

Supplementary Materials

Section S.1

Study Collection Site Coordinates

Collection Sites

Uruguayan Collection Sites:

Site #1 (Lake Sauce) Laguna Del Sauce (34 50' 59.78"S, 55 3' 0.98"W).

Site #2 (Lake Dario) Laguna Del Diario (34 53' 59.7"S 55° 00'29.3"W) near Maldonado, Uruguay.

Chinese Collection Sites:

Site #3 (Chinese Creek Site, 30°16'21.3"N 120°03'45.4"E) in Xi Xi National Park, Hangzhou, Zhejiang, China.

Site #4 (Chinese Lake Site, 30°16'26.5"N 120°03'47.4"E) in Xi Xi National Park, Hangzhou, Zhejiang, China.

Hawaiian Collection Site:

Site #5 (Kawainui Marsh Site, 21°23'02.9"N 157°45'37.3"W).

Location was 200 feet east of the Maunawilli Stream within Kawainui Marsh Oahu, Hawaii, USA.

Section S.2: Tables S1–S5 list of all individual detritus samples and apple snails (*Pomacea canaliculata*) from all five collection sites, the corresponding $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ values, and the calculated trophic level for all samples. Detritus samples served as a baseline for comparison between habitats; as such, the net value of the trophic levels for these samples, within each collection site, is and should be zero.

Table S1

Lake Sauce recorded stable isotope values ($\delta^{15}\text{N}$ and $\delta^{13}\text{C}$) and trophic level values for detritus and apple snails (<i>Pomacea canaliculata</i>)			
SAMPLE	$\delta^{15}\text{N}$	$\delta^{13}\text{C}$	
	(‰, air)	(‰, VPDB)	
Detritus	3.8	−26.6	
Detritus	2.7	−25.3	
Detritus	1.9	−27.1	
Detritus	3.5	−27.1	
Detritus	2.4	−26.3	
SAMPLE	$\delta^{15}\text{N}$	$\delta^{13}\text{C}$	TROPHIC LEVEL
<i>Pomacea</i>	5.0	−27.0	0.74
<i>Canaliculata</i>			
<i>Pomacea</i>	5.7	−28.7	0.95
<i>Canaliculata</i>			
<i>Pomacea</i>	4.3	−25.7	0.50
<i>Canaliculata</i>			
<i>Pomacea</i>	5.8	−27.3	1.01
<i>Canaliculata</i>			
<i>Pomacea</i>	5.6	−28.1	0.92
<i>Canaliculata</i>			
<i>Pomacea</i>	5.9	−26.7	1.03
<i>Canaliculata</i>			
<i>Pomacea</i>	5.0	−26.7	0.72
<i>Canaliculata</i>			
<i>Pomacea</i>	5.1	−27.1	0.76
<i>Canaliculata</i>			
<i>Pomacea</i>	5.2	−27.8	0.79
<i>Canaliculata</i>			
<i>Pomacea</i>	5.6	−27.7	0.91
<i>Canaliculata</i>			
<i>Pomacea</i>	5.7	−27.5	0.96
<i>Canaliculata</i>			

