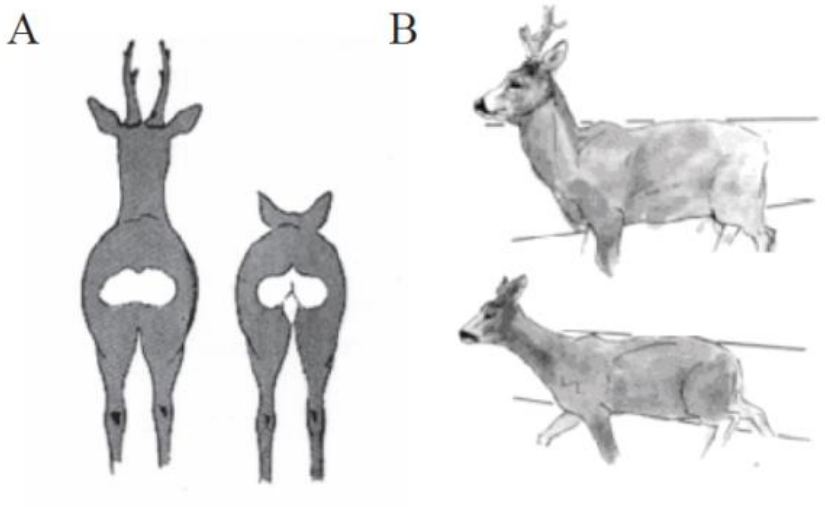

Figure 1 - (A) Determination of sex by the mirror (female to the right) or (B) body corpulence (female underside). Mirror corresponds to erectile light fur on the bottom.

Parameters		Notations	Units	Determination
White blood cells numeration		WBC	x103/µL	Flow cytometry
Proportions of WBC's subpopulation	**Neutrophils**	GNN%	%	Manual reading
	Monocytes	Mono%	%	Manual reading
	Lymphocytes	Lympho%	%	Manual reading
	Eosinophils	GNE%	%	Manual reading
Concentrations of WBC's subpopulation	**Neutrophils**	GNN	$x10^3/\mu L$	GNN=GNN%*WBC
	Monocytes	Mono	$x10^3/\mu L$	Mono=mono%*WBC
	Lymphocytes	Lympho	$x10^3/\mu L$	Lympho=Lympho%*WBC
	Eosinophils	GNE	$x10^3/\mu L$	GNE=GNE%*WBC
	Hemolysis	HL	$-\log_2$ (dilution)	Functional test
	Hemagglutination	HA	$-\log_2$ (dilution)	Functional test

Table 1- Immune parameters measured thanks to blood samples done during capture; their abbreviations, units and determination methods.

		2008	2009	2010	2011	2012	2013	2014	2015
protozoan	*Babesia.sp*	0%	5.9%	0%	0%	86.9%	67.7%	70%	M
		N=1	N=34	N=24	N=42	N=23	N=31	N=20	
	Toxoplasma gondii	24.4%	79.5%	55.8%	25.5%	34.9%	34.2%	31.4%	M
		N=41	N=44	N=43	N=51	N=43	N=38	N=35	
	Neospora caninum	2.4%	0%	2.3%	0%	23.5%	18.9%	0%	M
		N=41	N=44	N=43	N=44	N=37	N=36	N=31	
bacteria	*Anaplasma.sp*					63.4%	89.5%	79.5%	85.7%
						N=41	N=38	N=44	N=49
	Chlamydophila abortus	2.4%	11.9%	37.2%	27.4%	0%			
		N=41	N=42	N=43	N=51	N=43			
	Coxiella burnetii	24.4%	11.4%	2.3%	0%	2.3%	3.2%	6.8%	0%
		N=41	N=44	N=43	N=51	N=43	N=31	N=44	N=50
	Mycobacterium avium	0%	4.5%	0%	0%	0%			
		N=41	N=44	N=42	N=51	N=43			
	Mycoplasma agalactiae	34.1%	2.32%	0%	0%				
		N=41	N=43	N=42	N=51				
Virus	*Btv*	0%	0%	5.5%	0%	0%			
		N=2	N=43	N=36	N=51	N=43			
	Bvdv	46.3%	19%	0%	0%	0%			
		N=41	N=42	N=43	N=51	N=43			
	Ibr	0%	2.3%	2.6%	0%	18.6%			
		N=41	N=44	N=39	N=51	N=43			
	Schmallenberg					0%	73%	40%	M
						N=42	N=37	N=40	
	Caev	7.3%	2.4%	0%	0%	0%		0%	M
		N=41	N=44	N=43	N=50	N=41		N=40	

