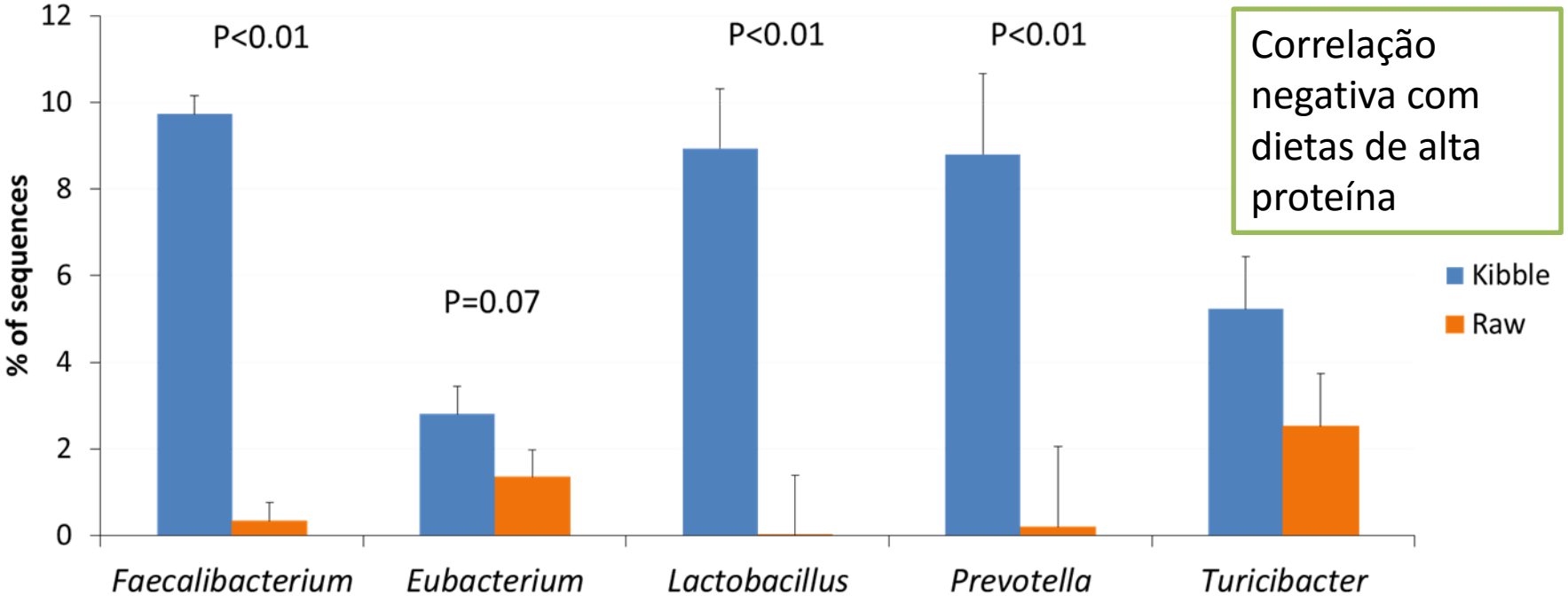




Beloshapka et al., 2011

Dietas: Carne Crua vs. Extrusadas

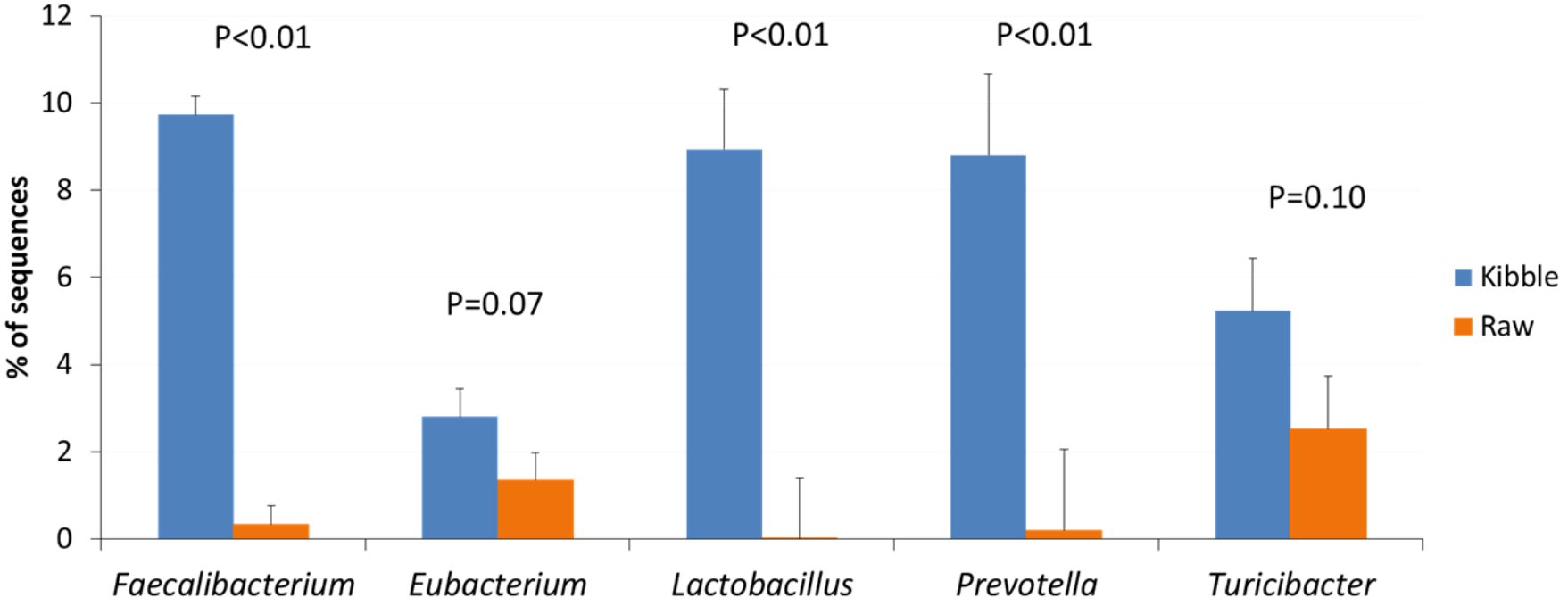
Metabolismo de carboidrato e síntese de ácido graxo



Correlação negativa com dietas de alta proteína

Beloshapka et al., 2011

Dietas: Carne Crua vs. Extrusadas



- Todos os animais de mantiveram saudáveis ao longo do estudo
- Importância das alterações microbianas a saúde do animal?

Beloshapka et al., 2011

Journal of proteome research

Article

pubs.acs.org/jpr

Effects of Dietary Fiber on the Feline Gastrointestinal Metagenome

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[†]Department of Animal Sciences, [¶]Division of Nutritional Sciences, and [▲]Department of Veterinary Clinical Medicine, and [○]The Institute for Genomic Biology, University of Illinois, Urbana, Illinois 61801, United States

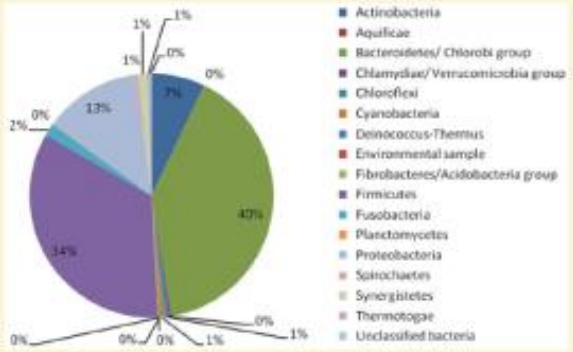
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[⊥]Gastrointestinal Laboratory, Texas A&M University, College Station, Texas 77843, United States

[#]CNRS, Universités Aix-Marseille I & II, Marseille, France

Supporting Information

ABSTRACT: Four healthy adult cats were used in a crossover design to determine phylogeny and metabolic functional capacity of the cat's gastrointestinal microbiota using a metagenomic approach. Healthy adult cats (1.7 years old) were fed diets containing 4% cellulose, fructooligosaccharides (FOS), or pectin for 30 d, at which time fresh fecal samples were collected. Fecal DNA samples from each cat consuming each diet were subjected to 454 pyrosequencing. Dominant phyla determined using two independent databases (MG-RAST and IMG/M) included Firmicutes (mean = 36.3 and 49.8%, respectively), Bacteroidetes (mean = 36.1 and 24.1%, respectively), and Proteobacteria (mean = 12.4 and 11.1%, respectively). Primary functional categories as determined by KEGG were associated with carbohydrates, clustering-based subsystems, protein metabolism, and amino acids and derivatives. Primary functional categories as determined by COG were associated with amino acid metabolism and transport, general function prediction only, and carbohydrate transport and metabolism. Analysis of carbohydrate-active enzymes revealed modifications in several glycoside hydrolases, glycosyl transferases, and carbohydrate-binding molecules with FOS and pectin consumption. While the cat is an obligate carnivore, its gut microbiome is similar regarding microbial phylogeny and gene content to omnivores.