<i>Pomacea</i>	5.3	−27.8	0.84
<i>Canaliculata</i>			
<i>Pomacea</i>	5.5	−27.7	0.88
<i>Canaliculata</i>			
<i>Pomacea</i>	6.6	−27.0	1.25
<i>Canaliculata</i>			
<i>Pomacea</i>	5.4	−27.4	0.88
<i>Canaliculata</i>			
<i>Pomacea</i>	6.4	−27.2	1.20
<i>Canaliculata</i>			
<i>Pomacea</i>	5.2	−27.8	0.78
<i>Canaliculata</i>			
<i>Pomacea</i>	6.4	−27.2	1.21
<i>Canaliculata</i>			
<i>Pomacea</i>	5.3	−27.6	0.82
<i>Canaliculata</i>			
<i>Pomacea</i>	6.2	−27.1	1.12
<i>Canaliculata</i>			
<i>Pomacea</i>	5.7	−27.0	0.97
<i>Canaliculata</i>			
<i>Pomacea</i>	5.5	−22.9	0.89
<i>Canaliculata</i>			
<i>Pomacea</i>	5.0	−27.6	0.73
<i>Canaliculata</i>			
<i>Pomacea</i>	5.0	−28.3	0.72
<i>Canaliculata</i>			
<i>Pomacea</i>	4.2	−26.8	0.46
<i>Canaliculata</i>			
<i>Pomacea</i>	3.6	−27.7	0.25
<i>Canaliculata</i>			
<i>Pomacea</i>	4.7	−26.9	0.62
<i>Canaliculata</i>			
<i>Pomacea</i>	4.0	−26.1	0.40
<i>Canaliculata</i>			
<i>Pomacea</i>	5.2	−26.8	0.78
<i>Canaliculata</i>			
<i>Pomacea</i>	4.8	−28.2	0.66
<i>Canaliculata</i>			
<i>Pomacea</i>	5.7	−27.1	0.96
<i>Canaliculata</i>			

<i>Pomacea</i>	4.3	−26.4	0.50
<i>Canaliculata</i>			
<i>Pomacea</i>	4.0	−28.5	0.40
<i>Canaliculata</i>			
<i>Pomacea</i>	4.7	−28.1	0.62
<i>Canaliculata</i>			
<i>Pomacea</i>	3.3	−28.6	0.14
<i>Canaliculata</i>			
<i>Pomacea</i>	4.5	−28.5	0.55
<i>Canaliculata</i>			
<i>Pomacea</i>	4.2	−27.5	0.45
<i>Canaliculata</i>			
<i>Pomacea</i>	3.4	−27.9	0.20
<i>Canaliculata</i>			
<i>Pomacea</i>	5.1	−28.3	0.77
<i>Canaliculata</i>			
<i>Pomacea</i>	4.2	−27.7	0.47
<i>Canaliculata</i>			
<i>Pomacea</i>	5.2	−28.2	0.79
<i>Canaliculata</i>			
<i>Pomacea</i>	4.2	−27.1	0.45
<i>Canaliculata</i>			
<i>Pomacea</i>	5.4	−27.2	0.87
<i>Canaliculata</i>			
<i>Pomacea</i>	3.8	−27.3	0.31
<i>Canaliculata</i>			
<i>Pomacea</i>	5.3	−27.8	0.81
<i>Canaliculata</i>			
<i>Pomacea</i>	4.6	−26.5	0.60
<i>Canaliculata</i>			
<i>Pomacea</i>	4.2	−21.3	0.45
<i>Canaliculata</i>			
<i>Pomacea</i>	3.6	−27.7	0.26
<i>Canaliculata</i>			
<i>Pomacea</i>	2.9	−28.0	0.01
<i>Canaliculata</i>			
<i>Pomacea</i>	3.6	−26.5	0.26
<i>Canaliculata</i>			

Table S2.

Lake Dario recorded stable isotope values ($\delta^{15}\text{N}$ and $\delta^{13}\text{C}$) and trophic level values for detritus and apple snails (<i>Pomacea canaliculata</i>)			
SAMPLE	$\delta^{15}\text{N}$	$\delta^{13}\text{C}$	
	(‰, air)	(‰, VPDB)	
Detritus	2.5	-27.6	
Detritus	1.4	-27.1	
Detritus	0.6	-28.5	
Detritus	0.5	-28.0	
Detritus	1.5	-28.7	
SAMPLE	$\delta^{15}\text{N}$	$\delta^{13}\text{C}$	TROPHIC LEVEL
<i>Pomacea</i>	2.5	-26.2	0.41
<i>Canaliculata</i>			
<i>Pomacea</i>	2.5	-26.0	0.40
<i>Canaliculata</i>			
<i>Pomacea</i>	1.9	-25.1	0.19
<i>Canaliculata</i>			
<i>Pomacea</i>	2.9	-26.4	0.52
<i>Canaliculata</i>			
<i>Pomacea</i>	1.8	-25.9	0.16
<i>Canaliculata</i>			
<i>Pomacea</i>	1.4	-25.3	0.04
<i>Canaliculata</i>			
<i>Pomacea</i>	2.3	-27.9	0.35
<i>Canaliculata</i>			
<i>Pomacea</i>	2.8	-27.0	0.49
<i>Canaliculata</i>			
<i>Pomacea</i>	3.4	-28.4	0.71
<i>Canaliculata</i>			
<i>Pomacea</i>	0.3	-25.9	-0.33
<i>Canaliculata</i>			
<i>Pomacea</i>	1.5	-26.0	0.06
<i>Canaliculata</i>			