Table 2- Parasites controlled (virus, bacteria and protozoan) by blood samples (and vaginal swabs). Their annual prevalences, in the population, are indicated in percentage. M is for missing values to this day. Blanked boxes indicated that parasites have not been searched. N is the number of individuals tested for the presence of parasites (N=378)

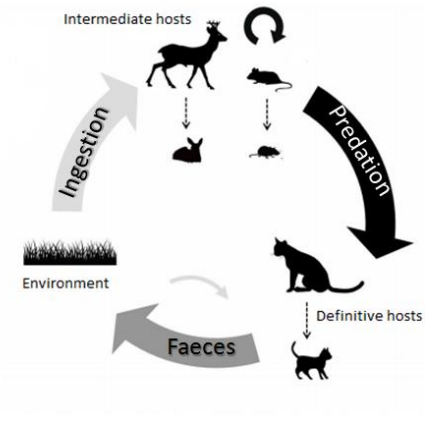

Figure 2- *Toxoplasma gondii* life cycle. Dotted arrows are for vertical transmission while full ones represent horizontal transmission (according to Gilot-Fromont 2012). Intermediate host gets infected by ingesting aliments or water contaminated by cats feces. Intermediate host is predated by definitive host (felines) and it has come full circle.

		2008	2009	2010	2011	2012	2013	2014	2015
nematodes	*Nematodirus*	**23.1%** N=39	**17.7%** N=45	**32.5%** N=43	**11.9%** N=42	**27.5%** N=40	**8.33%** N=36	**13.9%** N=43	**16%** N=50
	Dicrocoelium	Absent in the whole population							
	Nematodes gastrointestinal	**87.1%** N=39	**84.4%** N=45	**88.4%** N=43	**64.3%** N=42	**72.5%** N=40	**83.3%** N=36	**79.1%** N=43	**90%** N=50
	Strongyloides	**41%** N=39	**22.2%** N=45	**0%** N=43	**26.2%** N=42	**0%** N=40	**11.1%** N=36	**2.3%** N=43	**8%** N=50
	Haemonchus contortus							**2.6%** N=39	**2.4%** N=41
	Trichuris	**15.4%** N=39	**0%** N=45	**0%** N=43	**4.8%** N=42	**0%** N=39	**0%** N=40	**0%** N=43	**0%** N=50
	Oxyure	**15.4%** N=39	**0%** N=45	**0%** N=44	**4.8%** N=42	**0%** N=40	**0%** N=43		
	Capillaria	**2.6%** N=39	**0%** N=45	**0%** N=43	**0%** N=42	**0%** N=39	**0%** N=40		
protozoan	*Coccidian*	**41%** N=39	**43.5%** N=46	**25.5%** N=43	**0%** N=42	**5%** N=40	**0%** N=43	**2.1%** N=41	**14.6%** N=48
tapeworms	*Moniezia*	**11%** N=35	**2.5%** N=39	**2.3%** N=42	**5%** N=40	**0%** N=34	**0%** N=35	**0%** N=43	NA

Table 3- Parasites controlled by feces samples and their annual prevalences in the population. Blanked boxes indicate that parasite has not been searched. N is the number of individuals tested (N=378)