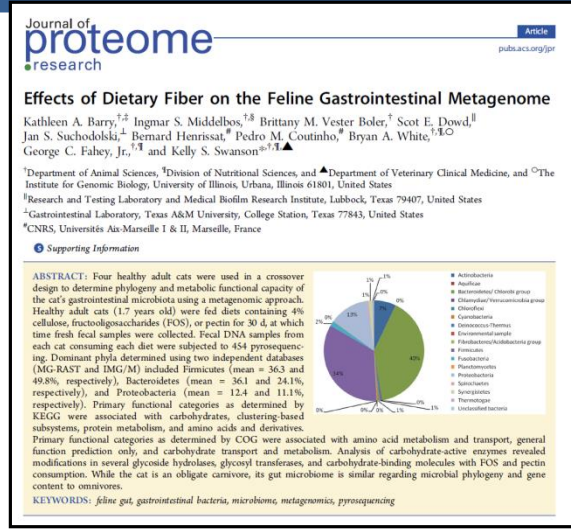
KEYWORDS: *feline gut, gastrointestinal bacteria, microbiome, metagenomics, pyrosequencing*

Barry et al., 2012

Fibra Dietética – Microbioma Felino

- Dietas
  - Controle (4% celulose)
  - FOS (4%)
  - Pectina (4%)
    - Arroz e farinha de víscera

- Período experimental e design
  - 30 dias (26 d adaptação; 4 d coleta)



Journal of proteome research — Article — pubs.acs.org/jpr

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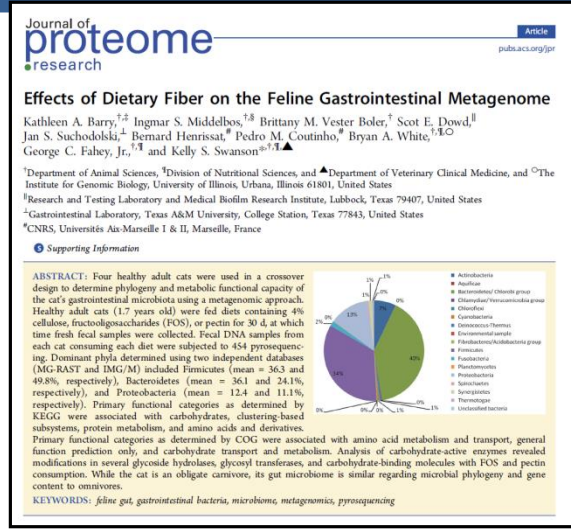
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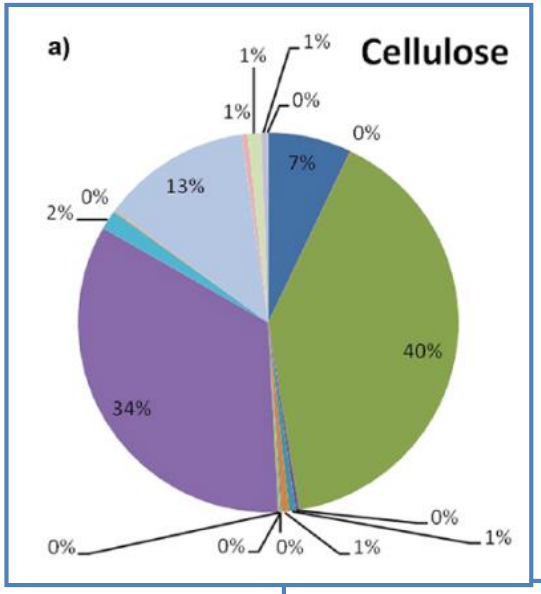
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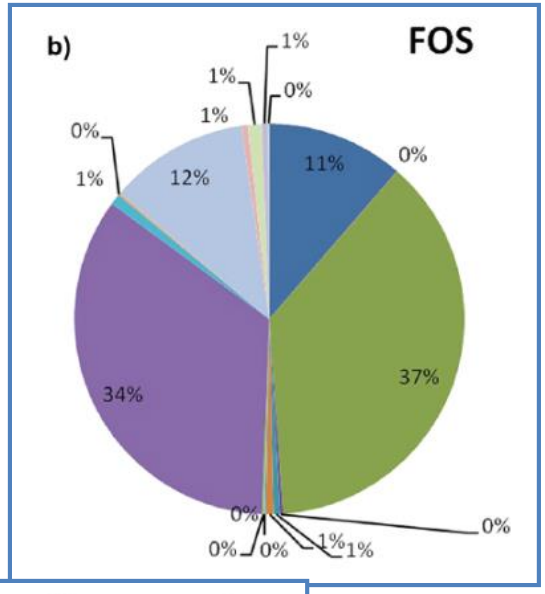
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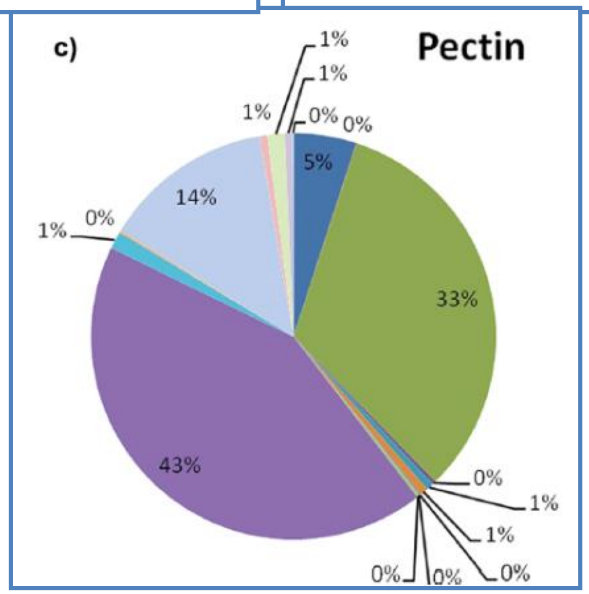
- Sequencimento DNA
  - Pirosequenciamento 454
    - Genoma inteiro
  - Kyoto encyclopedia of gene and genomes (KEGG)
  - Carbohydrate-active enzyme database (CAZy)
    - Função metabólica da microbiota

