

Supplementary Results

Table S1. Estimates for fixed and random effects of WNV viremia model. Time was treated as a factor in the linear mixed effects model. The control treatment is the reference group in the following output predicting host viremia (as determined via quantitative-PCR).

Linear mixed model fit by maximum likelihood ('lmerMod')

Formula: Viremia ~ CORTtreatment * Time + (1|BirdID)

Fixed Effects:

	Estimate	Std. Error	t value
Intercept	3.6751	0.4351	8.44
CORT++	0.7405	0.6153	1.204
CORT+	1.2545	0.6153	2.039
Day4	-0.2652	0.4327	-0.613
Day6	-1.4791	0.4474	-3.306
Day14	-3.6943	0.4474	-8.256
CORT++:Day4	1.7629	0.6245	2.823
CORT+:Day4	1.3159	0.6245	2.107
CORT++:Day6	3.3387	0.6874	4.857
CORT+:Day6	1.7651	0.6484	2.722
CORT++:Day14	2.6421	0.8171	3.233
CORT+:Day14	1.2491	0.6850	1.823

Random Effects:

Group	Variance	Std. Deviation
BirdID	0.9570	0.9783
Residual	0.9359	0.9674

Table S2. Estimates for fixed effects in the days infectious models, with cytokine expression levels considered individually. We fit generalized linear models to the reduced dataset (including only CORT+ and CORT++ birds, since Control birds were not detected with circulating viremia levels above the 10^5 PFU/mL threshold) specifying a Poisson distribution with or without inflation. Because of a high number of zeros in dataset, and because delta AIC scores were not greater than 2 between these two models, we report on the zero-inflated model in our manuscript, but provide output of both models, here. To confirm significance of individual effects in our Poisson models with and without inflation, we used the ‘anova’ function (likelihood ratio tests and associated p values) to compare alternative models with and without those single factors included. In initial exploratory analysis, we also examined identical models fit with a negative binomial distribution with and without zero inflation; both of these models performed worse than Poisson models, with delta AIC values > 2 . The figures (predicted effects plots) created to illustrate the days infectious analysis (Fig. 4A-B) are based on predicted values from a Poisson distribution, shown below.

Poisson Model (‘glm’)

Formula: DaysAboveThreshold ~ logCORTconcentration*logIL10expression + logCORTconcentration*logIFNexpression

Coefficients:

	Estimate	Std. Error	z-value	P
Intercept	-40.973	13.800	-2.969	0.0029
logCORTconcentration	16.521	5.580	2.961	0.0031
logIL10expression	9.796	3.278	2.988	0.0028
logIFN expression	3.490	6.014	0.580	0.5618
logCORTconcentration:logIL10expression	-3.708	1.314	-2.823	0.0048
logCORTconcentration:logIFNexpression	-1.894	2.374	-0.798	0.4250

Dispersion parameter for poisson family taken to be 1

Null deviance: 62.96 on 15 df

Residual deviance: 17.26 on 10 df

AIC: 57.4

Zero-Inflated Poisson Model (“glmmadmb”)

Formula: DaysAboveThreshold ~ logCORTconcentration*logIL10expression + logCORTconcentration*logIFNexpression

Coefficients:

	Estimate	Std. Error	z-value	P
Intercept	-36.03	18.73	-1.92	0.054
logCORTconcentration	14.59	7.45	1.96	0.050
logIL10expression	8.75	4.21	2.08	0.038
logIFN expression	2.71	6.29	0.43	0.667
logCORTconcentration:logIL10expression	-3.31	1.66	-1.99	0.046
logCORTconcentration:logIFNexpression	-1.53	2.53	-0.60	0.545

Zero-inflation: 0.0863 (st. err.: 0.2401)

Log-likelihood: -22.6281

AIC: 59.3

Likelihood Ratio Tests performed by comparing alternative zero-inflated Poisson models (glmmadmb), with main effects or interaction terms dropped from full model (above):

Full model vs model without main effect of **logCORTconcentration: P = 0.01**

Full model vs model without main effect of **logIL10expression: P = 0.007**

Full model vs model without main effect of logIFNexpression: P = 0.661

Full model vs model without main effect of **CORT X IL10 interaction: P = 0.01**

Full model vs model without CORT X IFN interaction: P = 0.532

Table S3. Estimates for fixed effects in the days infectious models using within-individual cytokine ratios as a predictor. As before, we investigated models fit with a Poisson distribution for predicted numbers of days infectious with and without zero inflation. We report on the zero inflated model, and our figure (Fig. 4C) is based on the Poisson distribution without zero inflation.

Poisson Model ('glm')

Formula: DaysAboveThreshold ~ logCORTconcentration*logCytokineRatio

Coefficients:

	Estimate	Std. Error	z-value	P
Intercept	-19.264	5.459	-3.529	0.0004
logCORTconcentration	7.494	2.008	3.732	0.0002
logCytokineRatio	-5.299	1.788	-2.963	0.0030
logCORTconcentration:logCytokineRatio	1.840	0.6754	2.725	0.0064

Dispersion parameter for poisson family taken to be 1

Null deviance: 62.96 on 15 df

Residual deviance: 20.88 on 12 df

AIC: 56.9

Zero-Inflated Poisson Model (“glmmadmb”)

Formula: DaysAboveThreshold ~ logCORTconcentration*logCytokineRatio

Coefficients:

	Estimate	Std. Error	z-value	P
Intercept	-15.387	5.956	-2.58	0.009
logCORTconcentration	6.110	2.178	2.81	0.005
logCytokineRatio	-4.452	1.848	-2.41	0.016
logCORTconcentration:logCytokineRatio	1.546	0.694	2.23	0.026

Zero-inflation: 0.18481 (st. err.: 0.17793)

Log-likelihood: -23.8073

AIC: 57.6

Likelihood Ratio Tests performed by comparing alternative zero-inflated Poisson models (glmmadmb), with main effects or interaction terms dropped from full model (above):

Full model vs model without main effect of **logCORTconcentration: P = 0.01523**

Full model vs model without main effect of **logCytokineRatio: P = 0.01558**

Full model vs model without main effect of **CORT X CytokineRatio interaction: 0.02439**