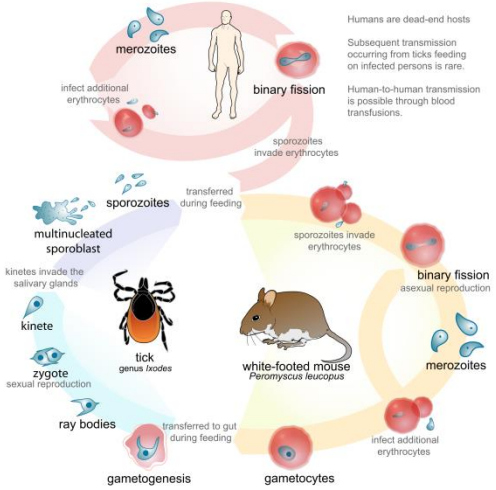

Figure 3- Transmission mode of *Babesia.sp* (source Mariana Ruiz Villarreal)

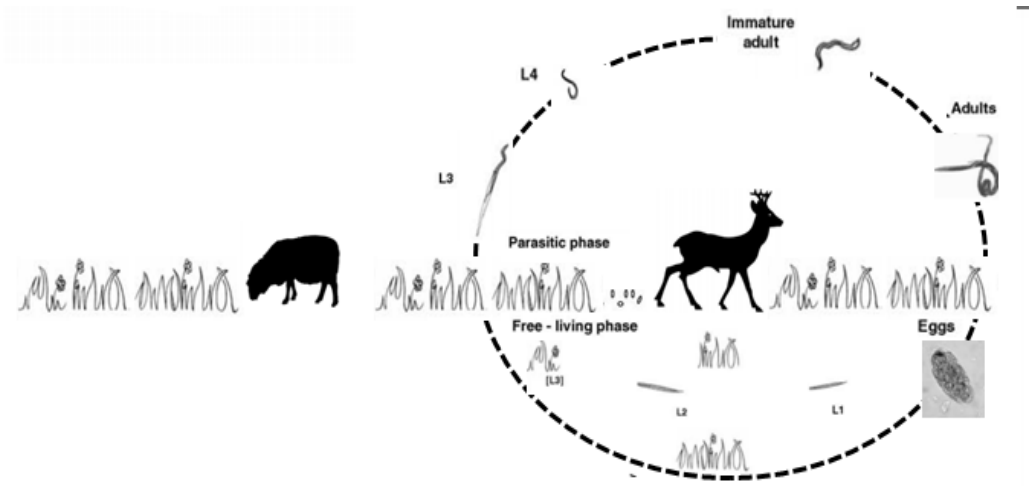

Figure 4- Life cycle of gastrointestinal nematodes, according to Hoste *et al.* 2010. Eggs are emitted in feces. L1, L2, L3 are for the larval stage.

Capture steps	Behaviours	Notations	Descriptions
In the net	Struggle	No struggle (0) Moderately Struggle(0.5) Strongly struggle(1)	Animal tries to escape giving punches.
In the box	Toss and turn	No (0) Yes(1)	Animal has turn upside down in the box
During Manipulation	Struggle	No Struggle (0)	Animal do not try to escape
		Struggle or pant(0.5)	Animal try to escape or pant
		Struggle and Pant(1)	Animal try to escape and pant.
At the release	Flight behavior	Trot (0)	Animal goes away without running
		Moderate run (0.5)	Animal goes away by running sinuously (hesitate)
		Speed run (1)	Animal goes away by running straight on (do not hesitate)
	Scrub the collar	No(0) Yes(1)	Animal tries to remove its collar

Ethogram 1- Description and notations of behavioral items measured during capture, at different capture steps.

