

Table 1. Statistical Analysis Framework

Complete analytical approach from laboratory development to field validation

Phase	Step	Research Question	Model	Method	Result	n	Perform.
Laboratory Development	Discovery	Can immune genes predict infection costs?	DISC-1	Linear regression (PC1, PC2 → weight loss)	Significant but modest prediction	n = 136	R ² = 0.10
Laboratory Development	Optimization	Can machine learning improve prediction?	DISC-2	Random forest (19 genes → weight loss)	Substantial improvement achieved	n = 136	R ² = 0.47
Laboratory Development	Validation	Is the model reliable?	DISC-3	Train-test cross-validation	Strong predictive accuracy	n = 95→41	r = 0.79*
Field Translation	Detection	Does the model work in wild populations?	FIELD-1	Predicted vs. observed infection status	Successfully detects infection	n = 305	+1.15%*
Field Translation	Discrimination	Can it distinguish parasite species?	FIELD-2	Predicted loss by species identity	Species-specific responses	n = 169	E.f: +2.06 E.r: +1.25
Field Translation	Scaling	Does it correlate with infection severity?	FIELD-3	Predicted loss vs. parasite load	Scales with infection intensity	n = 185	r = 0.233
Biological Validation	Physiological relevance	Does it capture real health impacts?	PROOF-1	Predicted loss vs. body condition	Correlates with actual body weight	n = 336	ρ = -0.11

¹ *p < 0.05, **p < 0.01, ***p < 0.001

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Biological Validation	Specificity	Is the response Eimeria-specific?	PROOF-2	Predicted loss vs. parasite community	Specific to Eimeria infections only	n = 305	p < 0.001

¹ *p < 0.05, **p < 0.01, ***p < 0.001