<i>Pomacea</i>	1.0	-24.4	-0.11
<i>Canaliculata</i>			
<i>Pomacea</i>	1.2	-25.9	-0.02
<i>Canaliculata</i>			
<i>Pomacea</i>	1.0	-27.0	-0.10
<i>Canaliculata</i>			
<i>Pomacea</i>	0.8	-26.3	-0.15
<i>Canaliculata</i>			
<i>Pomacea</i>	1.5	-28.7	0.08
<i>Canaliculata</i>			
<i>Pomacea</i>	1.5	-28.2	0.06
<i>Canaliculata</i>			
<i>Pomacea</i>	1.8	-28.5	0.18
<i>Canaliculata</i>			
<i>Pomacea</i>	1.9	-26.0	0.20
<i>Canaliculata</i>			
<i>Pomacea</i>	1.1	-22.3	-0.07
<i>Canaliculata</i>			
<i>Pomacea</i>	0.3	-25.9	-0.33
<i>Canaliculata</i>			
<i>Pomacea</i>	-0.1	-27.1	-0.46
<i>Canaliculata</i>			
<i>Pomacea</i>	2.3	-28.9	0.32
<i>Canaliculata</i>			
<i>Pomacea</i>	2.1	-28.2	0.26
<i>Canaliculata</i>			
<i>Pomacea</i>	0.5	-27.2	-0.27
<i>Canaliculata</i>			
<i>Pomacea</i>	1.9	-28.5	0.19
<i>Canaliculata</i>			
<i>Pomacea</i>	2.0	-28.9	0.25
<i>Canaliculata</i>			
<i>Pomacea</i>	0.4	-27.1	-0.28
<i>Canaliculata</i>			
<i>Pomacea</i>	1.7	-28.4	0.14
<i>Canaliculata</i>			
<i>Pomacea</i>	1.9	-28.9	0.22
<i>Canaliculata</i>			
<i>Pomacea</i>	1.5	-26.9	0.07
<i>Canaliculata</i>			

<i>Pomacea</i>	1.5	−28.1	0.07
<i>Canaliculata</i>			
<i>Pomacea</i>	2.3	−27.6	0.35
<i>Canaliculata</i>			
<i>Pomacea</i>	1.1	−28.3	−0.06
<i>Canaliculata</i>			
<i>Pomacea</i>	1.9	−28.5	0.19
<i>Canaliculata</i>			
<i>Pomacea</i>	1.9	−28.1	0.21
<i>Canaliculata</i>			
<i>Pomacea</i>	2.2	−27.4	0.32
<i>Canaliculata</i>			
<i>Pomacea</i>	1.5	−27.4	0.08
<i>Canaliculata</i>			
<i>Pomacea</i>	1.7	−26.7	0.12
<i>Canaliculata</i>			
<i>Pomacea</i>	2.5	−28.8	0.42
<i>Canaliculata</i>			
<i>Pomacea</i>	2.6	−28.4	0.45
<i>Canaliculata</i>			
<i>Pomacea</i>	3.2	−24.5	0.63
<i>Canaliculata</i>			
<i>Pomacea</i>	2.4	−23.6	0.37
<i>Canaliculata</i>			
<i>Pomacea</i>	1.3	−26.2	0.02
<i>Canaliculata</i>			
<i>Pomacea</i>	2.3	−26.9	0.33
<i>Canaliculata</i>			
<i>Pomacea</i>	2.9	−27.6	0.53
<i>Canaliculata</i>			
<i>Pomacea</i>	2.9	−26.6	0.54
<i>Canaliculata</i>			
<i>Pomacea</i>	2.1	−26.6	0.27
<i>Canaliculata</i>			
<i>Pomacea</i>	2.9	−28.2	0.53
<i>Canaliculata</i>			
<i>Pomacea</i>	2.7	−28.5	0.49
<i>Canaliculata</i>			