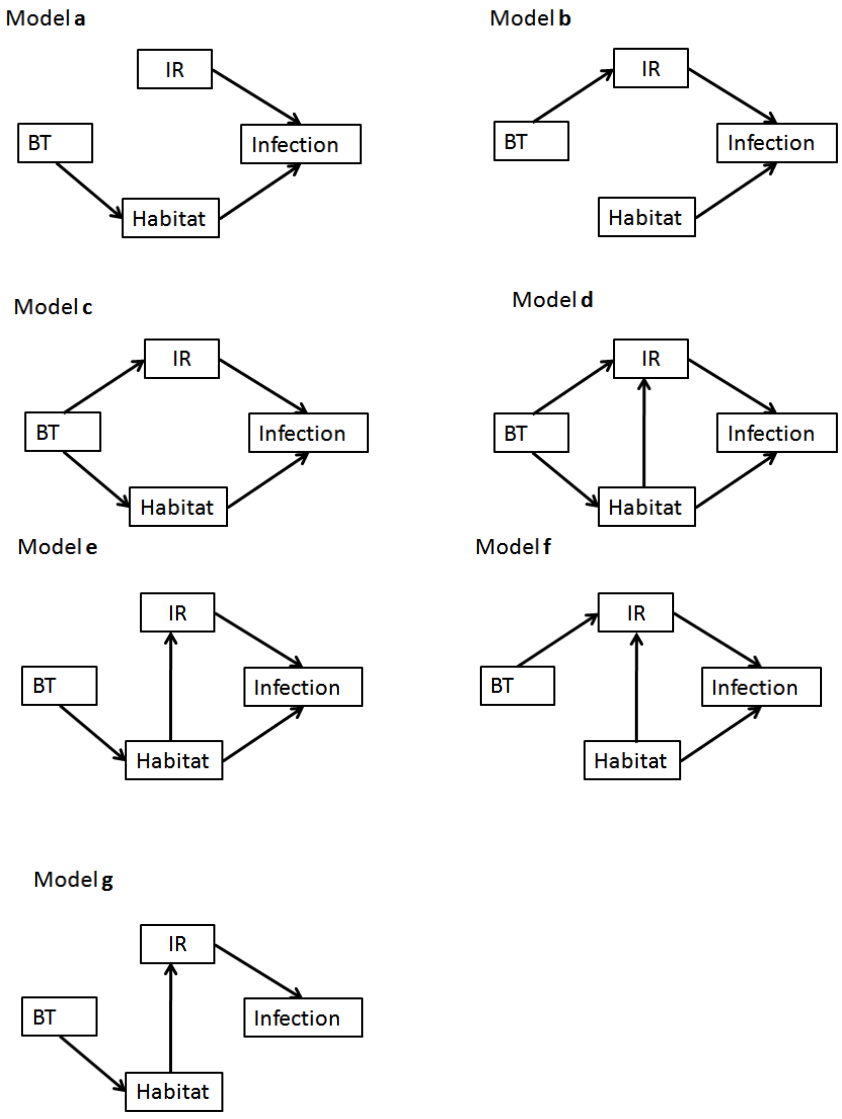

Figure 5- Different path models tested. BT stands for behavioural traits (Behavioural score, mobility) and IR for immune response. Arrows are for "causal links" tested.

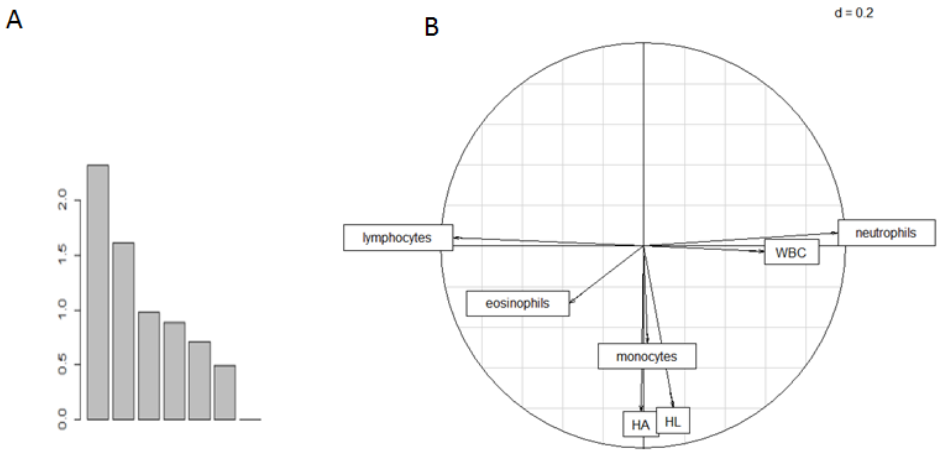

Figure 6- Principal Component Analysis for immune parameters. A: decomposition of variance among principal components B: correlation circle showing the projection of immune parameters on axis 1(x) and axis2(y). HA stands for hemagglutination HL stands for hemolysis and WBC for White Blood Cells counts.

