

Supplementary Material

Parasite-microbiota interactions with the vertebrate gut: synthesis through an ecological lens

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1 Supplementary Tables

Supplementary Table S1. Summary table of studies investigating helminth-induced alterations to the gut microbiota in vertebrates

Host	Helminth species	Infective dose	Sampling time (days p.i.)	Sample site(s)	Microbiota diversity	Microbiota composition			Reference
						Phylum	Family	Genus	
Swine									
Pig	<i>Trichuris suis</i>	2x10 ⁴	21	Luminal contents from colon	No change	↑Deferribacteres ↑Proteobacteria		↑ <i>Desulvibrio</i> ↑ <i>Mucispirillum</i> ↑ <i>Paraprevotella</i> ↓ <i>Asteroleplasma</i> ↓ <i>Blautia</i> ↓ <i>Coprobacillus</i> ↓ <i>Dorea</i> ↓ <i>Eubacterium</i> ↓ <i>Oribacterium</i> ↓ <i>Oscillibacter</i> ↓ <i>Peptococcus</i> ↓ <i>Scwartzia</i> ↓ <i>Selenomonas</i> ↓ <i>Spirochaeta</i> ↓ <i>Sporobacter</i> ↓ <i>Succinivibrio</i>	Li et al., 2012

Pig	<i>Trichuris suis</i>	2x10 ⁴	53	Luminal contents from colon	N/A	↓Fibrobacteres ↓Spirochaetes ↓Tenericutes ↓Gemmatimonadetes		↓ <i>Fibrobacter</i> ↓ <i>Treponema</i> ↓ <i>Spirochaeta</i> ↓ <i>Dorea</i> ↓ <i>Brachyspira</i> ↓ <i>Mycoplasma</i> ↓ <i>Thermotoga</i> ↓ <i>Actinobacillus</i> ↓ <i>Francisella</i> ↓ <i>Erysipelothrix</i> ↓ <i>Ruminococcus</i>	Wu et al., 2012
Pig	<i>Ascaris suum</i>	5000	14	Proximal gut	No change			↑ <i>Cellulosimicrobium</i> ↑ <i>Facklamia</i> ↑ <i>Haemophilus</i> ↑ <i>Succinivibrio</i> ↑ <i>Turicibacter</i> ↑Paraprevotellaceae uc. ↑Pasteurellaceae uc. ↑Planococcaceae uc. ↑Porphyromonadaceae uc. ↑Succinivibrionaceae uc. ↓ <i>Catenibacterium</i> ↓Veillonellaceae uc.	Williams et al., 2017
Rodent									
Mouse	<i>Trichuris muris</i>	20	14, 28, 42, 49, 56, 63, 70, 77, 84, 91	Feces	Decreased alpha diversity on days 41 and 91		↑Rikenellaceae ↑Family F16 from TM7 phylum	↑ <i>Mucispirillum</i> ↓ <i>Prevotella</i> ↓ <i>Parabacteroides</i>	Houlden et al., 2015
Mouse	<i>Trichuris muris</i>	20	13, 20, 27, 35	Feces for days 13, 20, 27; Luminal contents from colon on day 35	Decreased alpha, beta, and gamma diversity after day 27	↑Firmicutes ↑Proteobacteria ↓Bacteroidetes	↑Lactobacillaceae ↑Rikenellaceae ↓Desulfovibrionaceae ↓Ruminococceae ↓Erysipelotrichaceae	↑ <i>Bifidobacterium</i> ↑ <i>Lactobacillus</i> ↑ <i>Alistipes</i> ↑ <i>Odirobacter</i> ↑ <i>Oscillibacter</i> ↑ <i>Butyricicoccus</i> ↑ <i>Parasutterella</i> ↑ <i>Sphingomonas</i> ↑ <i>Halomonas</i> ↑ <i>Mucispirillum</i> ↓ <i>Parabacteroides</i> ↓ <i>Barnesiella</i> ↓ <i>Allobaculum</i> ↓ <i>Roseburia</i> ↓ <i>Sporobacter</i>	Holm et al., 2015

