Hypothesis test results for analysis of estrous cyclicity using the continuous-time Markov model

Stage ^a	Comparison ^b	p-value ^c	Significance ^d	Stage Length Difference ^e (days)
Diestrus	Low-Control	0.915	None	1.0
Diestrus	Mid-Control	1.000	None	-0.1
Diestrus	High-Control	0.399	None	-0.9
Proestrus	Low-Control	0.153	None	-0.2
Proestrus	Mid-Control	0.153	None	-0.2
Proestrus	High-Control	0.018	p < 0.05	-0.3
Estrus	Low-Control	1.000	None	0.0
Estrus	Mid-Control	1.000	None	0.1
Estrus	High-Control	1.000	None	0.1

a: Insufficient data to evaluate metestrus stage.

b: Sample sizes for the Control, Low, Mid, and High dose groups respectively were n = 10, 10, 10, 10. Dose levels were 0, 125, 250, 500 mg/L respectively.

c: The p-values shown were calculated using a permutation null hypothesis testing method and have been adjusted for multiple comparisons using a Hommel correction within each stage.

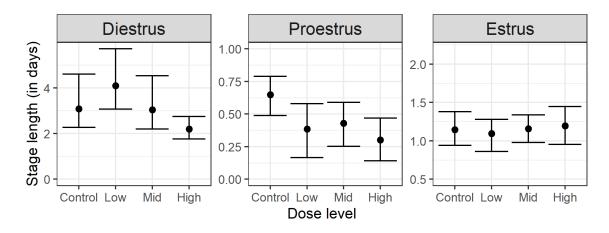
d: Significance is based on the adjusted p-value with a significance level of α = 0.05.

e: A positive number indicates the estimated stage length in the treated group is longer than in the control group.

Markov model estimates	of stage lengtl	h and 95%	confidence i	intervals

	Control (0 mg/L)		Low dose (125 mg/L)		Mid dose (250 mg/L)		High dose (500 mg/L)	
	Stage Length (days)	95% CI						
Diestrus	3.1	(2.3, 4.6)	4.1	(3.1, 5.7)	3.0	(2.2, 4.5)	2.2	(1.8, 2.7)
Proestrus	0.6	(0.5, 0.8)	0.4	(0.2, 0.6)	0.4	(0.2, 0.6)	0.3	(0.1, 0.5)
Estrus	1.1	(0.9, 1.4)	1.1	(0.9, 1.3)	1.2	(1.0, 1.3)	1.2	(0.9, 1.4)
Metestrus ^a	0.1		0.1		0.1		0.1	

a: Due to a very low number of observations of metestrus, stage lengths were estimated using a profile likelihood approach. As a result, confidence intervals are not available for the metestrus stage length estimate.



Estimates of stage length shown as dots, with bars indicating 95% confidence intervals. Estimates for lengths of metestrus are not shown here due to very low numbers of observations of this stage.