Model	Age	Sex	Axis 1	Body Mass	BS	Pi	habitat	df	AICc	deltaAICc	Weight
1			+		+	+	+	5	179.3	0.00	0.17
2			+		+	+		4	179.6	0.25	0.15
3	+		+		+	+	+	7	180.2	0.85	0.11
4			+	+	+	+	+	6	180.4	1.05	0.10
5			+	+	+	+		5	180.4	1.12	0.10
6		+	+		+	+	+	6	180.5	1.16	0.10
7	+		+		+	+		6	180.6	1.25	0.09
8		+	+		+	+		5	181.0	1.66	0.07
9	+		+	+	+	+	+	8	181.2	1.86	0.07

Table 4 - Models retained after selection by AICc, representing the effect of behavioural score (BS), immune response (axes 1&2), habitat and confounding variables. Model 1, with the lowest AICc was retained in the aim of Path Analysis.

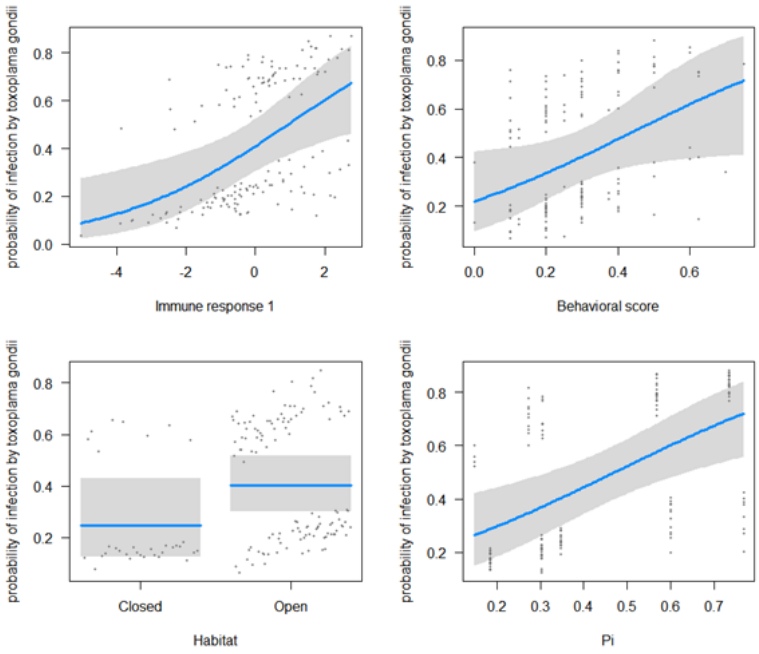

Figure 7- Representation of prediction for the different independent variables having an effect on probability of being infected by *Toxoplasma gondii*. Axis Y represents the probability of being infected by *toxoplasma gondii*; axis X represents from left to right: immune response 1, behavioural score for up plots and habitat and probability of getting infected in population, for bottom plots**.** In blue the predictions, in light the confidence intervals and the points are the partial residuals.

Model	Axis1	Axis2	Body Mass	Mobility	Pi	habitat	df	AICc	deltaAICc	Weight
1	+		+	-	+	+	6	95.4	0.00	0.27
2	+			-	+	+	5	96.3	0.84	0.18
3	+		+	-		+	5	96.5	1.07	0.16
4	+				+	+	5	96.8	1.33	0.14
5	+	+	+	-	+	+	7	97.1	1.64	0.12
6	+				+	+	4	97.4	1.94	0.10

Table 5- Models with a difference in AICc below 2 units, representing the effect of mobility, immune response (axes 1&2), habitat and confounding variables on infection by *Toxoplasma gondii*. Model 1, with the lowest AICc was retained in the aim of Path Analysis.