Barry et al., 2012

Fibra Dietética – Microbioma Felino



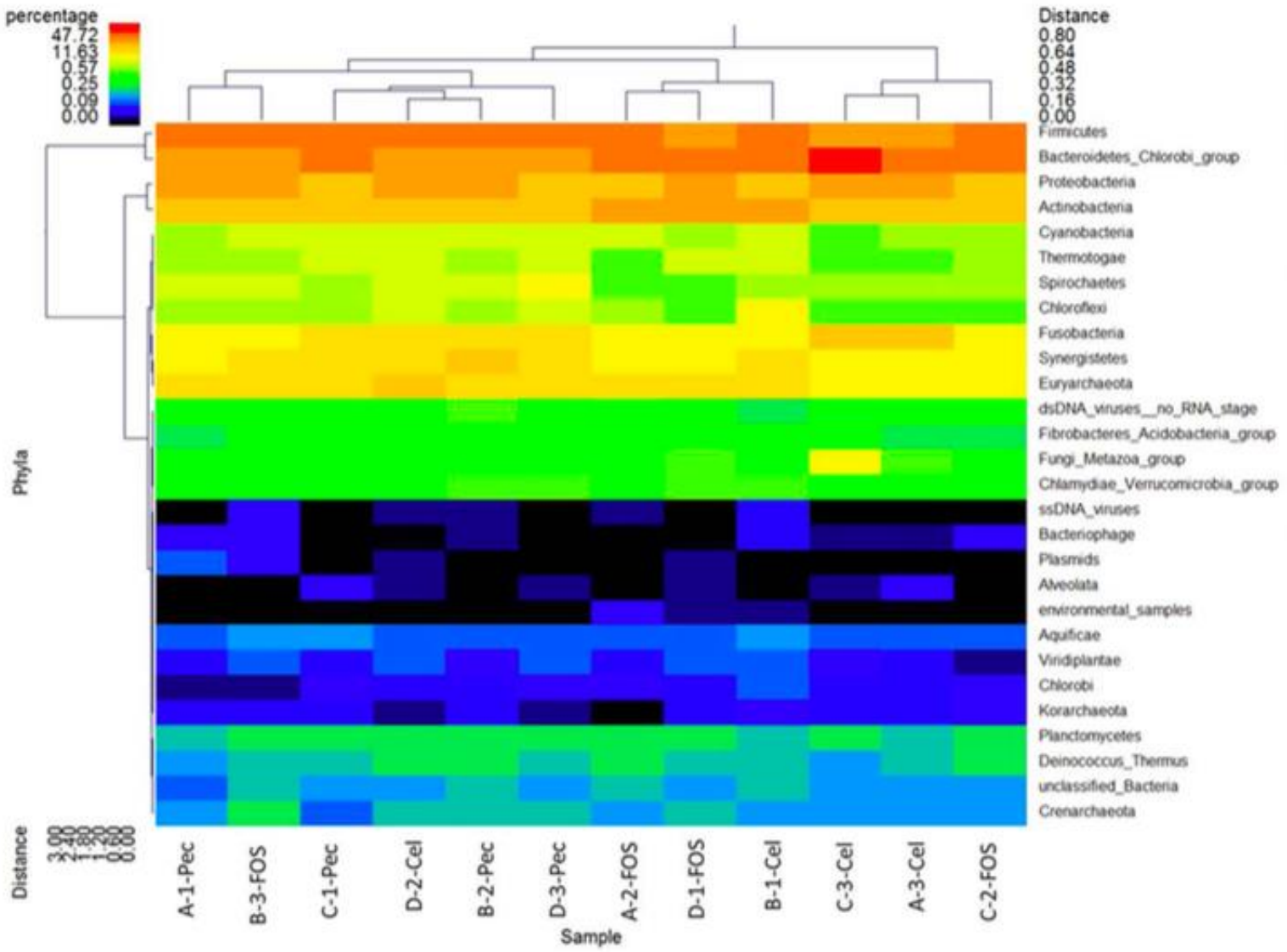




- Actinobacteria
- Aquificae
- Bacteroidetes/ Chlorobi group
- Chlamydiae/ Verrucomicrobia group
- Chloroflexi
- Cyanobacteria
- Deinococcus-Thermus
- Environmental sample
- Fibrobacteres/Acidobacteria group
- Firmicutes
- Fusobacteria
- Planctomycetes
- Proteobacteria
- Spirochaetes
- Synergistetes
- Thermotogae
- Unclassified bacteria

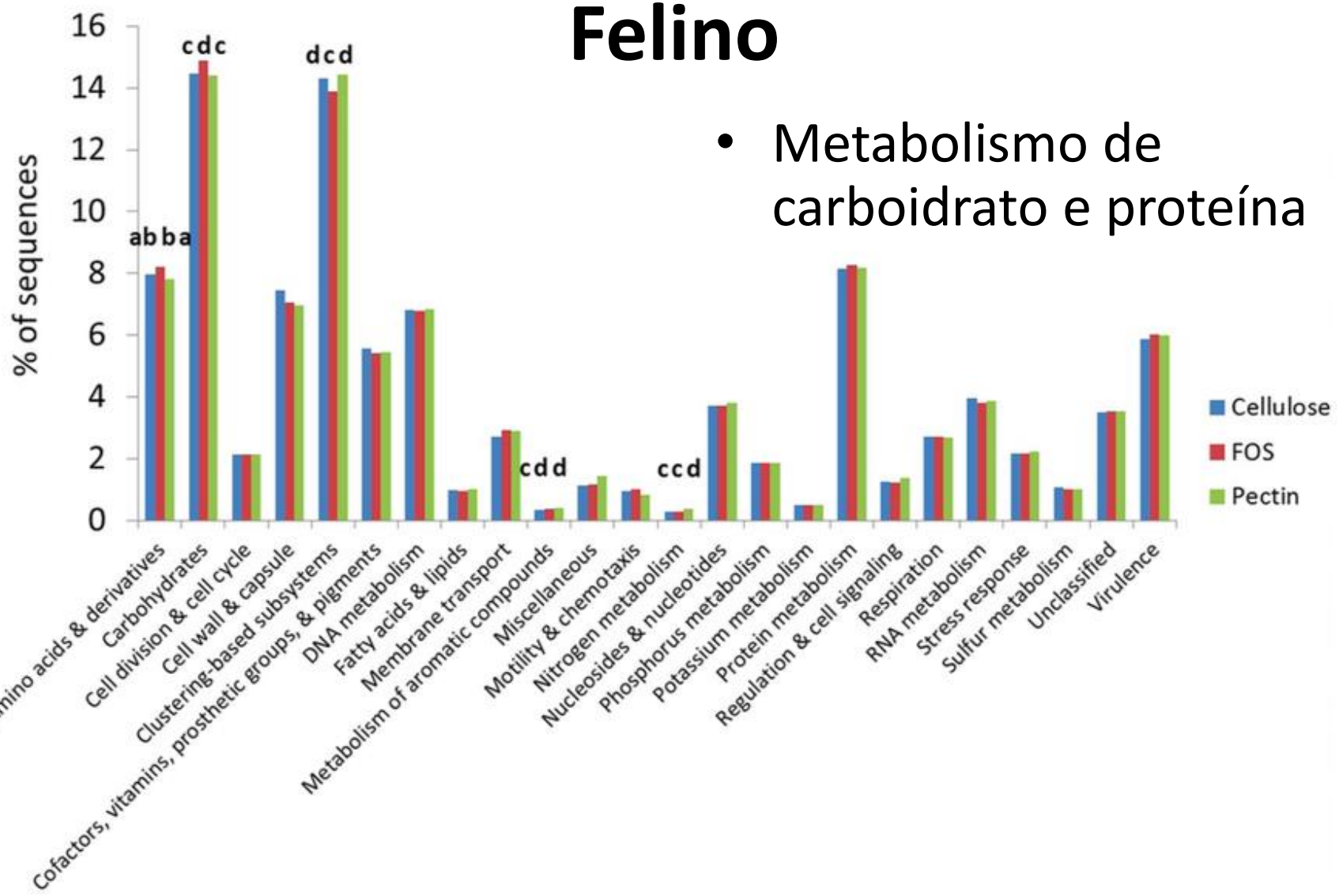
Barry et al., 2012

Fibra Dietética – Microbioma Felino



Barry et al., 2012

Função Metabólica– Microbioma Felino



- Metabolismo de carboidrato e proteína

Barry et al., 2012

British Journal of Nutrition (2013), **109**, 1637–1646
doi:10.1017/S0007114512003479
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The gut microbiome of kittens is affected by dietary protein:carbohydrate ratio and associated with blood metabolite and hormone concentrations