<i>Pomacea</i>	2.2	−26.4	0.29
<i>Canaliculata</i>			
<i>Pomacea</i>	2.6	−27.1	0.45
<i>canaliculata</i>			
<i>Pomacea</i>	3.6	−28.3	0.76
<i>canaliculata</i>			
<i>Pomacea</i>	2.4	−25.9	0.35
<i>canaliculata</i>			
<i>Pomacea</i>	3.4	−27.5	0.69
<i>canaliculata</i>			
<i>Pomacea</i>	2.6	−26.6	0.44
<i>canaliculata</i>			
<i>Pomacea</i>	2.4	−27.5	0.38
<i>canaliculata</i>			
<i>Pomacea</i>	2.3	−27.6	0.34
<i>canaliculata</i>			
<i>Pomacea</i>	2.4	−26.7	0.37
<i>canaliculata</i>			
<i>Pomacea</i>	2.9	−26.8	0.53
<i>canaliculata</i>			
<i>Pomacea</i>	2.7	−27.1	0.46
<i>canaliculata</i>			
<i>Pomacea</i>	3.0	−26.1	0.59
<i>canaliculata</i>			
<i>Pomacea</i>	3.1	−28.3	0.61
<i>canaliculata</i>			
<i>Pomacea</i>	4.2	−28.6	0.98
<i>canaliculata</i>			

Table S3

Chinese Lake Site recorded stable isotope values ($\delta^{15}\text{N}$ and $\delta^{13}\text{C}$) and trophic level values for detritus and apple snails (<i>Pomacea canaliculata</i>)			
SAMPLE	$\delta^{15}\text{N}$	$\delta^{13}\text{C}$	
	(‰, air)	(‰, VPDB)	
Detritus	2.4	−30.4	
Detritus	4.2	−26.8	
Detritus	2.0	−29.2	
Detritus	2.1	−29.8	
Detritus	3.6	−30.0	
SAMPLE	$\delta^{15}\text{N}$	$\delta^{13}\text{C}$	TROPHIC LEVEL
<i>Pomacea canaliculata</i>	3.2	−28.9	0.11
<i>Pomacea canaliculata</i>	2.9	−28.0	0.02
<i>Pomacea canaliculata</i>	3.6	−27.6	0.26
<i>Pomacea canaliculata</i>	3.5	−28.7	0.21
<i>Pomacea canaliculata</i>	4.1	−25.0	0.43
<i>Pomacea canaliculata</i>	3.0	−29.1	0.06
<i>Pomacea canaliculata</i>	2.8	−29.5	−0.02
<i>Pomacea canaliculata</i>	2.8	−28.0	−0.01
<i>Pomacea canaliculata</i>	4.1	−29.3	0.42
<i>Pomacea canaliculata</i>	3.5	−28.2	0.20
<i>Pomacea canaliculata</i>	3.8	−28.7	0.32
<i>Pomacea canaliculata</i>	1.8	−27.7	−0.36