Mouse	<i>Trichuris muris</i>	25	21, 35	Feces, SI mucosa	Decreased alpha diversity in WT infected animals, but increased alpha diversity in Nod2 ^{-/-}		↑Lachnospiraceae ↑Clostridiales (order)	↓ <i>Prevotella</i> ↓ <i>Bacteroides</i>	Ramanan et al., 2016
Mouse	<i>Trichuris muris</i>	200	20-22, 26-29	Feces	Decreased alpha diversity in re-wilded mice			In the lab: ↑ <i>Alistipes</i> (reversed in re-wilded mice) ↓ <i>Ruminococcus</i> ↓ <i>Allobaculum</i> ↓ <i>Barnesiella</i> (reversed in re-wilded mice)	Leung et al., 2018
Mouse	<i>Heligmosomoides polygyrus</i>	200	12, 35	Feces, SI mucosa	N/A		↑Clostridiales (order)	↓ <i>Bacteroides</i>	Ramanan et al., 2016
Mouse	<i>Heligmosomoides polygyrus bakeri</i>	200	6, 14, 28	Luminal contents from ileum, cecum, and colon	N/A	↑g-Proteobacterium	↑Enterobacteriaceae ↑Porphyromonadaceae	↑ <i>Lactobacillus</i> ↑ <i>Bacteroides</i> ↑ <i>Prevotella</i> ↓ <i>Paenibacillus</i>	Rausch et al., 2013
Mouse	<i>Heligmosomoides polygyrus bakeri</i>	200	28	Duodenum, feces	N/A		↑Enterobacteriaceae	↑ <i>Lactobacillus</i>	Reynolds et al., 2014
Mouse	<i>Heligmosomoides polygyrus</i>	N/A	14	Ileum, cecum tissue	N/A		↑Lactobacillaceae ↑Clostridaceae ↑Porphyromonadaceae ↓Erysipelotrichaceae ↓Clostridiales (order)		Walk et al., 2010
Mouse	<i>Heligmosomoides polygyrus bakeri</i>	200	21	Cecal contents	Not consistent		↑Clostridiales (order)	↑ <i>HA-107 E. coli</i>	Zaiss et al., 2015
Mouse	<i>Nippostrongylus brasiliensis</i>	500	11	SI lumen; feces	No change	↑ <i>Bacteroides</i> ↑Actinobacteria ↓Firmicutes	↑Lactobacillaceae ↑S24-7 Family ↑Coriobacteriaceae ↓Peptostreptococcaceae ↓Clostridiaceae ↓Turicibacteraceae		Fricke et al., 2015

Mouse	<i>Trichinella spiralis</i>	300-500	12	SI and LI luminal contents	N/A		↑Clostridiales (order) ↑Ruminococcaceae ↑Lachnospiraceae ↑Lactobacillaceae ↓Clostridiceae ↓Turicibacteraceae		Osborne et al., 2014
Wild mouse	<i>Heligmosomoides polygyrus</i> ; <i>Syphacia</i> spp.; <i>Hymenolepis</i> spp.	N/A	N/A	Lumen of stomach, SI, cecum, and distal colon	No change	<i>H. polygyrus</i> : ↑Firmicutes ↓Bacteroidetes <i>Syphacia</i> spp: ↑Bacteroidetes ↓Firmicutes	<i>H. polygyrus</i> & <i>Syphacia</i> spp: ↓Lachnospiraceae ↓Lactobacillaceae ↓Ruminococcaceae ↓Acetobacteraceae ↓Sphingomonadaceae ↓S24-7 <i>Hymenolepis</i> spp: ↑S24-7 ↑Lactobacillaceae		Kreisinger et al., 2015
Wild mouse	<i>Heligmosomoides polygyrus</i>	N/A	N/A	Feces	N/A			↑Escherichia ↓Lachnospiraceae uc.	Maurice et al., 2015
Rat	<i>Hymenolepis diminuta</i>	4	62	Luminal contents of cecum	No change		↑Peptostreptococcaceae	↓ <i>Turicibacter</i>	McKenney et al., 2015
Rat	<i>Hymenolepis diminuta</i>	10 each for 3 days	3 consecutive days followed by a 7-10 day gap for 50 days	Feces	No change in alpha diversity; shifts in beta diversity		↑Erysipelotrichaceae ↑S24-7 ↑Ruminococcaceae ↑Mollicutes order RF39	↑ <i>Turicibacter</i> ↑ <i>Sutterella</i>	Parfrey et al., 2017
Hamster	<i>Opisthorchis viverrini</i>	50	42	Feces from colon and rectum; bile from bile duct	Increased alpha diversity	↑Spirochaetes	↑Ruminococcaceae ↑Lachnospiraceae ↓Porphyromonadaceae ↓Erysipelotrichaceae	↑ <i>Lactobacillus</i>	Plieskett et al., 2013
Rabbit	<i>Trichostrongylus retortaeformis</i>	1000 every 7 days	0, 15, 30, 60	Mucosa of duodenum	Decreased alpha diversity	↑Proteobacteria ↑Spirochaetes ↓Firmicutes	↑Leptosiraceae ↑Desulfobacteraceae ↓Ruminococcaceae ↓Porphyromonadaceae ↓Bacteroidaceae	↑ <i>Leptomna</i> ↑ <i>Desulfocella</i> ↓ <i>Ruminococcus</i> ↓ <i>Bacteroides</i>	Cattadori et al., 2016
Ruminant									
Goat	<i>Haemonchus contortus</i>	5,000	50	Lumen of abomasum	No change	↓Euryarchaeota	↑Pasteurellales (order) ↑Prevotellaceae	↑ <i>Prevotella</i> ↑ <i>Selenomonas ruminantium</i>	Li et al., 2016