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(Submitted 24 February 2012 – Final revision received 28 May 2012 – Accepted 5 July 2012 – First published online 31 August 2012)

Abstract

High-protein, low-carbohydrate (HPLC) diets are common in cats, but their effect on the gut microbiome has been ignored. The present study was conducted to test the effects of dietary protein:carbohydrate ratio on the gut microbiota of growing kittens. Male domestic short-hair kittens were raised by mothers fed moderate-protein, moderate-carbohydrate (MPMC; *n* 7) or HPLC (*n* 7) diets, and then weaned at 8 weeks onto the same diet. Fresh faeces were collected at 8, 12 and 16 weeks; DNA was extracted, followed by amplification of the V4–V6 region of the 16S rRNA gene using 454 pyrosequencing. A total of 384 588 sequences (average of 9374 per sample) were generated. Dual hierarchical clustering indicated distinct clustering based on the protein:carbohydrate ratio regardless of age. The protein:carbohydrate ratio affected faecal bacteria. Faecal Actinobacteria were greater ($P<0·05$) and Fusobacteria were lower ($P<0·05$) in MPMC-fed kittens. Faecal *Clostridium*, *Faecalibacterium*, *Ruminococcus*, *Blautia* and *Eubacterium* were greater ($P<0·05$) in HPLC-fed kittens, while *Dialister*, *Acidaminococcus*, *Bifidobacterium*, *Megasphaera* and *Mitsuokella* were greater ($P<0·05$) in MPMC-fed kittens. Principal component analysis of faecal bacteria and blood metabolites and hormones resulted in distinct clusters. Of particular interest was the clustering of blood TAG with faecal Clostridiaceae, Eubacteriaceae, Ruminococcaceae, Fusobacteriaceae and Lachnospiraceae; blood ghrelin with faecal Coriobacteriaceae, Bifidobacteriaceae and Veillonellaceae; and blood glucose, cholesterol and leptin with faecal Lactobacillaceae. The present results demonstrate that the protein:carbohydrate ratio affects the faecal microbiome, and highlight the associations between faecal microbes and circulating hormones and metabolites that may be important in terms of satiety and host metabolism.

Key words: **Kittens: Faecal microbiome: Protein:carbohydrate ratio**

Hooda et al., 2013

Proteína: Carboidrato Dietético – Microbiota de Gatos (filhotes)

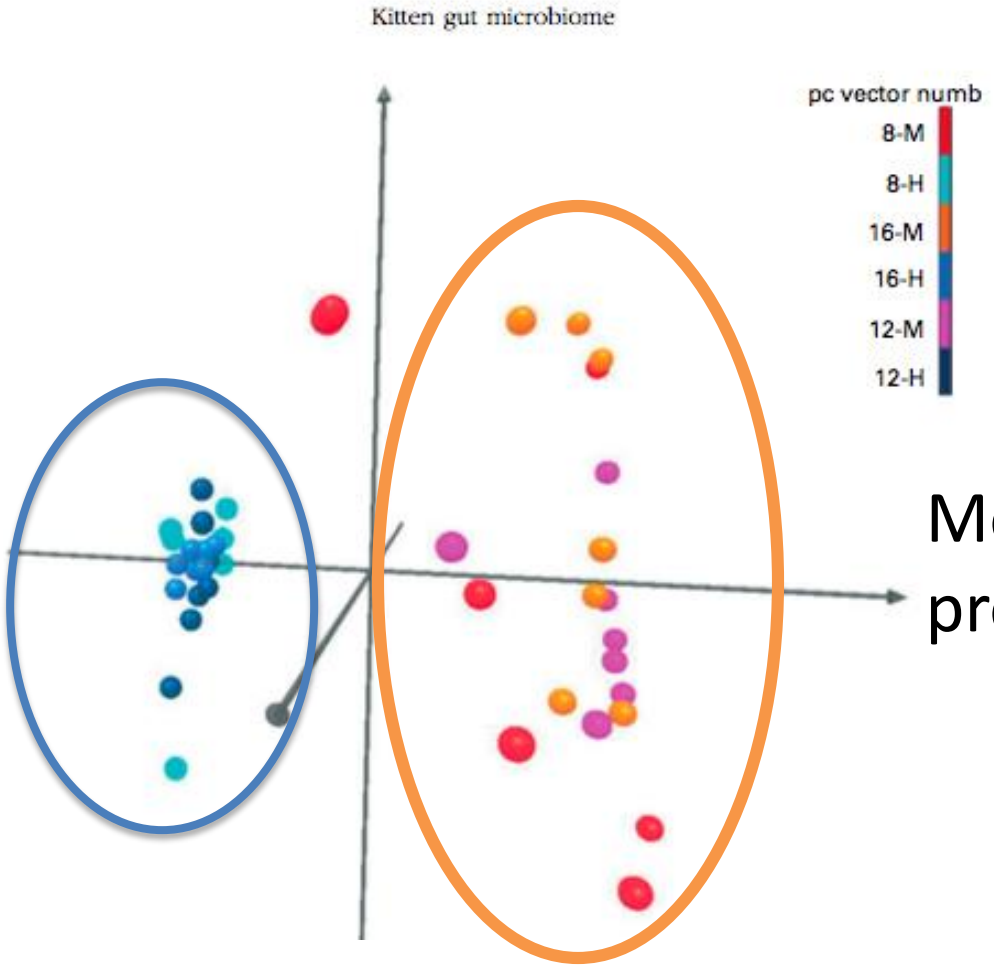
- Dietas
  - Proteína e carboidrato moderado
    - 34% CP, 19% AHF, 6% TDF
  - Alta protéina e baixo carboidrato
    - 53% CP, 24% AHF, 2% TDF

- Animais e design experimental
  - 7 filhotes de gatos/ tratamento
  - Completamente casualizado
  - Coletas 8, 12 e 16 semanas de vida

Hooda et al., 2013

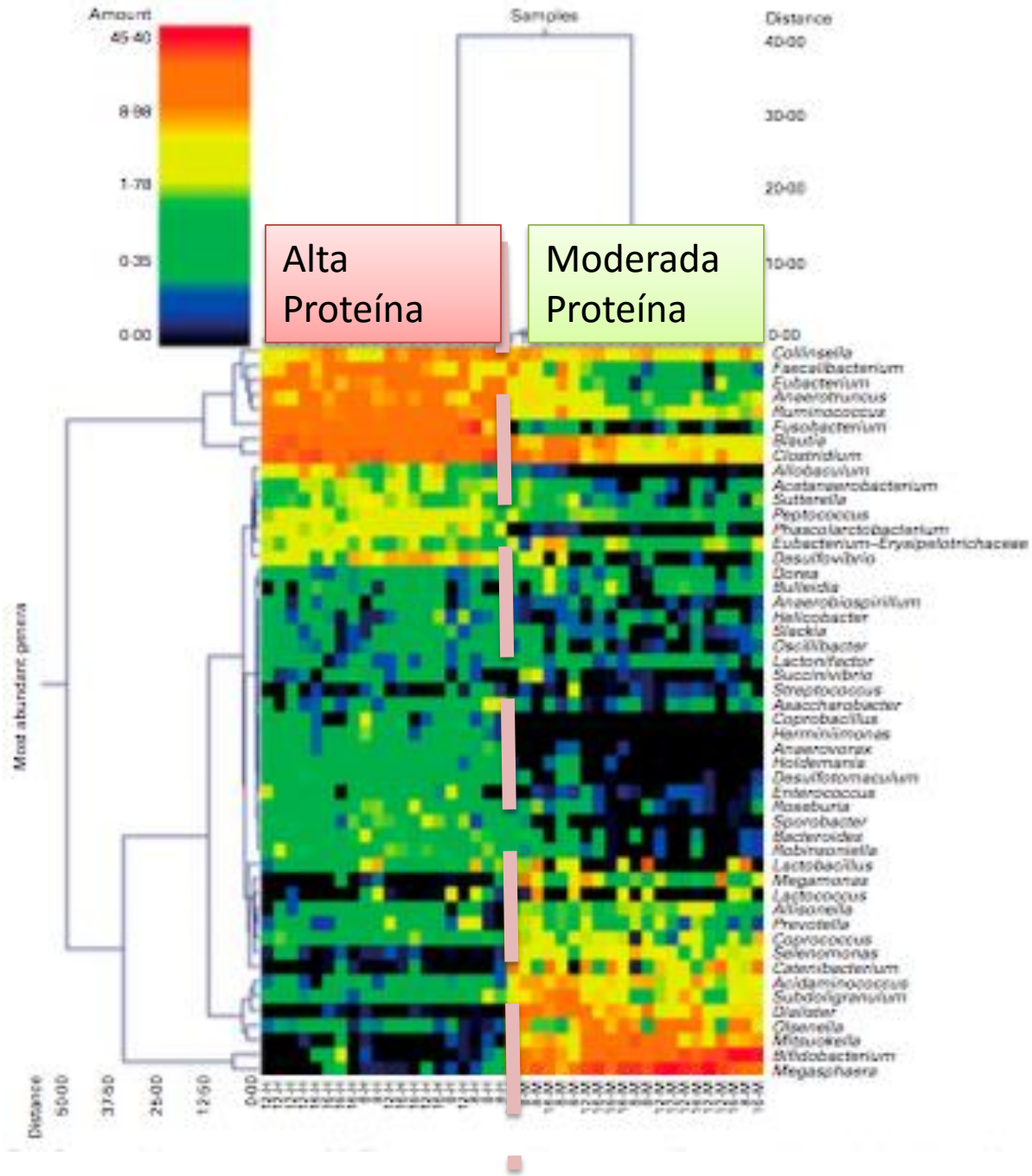
Proteína: Carboidrato Dietético – Microbiota de Gatos (filhotes)