<i>Pomacea</i>	3.4	−28.4	0.17
<i>canaliculata</i>			
<i>Pomacea</i>	2.3	−28.5	−0.19
<i>canaliculata</i>			
<i>Pomacea</i>	3.4	−28.4	0.17
<i>canaliculata</i>			
<i>Pomacea</i>	2.6	−27.6	−0.09
<i>canaliculata</i>			
<i>Pomacea</i>	3.1	−28.3	0.08
<i>canaliculata</i>			
<i>Pomacea</i>	3.2	−29.0	0.12
<i>canaliculata</i>			
<i>Pomacea</i>	3.5	−26.8	0.23
<i>canaliculata</i>			
<i>Pomacea</i>	2.7	−28.6	−0.04
<i>canaliculata</i>			
<i>Pomacea</i>	2.9	−27.5	0.00
<i>canaliculata</i>			
<i>Pomacea</i>	2.9	−29.4	0.03
<i>canaliculata</i>			
<i>Pomacea</i>	3.3	−26.8	0.13
<i>canaliculata</i>			
<i>Pomacea</i>	2.5	−28.2	−0.12
<i>canaliculata</i>			
<i>Pomacea</i>	2.7	−28.1	−0.06
<i>canaliculata</i>			
<i>Pomacea</i>	5.7	−28.5	0.94
<i>canaliculata</i>			
<i>Pomacea</i>	4.7	−28.2	0.61
<i>canaliculata</i>			
<i>Pomacea</i>	3.9	−26.7	0.35
<i>canaliculata</i>			
<i>Pomacea</i>	4.5	−28.6	0.56
<i>canaliculata</i>			
<i>Pomacea</i>	5.7	−27.8	0.95
<i>canaliculata</i>			
<i>Pomacea</i>	4.7	−27.7	0.60
<i>canaliculata</i>			

<i>Pomacea</i>	5.1	−28.6	0.74
<i>canaliculata</i>			
<i>Pomacea</i>	5.4	−27.7	0.84
<i>canaliculata</i>			
<i>Pomacea</i>	5.3	−28.6	0.83
<i>canaliculata</i>			
<i>Pomacea</i>	4.4	−27.8	0.52
<i>canaliculata</i>			
<i>Pomacea</i>	5.2	−28.8	0.77
<i>canaliculata</i>			
<i>Pomacea</i>	4.8	−28.2	0.64
<i>canaliculata</i>			
<i>Pomacea</i>	5.0	−28.7	0.70
<i>canaliculata</i>			
<i>Pomacea</i>	4.5	−27.9	0.55
<i>canaliculata</i>			
<i>Pomacea</i>	4.8	−28.1	0.67
<i>canaliculata</i>			
<i>Pomacea</i>	4.6	−27.6	0.58
<i>canaliculata</i>			
<i>Pomacea</i>	5.1	−27.9	0.76
<i>canaliculata</i>			
<i>Pomacea</i>	4.5	−27.9	0.54
<i>canaliculata</i>			
<i>Pomacea</i>	4.8	−28.4	0.64
<i>canaliculata</i>			
<i>Pomacea</i>	5.5	−28.1	0.88
<i>canaliculata</i>			
<i>Pomacea</i>	5.1	−27.9	0.74
<i>canaliculata</i>			
<i>Pomacea</i>	5.2	−28.7	0.79
<i>canaliculata</i>			
<i>Pomacea</i>	4.5	−28.2	0.56
<i>canaliculata</i>			
<i>Pomacea</i>	4.1	−28.4	0.43
<i>canaliculata</i>			
<i>Pomacea</i>	4.8	−28.5	0.65
<i>canaliculata</i>			

Table S4

Chinese Creek Site recorded stable isotope values ($\delta^{15}\text{N}$ and $\delta^{13}\text{C}$) and trophic level values for detritus and apple snails (*Pomacea canaliculata*)