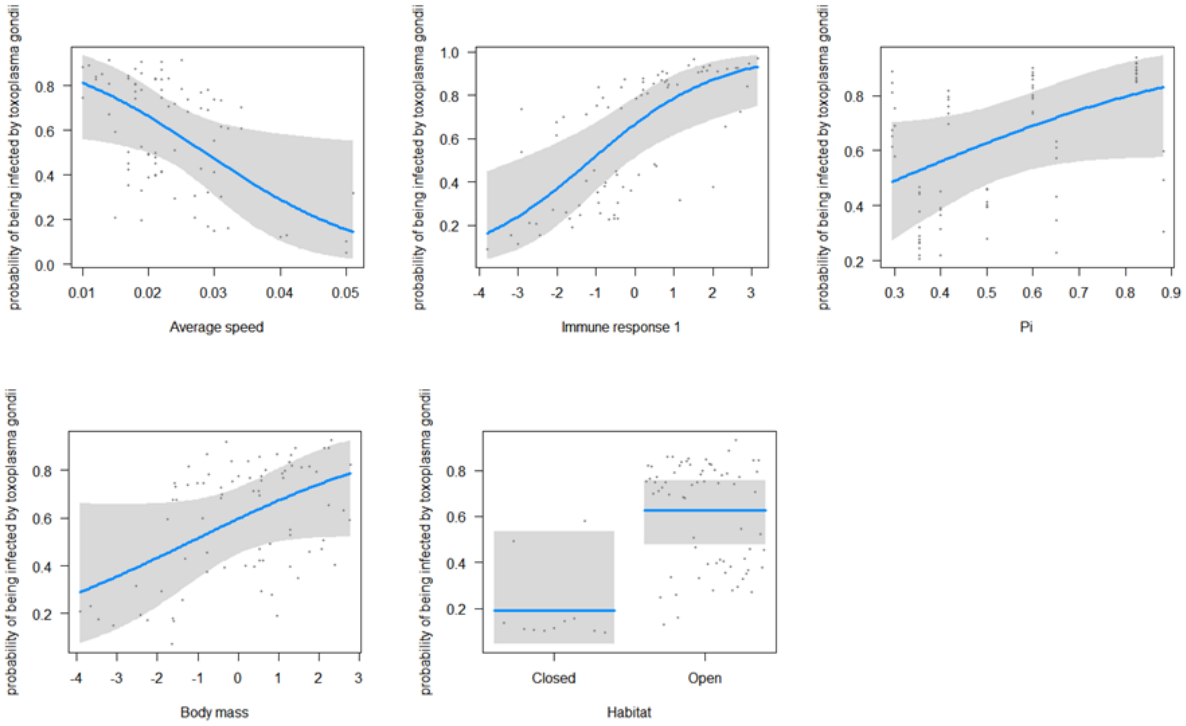

Figure 8- Representation of predictions for the different independent variables having an effect on probability of being infected by *Toxoplasma gondii*. Axis Y represents the probability of being infected by *Toxoplasma gondii*; axis X represents from left to right: Average speed, Immune response 1, prevalence in the population for up plots and body mass and habitat, for bottom plots. In blue the predictions, in light the confidence intervals and the points are the partial residuals.

Models	Sex	Pi	Body mass	BS	Habitat	df	AICc	DeltaAICc	Weight
1	+	+	-	-	+	6	45.6	0	0.17
2			-	-		3	45.7	0.13	0.16
3			-	-	+	4	45.7	0.15	0.16
4	+		-	-	+	5	46.2	0.60	0.13
5	+		-	-		4	46.5	0.95	0.11
6	+	+	-	-		5	46.8	1.21	0.09
7		+	-	-		4	47.2	1.61	0.08
8		+	-	-	+	5	47.2	1.66	0.07

Table 6- Models with a difference in AICc below 2 units. Models selection was based on the influence of immune response 1 and 2, habitat, behavioural score (BS) and confounding variable on infection by *Babesia.sp*. No model were retained in the aim of Path analyses.