Alta proteína

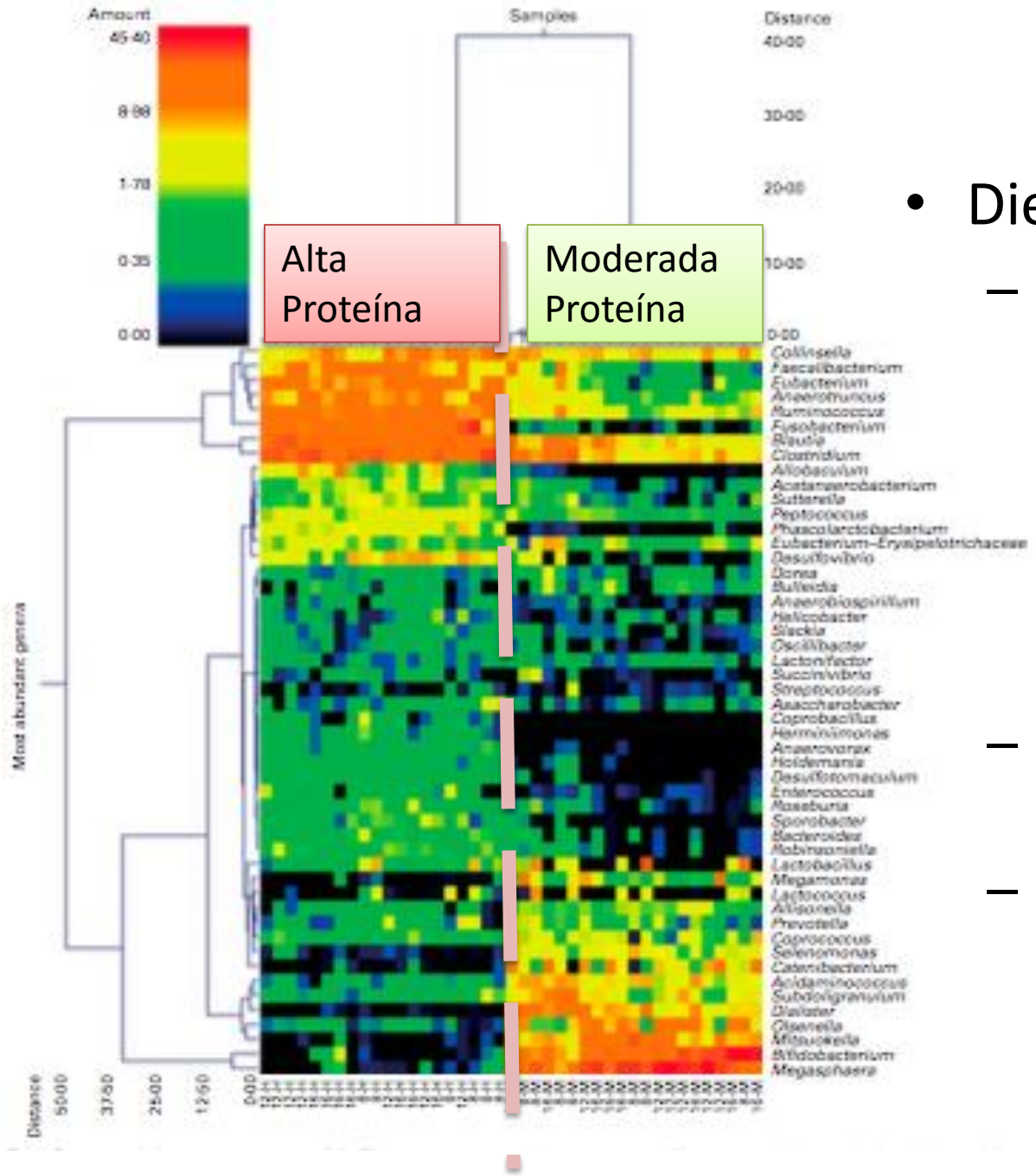


Moderada proteína

Hooda et al., 2013



Hooda et al., 2013



- Dieta: Alta proteína
  - ↓Firmicutes
    - ↑ Clostridiaceae
    - ↓ Veilonellaceae
      - ↓Megasphaera
      - Sint. butirato
    - ↓ Lactobacillus (desmame)
  - ↓Actinobacteria
    - ↓Bifidobacterium
  - ↑Fusobacteria

Hooda et al., 2013

OPEN ACCESS Freely available online

PLOS ONE

Deep Illumina-Based Shotgun Sequencing Reveals Dietary Effects on the Structure and Function of the Fecal Microbiome of Growing Kittens

Oliver Deusch[1], Ciaran O'Flynn[1], Alison Colyer[1], Penelope Morris[1], David Allaway[1], Paul G. Jones[1], Kelly S. Swanson[2,3,4]*

1 WALTHAM Centre for Pet Nutrition, Waltham-on-the-Wolds, Leicestershire, United Kingdom, 2 Department of Animal Sciences, University of Illinois, Urbana, Illinois, United States of America, 3 Division of Nutritional Sciences, University of Illinois, Urbana, Illinois, United States of America, 4 Department of Veterinary Clinical Medicine, University of Illinois, Urbana, Illinois, United States of America

Abstract

Background: Previously, we demonstrated that dietary protein:carbohydrate ratio dramatically affects the fecal microbial taxonomic structure of kittens using targeted 16S gene sequencing. The present study, using the same fecal samples, applied deep Illumina shotgun sequencing to identify the diet-associated functional potential and analyze taxonomic changes of the feline fecal microbiome.