SAMPLE	$\delta^{15}\text{N}$	$\delta^{13}\text{C}$	
	(‰, air)	(‰, VPDB)	
Detritus	-5.6	-22.6	
Detritus	1.3	-22.4	
Detritus	1.5	-18.7	
Detritus	-0.4	-23.1	
Detritus	2.8	-18.2	
SAMPLE	$\delta^{15}\text{N}$	$\delta^{13}\text{C}$	TROPHIC LEVEL
<i>Pomacea canaliculata</i>	3.4	-30.5	1.12
<i>Pomacea canaliculata</i>	5.9	-30.9	1.96
<i>Pomacea canaliculata</i>	5.5	-30.8	1.81
<i>Pomacea canaliculata</i>	5.2	-30.7	1.71
<i>Pomacea canaliculata</i>	2.7	-31.3	0.87
<i>Pomacea canaliculata</i>	6.6	-30.3	2.18
<i>Pomacea canaliculata</i>	7.4	-28.6	2.47
<i>Pomacea canaliculata</i>	3.7	-31.2	1.20
<i>Pomacea canaliculata</i>	9.4	-28.9	3.14
<i>Pomacea canaliculata</i>	4.8	-30.2	1.58
<i>Pomacea canaliculata</i>	8.3	-29.3	2.76

<i>Pomacea</i>	7.1	−29.8	2.37
<i>canaliculata</i>			
<i>Pomacea</i>	7.1	−30.5	2.35
<i>canaliculata</i>			
<i>Pomacea</i>	3.7	−30.9	1.21
<i>canaliculata</i>			
<i>Pomacea</i>	9.1	−28.5	3.03
<i>canaliculata</i>			
<i>Pomacea</i>	9.8	−28.4	3.28
<i>canaliculata</i>			
<i>Pomacea</i>	6.9	−30.1	2.29
<i>canaliculata</i>			
<i>Pomacea</i>	6.0	−30.1	1.99
<i>canaliculata</i>			

Table S5

Kawainui Marsh Site recorded stable isotope values ($\delta^{15}\text{N}$ and $\delta^{13}\text{C}$) and trophic level values for the detritus and apple snails (<i>Pomacea canaliculata</i>)			
SAMPLE	$\delta^{15}\text{N}$	$\delta^{13}\text{C}$	
	(‰, air)	(‰, VPDB)	
Detritus	3.5	-13.9	
Detritus	4.4	-17.5	
Detritus	2.5	-16.3	
Detritus	4.9	-17.9	
Detritus	1.5	-15.3	
SAMPLE	$\delta^{15}\text{N}$	$\delta^{13}\text{C}$	TROPHIC LEVEL
<i>Pomacea</i>	8.5	-18.0	1.72
<i>canaliculata</i>			
<i>Pomacea</i>	7.3	-19.4	1.30
<i>canaliculata</i>			
<i>Pomacea</i>	7.5	-19.8	1.38
<i>canaliculata</i>			
<i>Pomacea</i>	8.8	-25.0	1.81
<i>canaliculata</i>			
<i>Pomacea</i>	5.5	-24.9	0.71
<i>canaliculata</i>			
<i>Pomacea</i>	8.0	-22.1	1.55
<i>canaliculata</i>			
<i>Pomacea</i>	9.8	-18.2	2.16
<i>canaliculata</i>			
<i>Pomacea</i>	10.2	-26.6	2.31
<i>canaliculata</i>			
<i>Pomacea</i>	9.5	-23.9	2.04
<i>canaliculata</i>			
<i>Pomacea</i>	7.2	-19.6	1.29
<i>canaliculata</i>			
<i>Pomacea</i>	8.3	-20.1	1.67
<i>canaliculata</i>			

<i>Pomacea</i>	8.5	−20.3	1.72
<i>canaliculata</i>			
<i>Pomacea</i>	7.5	−16.5	1.38
<i>canaliculata</i>			
<i>Pomacea</i>	7.4	−18.7	1.34
<i>canaliculata</i>			
<i>Pomacea</i>	7.5	−22.9	1.37
<i>canaliculata</i>			
<i>Pomacea</i>	7.9	−24.7	1.53
<i>canaliculata</i>			
<i>Pomacea</i>	8.5	−25.7	1.73
<i>canaliculata</i>			

Section S.3: Animal collections catalogued and the corresponding means of for the identification of animals collected, and corresponding cytochrome oxidase sub-unit I (COI) sequence data, where applicable, from all collection sites during this study.