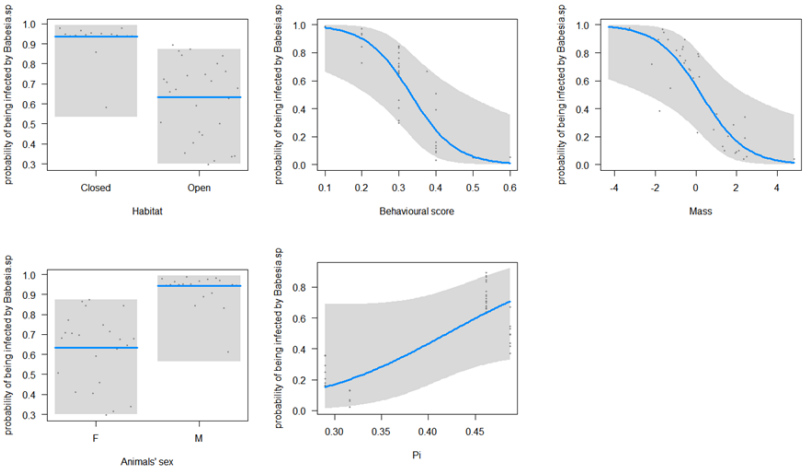

Figure 9- Predictions of the independent variables on probability of being infected by *Babesia.Sp*. X axis represents from left to right: habitat, behavioural score, body mass for up plots and animals' sex and prevalence in the population for bottom plots. In blue the predictions, in light the confidence intervals and the points are the partial residuals.

Models	Sex	Axis	Axis2	Body Mass	Pi	Habitat	df	AICc	deltaAICc	Weight
1	+						2	22.7	0.00	0.19
2	+		-				3	23.0	0.27	0.17
3	+	-					3	23.4	0.71	0.13
4	+				+		3	24.1	1.39	0.09
5	+			-			3	24.4	1.72	0.08
6	+					+	3	24.5	1.77	0.08
7	+	-	-				4	24.5	1.84	0.07
8	+		-			+	4	24.6	1.90	0.07
9			-		+		5	24.6	1.92	0.07

Table 7- Models with a difference in AICc below 2 units. Models selection was based on the influence of immune response (axes 1&2), habitat, mobility and confounding variable on infection by *Babesia.sp*. No models were retained in the aim of Path analyses.

Model	Axis 1	Axis 2	Age	Body mass	BS	Pi	df	AICc	delta AICc	Weight
1	+			-			4	421.0	0.00	0.23
2	+			-	-		5	422.0	0.93	0.14
3	+						3	422.3	1.27	0.12
4	+			-			3	422.7	1.61	0.10
5		-		-			5	422.7	1.64	0.10
6	+		+	-			6	422.8	1.80	0.09
7	+				-		4	422.9	1.81	0.09
8	+			-		+	5	422.9	1.86	0.09

Table 8- Models with a difference in AICc below 2 units. Models selection was based on the influence of immune response (axes 1&2), habitat, behavioural score (BS) and confounding variables on infection by gastrointestinal nematodes. No models were retained, in the aim of Path analyses.