Methodology & Principal Findings: Fecal samples from kittens fed one of two diets differing in protein and carbohydrate content (high–protein, low–carbohydrate, HPLC; and moderate-protein, moderate-carbohydrate, MPMC) were collected at 8, 12 and 16 weeks of age (n = 6 per group). A total of 345.3 gigabases of sequence were generated from 36 samples, with 99.75% of annotated sequences identified as bacterial. At the genus level, 26% and 39% of reads were annotated for HPLC- and MPMC-fed kittens, with HPLC-fed cats showing greater species richness and microbial diversity. Two phyla, ten families and fifteen genera were responsible for more than 80% of the sequences at each taxonomic level for both diet groups, consistent with the previous taxonomic study. Significantly different abundances between diet groups were observed for 324 genera (56% of all genera identified) demonstrating widespread diet-induced changes in microbial taxonomic structure. Diversity was not affected over time. Functional analysis identified 2,013 putative enzyme function groups were different ($p<0.000007$) between the two dietary groups and were associated to 194 pathways, which formed five discrete clusters based on average relative abundance. Of those, ten contained more ($p<0.022$) enzyme functions with significant diet effects than expected by chance. Six pathways were related to amino acid biosynthesis and metabolism linking changes in dietary protein with functional differences of the gut microbiome.

Conclusions: These data indicate that feline feces-derived microbiomes have large structural and functional differences relating to the dietary protein:carbohydrate ratio and highlight the impact of diet early in life.

Citation: Deusch O, O'Flynn C, Colyer A, Morris P, Allaway D, et al. (2014) Deep Illumina-Based Shotgun Sequencing Reveals Dietary Effects on the Structure and Function of the Fecal Microbiome of Growing Kittens. PLoS ONE 9(7): e101021. doi:10.1371/journal.pone.0101021

Editor: John Parkinson, Hospital for Sick Children, Canada

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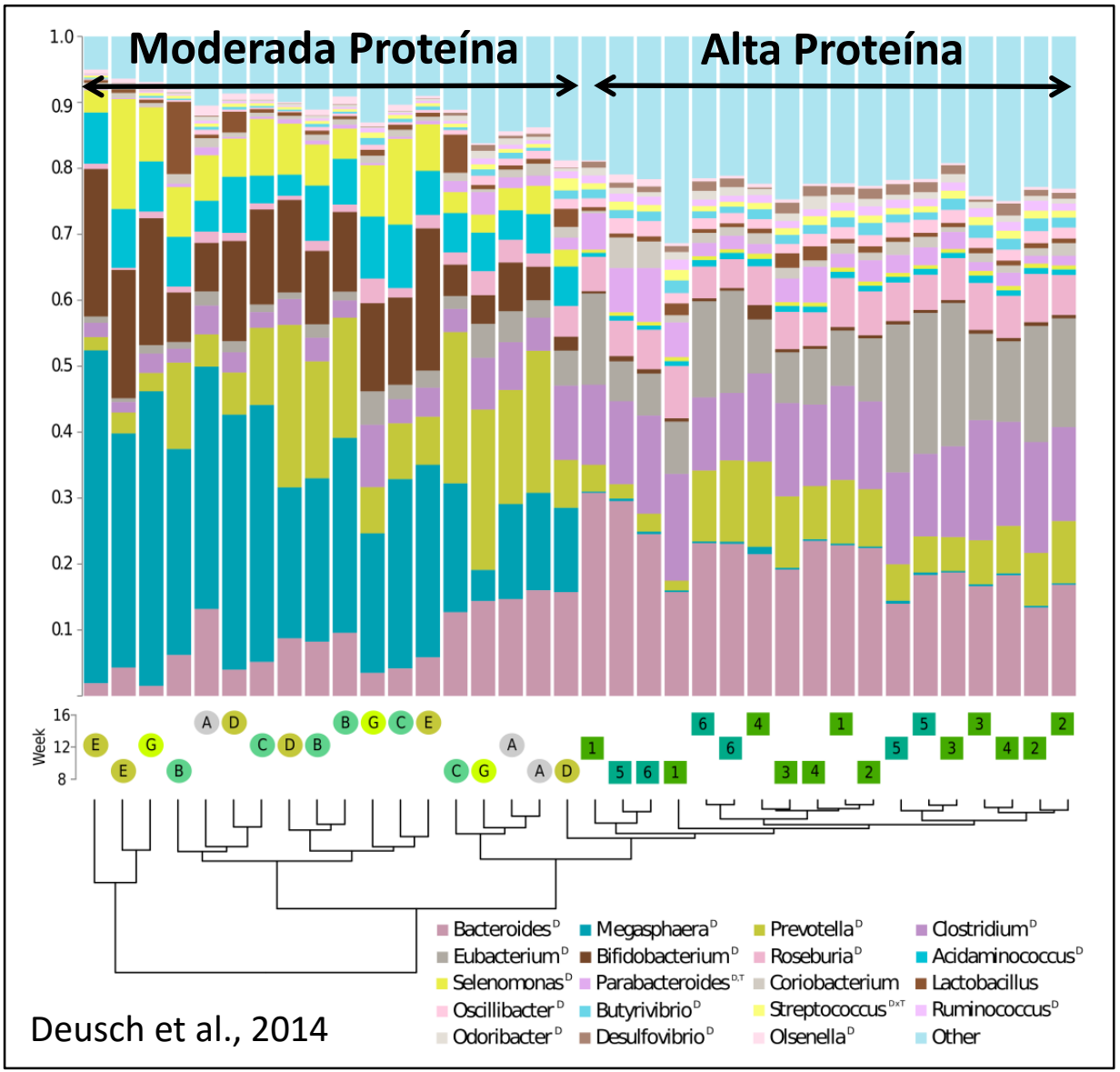
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Funding: Funding was provided by Mars Petcare. The funders had no role in study design, data collection, and decision to publish. [was the role of KSS]. KSS, OD, and CD were the primary individuals that analyzed the data and wrote the manuscript.

Competing Interests: The authors have the following interests. Funding for this study was provided by Mars Petcare. OD, CO, AC, PM, DA and PJ are employed

Deusch et al., 2014

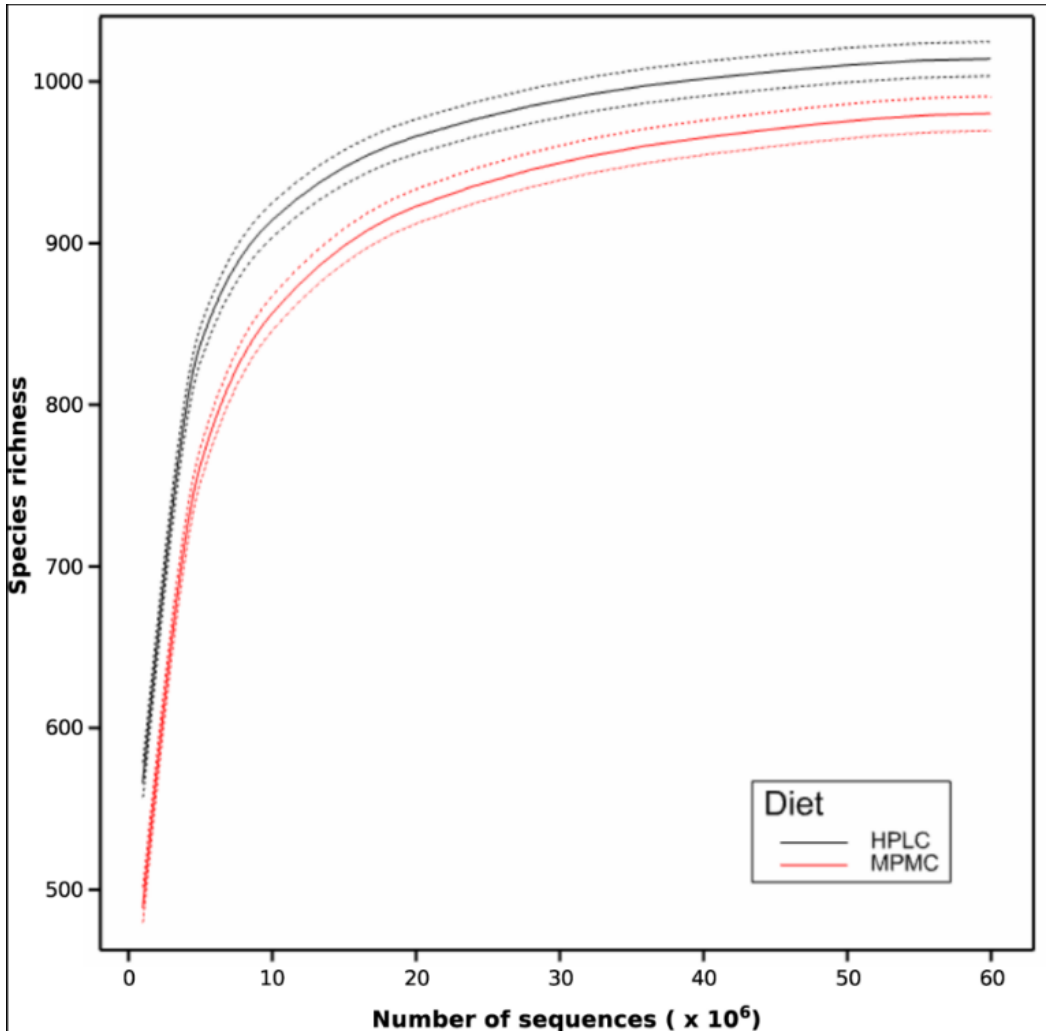
Proteína: Carboidrato Dietético – Microbioma de Gatos (filhotes)