Sheep	<i>Haemonchus contortus</i>	5,000	7, 50	Rumen and abomasum fluids	Increased alpha diversity	In abomasum fluids: ↑Lentisphaerae* ↑Bacteroidetes* ↑Tenericutes* ↑Candidate_division_TM7* ↑Synergistetes ↑Firmicutes* ↑Elusimicrobia ↑Fibrobacteres* ↑Proteobacteria* ↑Cyanobacteria ↑Actinobacteria* ↑Spirochaetae *Also ↑ in rumen fluid		↑ <i>Prevotella</i>	El-Ashram et al., 2017
Calf	<i>Ostertagia ostertagi</i>	1x10 ⁵	14	Lumen of abomasum	No change			↑ <i>Ethanoligenes</i> ↓ <i>Subdoligranulum</i>	Li et al., 2011
Companion animal									
Dog	<i>Ancylostoma caninum</i>	N/A	N/A	Feces	No change				Slapeta et al., 2015
Cat	<i>Toxocara cati</i>	N/A	N/A	Feces	No Change	↑Actinobacteria	↑Coriobacteriaceae ↑Enterococcoceae	↑ <i>Collinsella</i> ↑ <i>Enterococcus</i> ↑ <i>Dorea</i> ↑ <i>Ruminococcus</i> ↓ <i>Bulleidia</i> ↓ <i>Jeotgalicoccus</i>	Duarte et al., 2016
Primate									
Macaque	<i>Trichuris trichiura</i>	1,000	98	Colon mucosa	Increased alpha diversity (although not statistically significant)	↑Tenericutes ↑Bacteroidetes ↑Elusimicrobia ↓Cyanobacteria ↓ZB2		↓ <i>Streptophyta</i>	Broadhurst et al., 2012
Human with Celiac's Disease	<i>Necator americanus</i>	20	0, 56	Feces	No change				Cantacessi et al., 2014
Human with Celiac's Disease	<i>Necator americanus</i>	20	168, 252	Mucosa of duodenum	Increased alpha diversity at 168 days; returned to baseline at 252 days	↑Bacteroidetes			Giacomin et al., 2016

Human	Mix of <i>Trichuris</i> spp., <i>Ascaris</i> spp., and hookworms	N/A	N/A	Feces	No difference in alpha diversity; Increased beta diversity		<p>↑Verrucomicrobiaceae ↑Enterobacteriaceae</p> <p>↓Bacteroidaceae ↓Leuconostocaceae</p>	<p>↑<i>Lactococcus</i> ↑<i>Akkermansia</i> ↑Undefined Enterobacteriaceae</p> <p>↓<i>Bacteroides</i></p>	Jenkins et al., 2017
Human	Mix of <i>Trichuris</i> spp., <i>Ascaris</i> spp., and hookworms	N/A	N/A	Feces	Increased alpha diversity		↑Paraprevotellaceae	↓ <i>Bifidobacterium</i>	Lee et al., 2014
Human	Mix of <i>Trichuris trichiura</i> and <i>Ascaris lumbricoides</i>	N/A	N/A	Feces	<p><i>T. trichiura</i> only: No change</p> <p>Mix of <i>T. trichiura</i> & <i>A. lumbricoides</i>: Decreased alpha diversity</p>			<p>Mix of <i>T. trichiura</i> and <i>A. lumbricoides</i>: ↑<i>Streptococcus</i></p>	Cooper et al., 2013
Human	Mix of <i>Trichuris</i> spp., <i>Ascaris</i> spp. and hookworms	N/A	N/A	Feces	Increased alpha diversity	After self-clearing*: ↑Synergistetes (*Note: These are individuals going from worm-positive to worm-negative)	<p>After deworming*: ↓Sutterellaceae</p> <p>After self-clearing*: ↑Porphyromonadaceae ↑Bacteroidaceae (*Note: These are individuals going from worm-positive to worm-negative)</p>	<p>After deworming*: ↑<i>Sphingobacterium</i> ↑<i>Clostridium_XVIII</i> ↓<i>Xylanibacter</i> ↓<i>Leuconostoc</i> ↓<i>Butyricimonas</i></p> <p>After self-clearing*: ↑<i>Parabacteroides</i> ↑<i>Bacteroides</i> ↓<i>Olsenella</i> (*Note: These are individuals going from worm-positive to worm-negative)</p>	Rosa et al., 2018
Human	<i>Enterobius vermicularis</i>	N/A	N/A	Feces	Increased alpha diversity			<p>↑<i>Alistipes</i> ↑<i>Faecalibacterium</i></p> <p>↓<i>Fusobacterium</i> ↓<i>Veilonella</i> ↓<i>Megashpaera</i> ↓<i>Acidaminococcus</i> (Note: The corrected p-values (FDRs) for all these taxa were >0.05.)</p>	Yang et al., 2017