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	1.000	None	0.1	
Diestrus	Mid-Control	1.000	None	-0.1	
Diestrus	High-Control	1.000	None	0.1	
Estrus	Low-Control	1.000	None	0.1	
Estrus	Mid-Control	1.000	None	-0.0	
Estrus	High-Control	1.000	None	0.0	
Metestrus	Low-Control	0.557	None	0.1	
Metestrus	Mid-Control	1.000	None	0.0	
Metestrus	High-Control	0.644	None	-0.1	

a: Insufficient data to evaluate proestrus stage.

b: Sample sizes for the Control, Low, Mid, and High dose groups respectively were n = 10, 10, 9, 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.

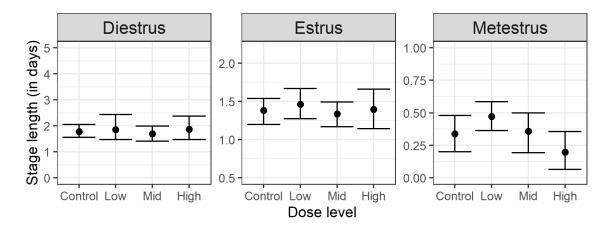
d: Significance is based on the adjusted p-value with a significance level of α = 0.05.

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 length and 95% confidence intervals	Markov mode	l estimates of s	stage length a	and 95% c	onfidence intervals
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	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	1.8	(1.6, 2.0)	1.8	(1.5, 2.4)	1.7	(1.4, 2.0)	1.9	(1.5, 2.4)
Proestrus ^a	0.2		0.2		0.2		0.2	
Estrus	1.4	(1.2, 1.5)	1.5	(1.3, 1.7)	1.3	(1.2, 1.5)	1.4	(1.1, 1.7)
Metestrus	0.3	(0.2, 0.5)	0.5	(0.4, 0.6)	0.4	(0.2, 0.5)	0.2	(0.1, 0.4)

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



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