Deusch et al., 2014

- 324 gêneros alterados pela dieta
  - 2,000 genes and 194 rotas metabólicas modificados
  - Diferenças na microbiota concordam com estudo anterior (Hooda et al., 2013)

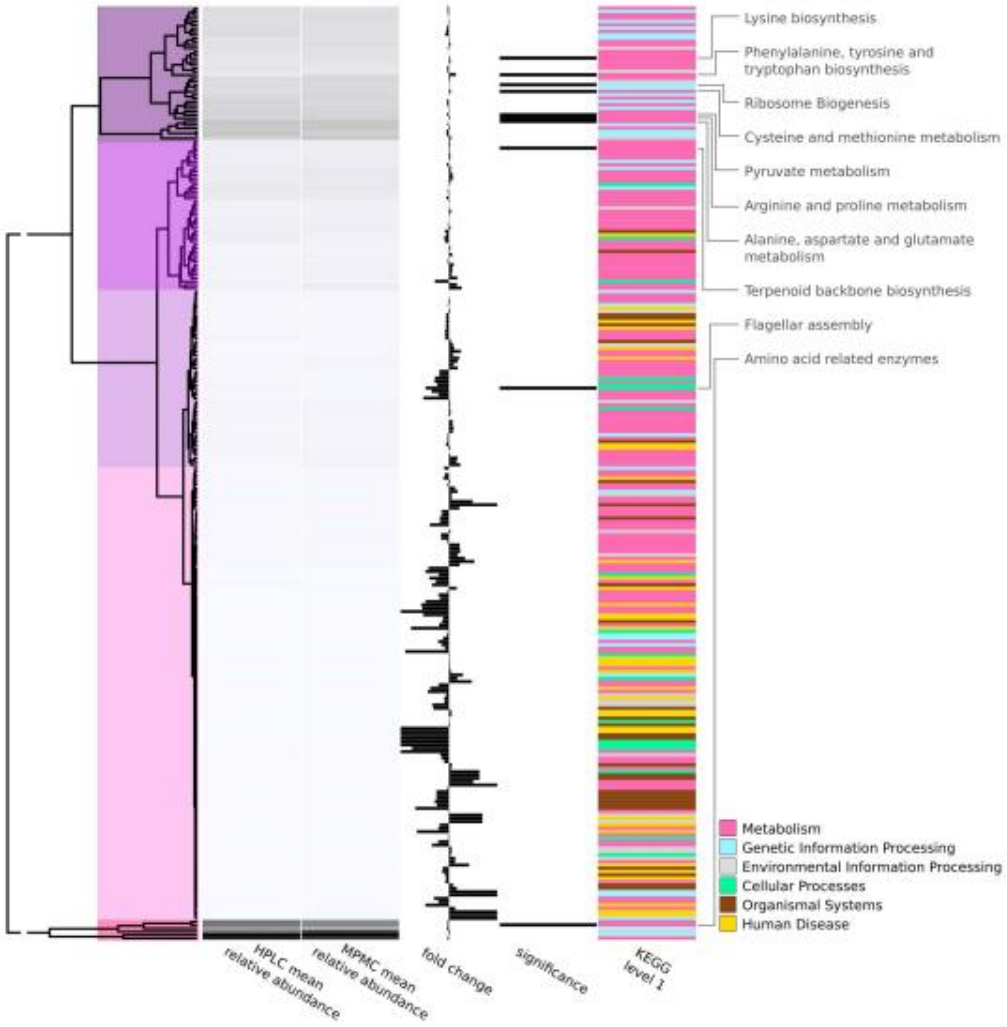
Proteína: Carboidrato Dietético – Microbioma de Gatos (filhotes)



- Alta proteína
  - Maior diversidade e menor variação entre animais
    - Microbiota mais especializada

Deusch et al., 2014

Proteína: Carboidrato Dietético – Microbioma de Gatos (filhotes)



10 rotas metabolicas

- 6 metabolismo de amino ácidos
  - ↑ proteína moderada
- Genes relacionados a degradação de mucina
  - ↑ proteína alta
    - ↑ Bacteroides

Deusch et al., 2014

Metabolomics
DOI 10.1007/s11306-013-0617-7

ORIGINAL ARTICLE

Effects of dietary macronutrient composition on the fasted plasma metabolome of healthy adult cats

Ping Deng · Janice C. Jones · Kelly S. Swanson

Received: 25 September 2013 / Accepted: 10 December 2013
© Springer Science+Business Media New York 2013

Abstract Metabolomics assays have recently been used in humans for the identification of biomarkers for dietary assessment and diseases. The application of metabolomics to feline nutrition, however, has been very limited. The objective of this study was to identify how the feline blood metabolome changed in response to dietary macronutrient composition. Twelve adult domestic cats were fed four nutritionally complete diets [control, high-fat (HF), high-protein (HP), high-carbohydrate (HC)] at amounts to maintain ideal body weight and body condition score for 16 days. Overnight fasted plasma samples were collected on day 16 and subjected to liquid/gas chromatography and mass spectrometry. Principal component analysis showed that metabolite profiles of cats fed HP, HF, and HC dietary regimes formed distinct clusters. Cats fed the HP diet had a metabolite profile associated with decreased nucleotide catabolism, but increased amino acid metabolism and ketone bodies, indicating a greater use of protein and fat for energy. Cats fed the HP diet had a significant increase in metabolites associated with gut microbial metabolism. Cats fed the HF diet had metabolites indicative of increased lipid metabolism, including free fatty acids, monoacylglycerols, glycerol-3-phosphate, cholesterol, ketone bodies, and markers of oxidative stress. γ-glutamylleucine, 3-hydroxyisobutyrate, and 3-indoxyl sulfate were identified by random forest analysis to distinguish cats fed the three macronutrient-rich diets. In conclusion, macronutrient-rich diets primarily altered markers of amino acid and lipid metabolism, with little changes in markers of carbohydrate and energy metabolism. Moreover, the HP diet influenced several metabolites originating from gut microbial metabolism.