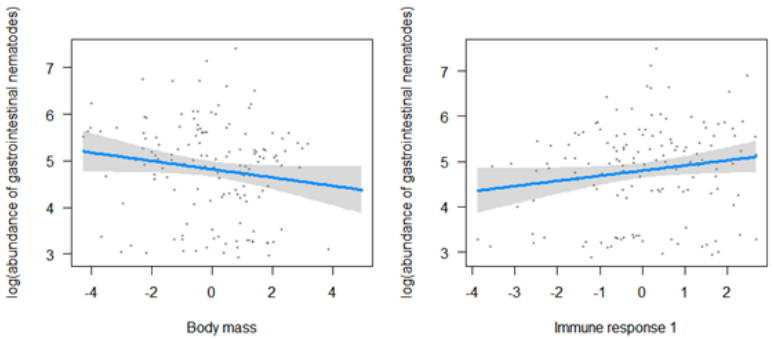

Figure 10- Predictions for gastrointestinal nematodes. X axis represents body mass (left) and immune response 1 (right). In blue the predictions, in light the confidence intervals and the points are the partial residuals. On the x axis body mass and on Y axis the log abundance of gastrointestinal nematodes.

Causal models	C-value	d.f	P-value	AIcc	deltaAIcc
b	**7.34**	**6**	**0.28**	**22.14**	**0**
c	**5.11**	**4**	**0.27**	**22.14**	**0**
a	9.10	6	0.16	23.90	1.76
f	7.05	4	0.13	24.09	1.95
d	5.15	2	0 .07	24.45	2.31
e	9.05	4	0.05	26.09	3.95
g	17.06	6	<0.01	31.86	9.69

Table 9- Statistics used to discriminate between 7 competing models for proactivity-reactivity axis. Competing model with a C-value that follows a Chi-squared distribution are not rejected. P-value represents the probability that C value follows this distribution. A model fit was assessed using AICc. Models were compared thanks to delta AICc. Causal model with the lowest AICc and a delta AICc lower than 2 units were considered as best models (here in bold).

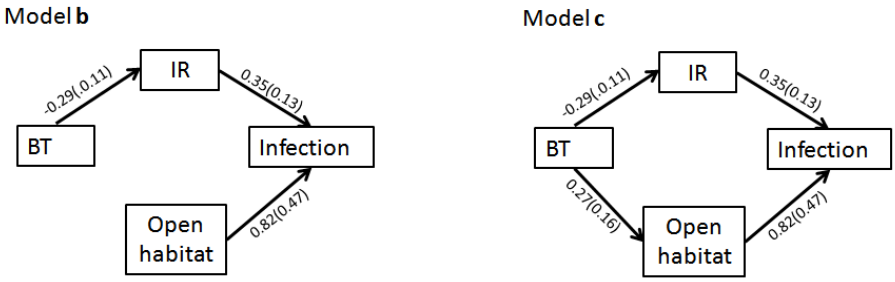

Figure 11- Selected path model that best explained infection by *Toxoplasma gondii*, with standardized path coefficients. BT stands for behavioural traits (here proactivity), IR stands for immune response.

Causal models	C-value	d.f	P-value	AIcc	deltaAIcc
a	**4.34**	**6**	**0.63**	**19.14**	**0**
e	3.46	4	0.48	20.49	1.35
c	4.33	4	0.36	21.37	2.23
b	6.92	6	0.32	21.72	2.58
d	3.37	2	0.18	22.67	3.53
f	5.83	4	0.21	22.87	3.73
g	11.55	6	0.07	26.35	7.21

Table 10- Statistics used to discriminate between 7 competing models for mobility. Competing model with a C-value that follows a Chi-squared distribution are not rejected. P-value represents the probability that C value follows this distribution. A model fit was assessed using AICc. Models were compared thanks to delta AICc. Causal model with the lowest AICc and a delta AICc lower than 2 units were considered as best models (here in bold).

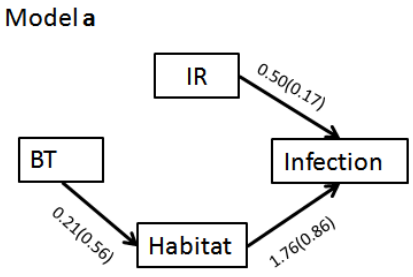

Figure 12- Selected path model that best explained infection by *Toxoplasma gondii*, with standardized path coefficients. BT stands for behavioural traits (here mobility), IR stands for immune response.