Composição Macronutrientes – Metaboloma Felino

- Animais e dietas
  - 12 gatos adultos
  - Dietas
    - Alta-proteína(50% kcal)
    - Alta-gordura(50% kcal)
    - Alto-carboidrato(50% kcal)
    - Controle (30-35% kcal – cada macronutriente)
  - Quadrado latino replicado 4 x4
    - Período = 16 d
  - Perfil de metabólitos no plasma
    - Análise não direcionada (untargeted) GC/LC/MS

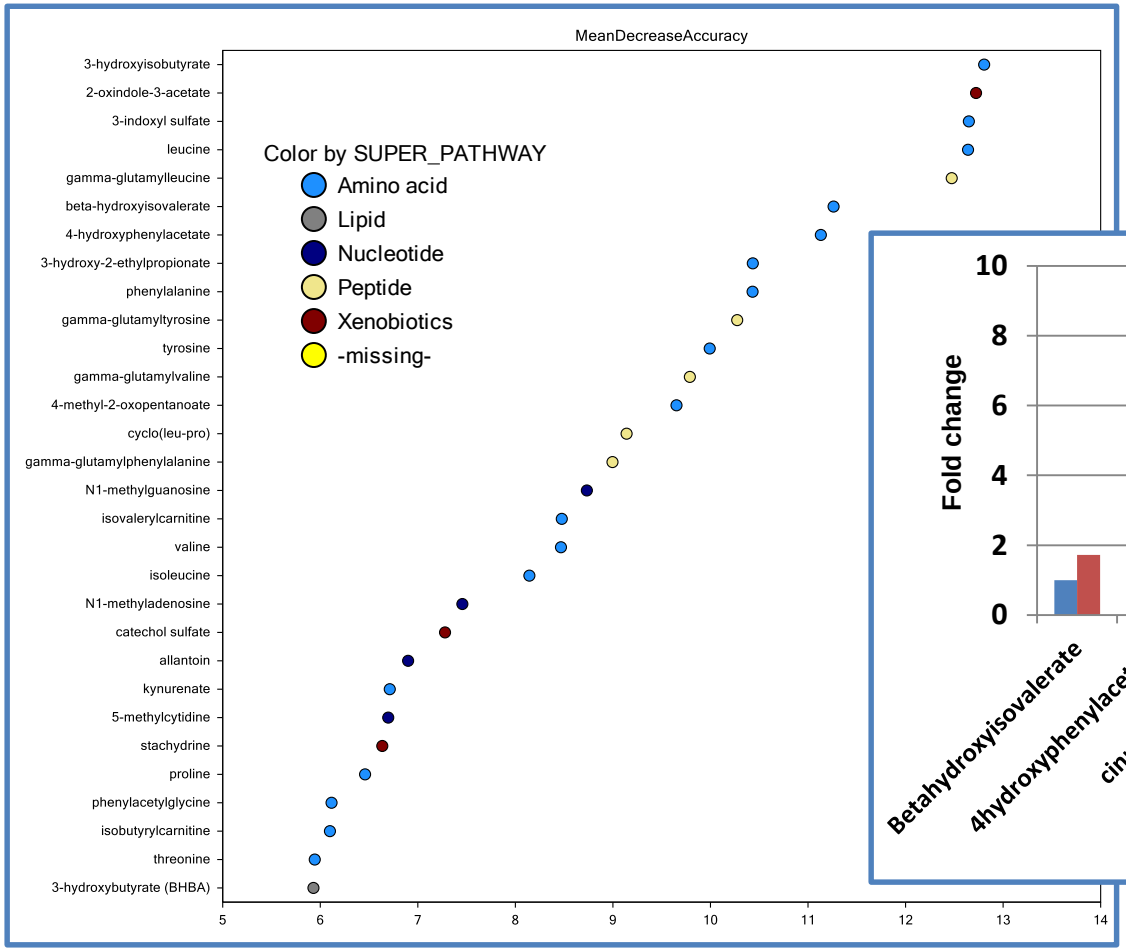
Deng et al., 2014

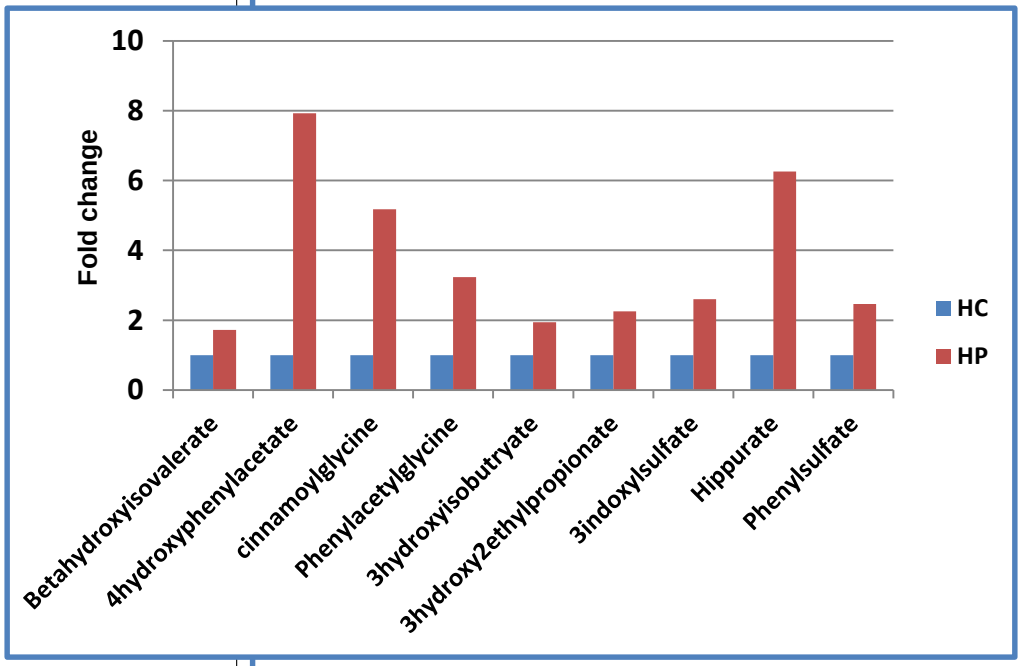
Composição Macronutrientes – Metaboloma Felino



Alta Proteína vs. Alto Carboidrato

- Alterações metabólitos associados a microbiota





Deng et al., 2014

Quase no Fim!!!



Próximos Passos…

- Existência de um núcleo comum microbiano e sua função em cães e gatos
  - Relação microbiota-microbiota e microbiota-hospedeiro
- Quais são as variações temporais na microbiota intestinal, e em outras partes do corpo, de cães e gatos
  - Fatores influenciam modulação e em que extensão

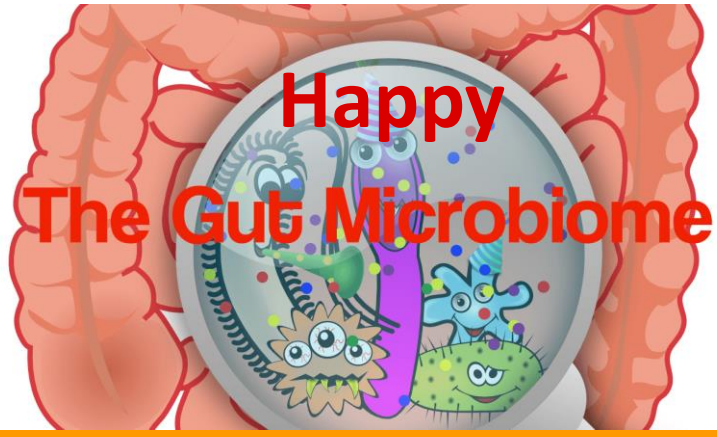
Próximos Passos…

- Necessário
  - Sequenciamento mais profundo
    - Espécies e estirpes
  - Estudos longitudinais
    - Determinar diferenças microbianas desde o nascimento até idade geriátrica, diferentes partes do corpo, ou ao longo do TGI
      - Taxa dominantes e raras (subdominates)
      - Relevância saúde ou patologias
      - Keystone (fundamental) microbiota

Objetivo Final...



- Desenvolver estratégias nutricionais e terapêuticas para ajudar na manutenção do microbioma “saudável” ou ajudar no reestabelecimento de uma microbiota “normal” em quadros patológicos



Obrigada!

UNIVERSITY OF ILLINOIS
AT URBANA - CHAMPAIGN

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Probióticos & Antibióticos

- Área emergente de pesquisa
  - Poor quality control of commercial products
  - ↑ in probiotic bacteria in gut
  - Little evidence of clinical benefits
  - Shift in microbiome?
  - Which strains?
  - Effective dose?