Lake Sauce Maldonado, Uruguay

Ten (10) distinct arachnid species (nine (9) terrestrial and one (1) aquatic) were collected from Lake Sauce in Maldonado, Uruguay. Of these ten (10) arachnid species, only one (1) was identified to the taxonomical level of family (Araneidae) via COI (cytochrome oxidase subunit-I) sequencing data and comparisons to available barcode databases (e.g., NCBI). Aside from arachnids, one hundred and six (106) other individual (non-arachnid) macroinvertebrates, representing twenty (20) distinct species, were collected from Lake Sauce in Maldonado, Uruguay. Altogether, ten (10) of these (non-arachnid) macroinvertebrate species were identified at least to the taxonomical level of family via COI (cytochrome oxidase subunit-I) sequencing data and/or comparisons to available barcode databases (e.g., NCBI); including invasive apple snails (*Pomacea canaliculata*).

Thirty (30) adult fish were collected and categorized into what were thought to be nine (9) distinct fish species by collaborators. Preliminary species identifications for these nine (9) fish species and a single (1) species of larval fish were made by Dr. Marianna Meerhoff (of the CURE Institute in Maldonado, Uruguay). Subsequently, five (5) of these fish species were identified via COI (cytochrome oxidase subunit-I) sequencing data and comparisons to available barcode databases (e.g., NCBI). All species identifications from Lake Sauce, and the means by which these identifications were made, are listed below; corresponding sequence data is available in **Section S.4**.

List of all animals collected from Lake Sauce in Maldonado, Uruguay

<u>Arachnids</u>	<u>Sample Size (n)</u>	<u>Species ID</u>	<u>Means of ID</u>
Arachnid Sp. 9	2		
Arachnid Sp. 8	1		
Arachnid Sp. 7	1		
Arachnid Sp. 6	1		
Arachnid Sp. 5	1		
Arachnid Sp. 4	8		
Arachnid Sp. 3	1		
Arachnid Sp. 2	1		
Arachnid Sp. 1	2	Family Araneidae	COI
Aquatic Arachnid Sp.1	1		
<u>Other Macroinvertebrates</u>	<u>Sample Size (n)</u>	<u>Species ID</u>	<u>Means of ID</u>
Coleoptera Species 1	1		
Diptera Species 1	3	<i>Poeciloderas quadripunctatus</i>	COI
Diptera Species 2	2	Family Tabanidae	COI
Hemiptera Species 1	2		
Hymenoptera Species 1	1		
Hymenoptera Species 2	1		
<i>Odonata</i> species 1	4		
<i>Odonata</i> Species 2	3	<i>Sympetrum</i> sp.	COI
<i>Odonata</i> Species 3	3		
<i>Odonata</i> Species 4	1		
<i>Odonata</i> Species 5	10		
<i>Odonata</i> Species 6	1		

<i>Odonata</i> Species 7	7	<i>Pantala</i> <i>flavescens</i>	COI
<i>Odonata</i> Species 8	2	<i>Aeshna cyanea</i>	COI
<i>Odonata</i> Species 9	1		
Orthoptera Species 1	2		
Orthoptera Species 2	6	<i>Dilobopterus dispa</i>	COI
Orthoptera Species 3	1	<i>Neonemobius cubensis</i>	COI
Shrimp Species 1	30	Family Alpheidae	COI
Apple snails	25	<i>Pomacea canaliculata</i>	COI
Fish	Sample Size (n)	Field ID	Means of ID
Fish Species 1	5	<i>Oligosarcus</i> sp.	
Fish Species 1 Larval	1	<i>Oligosarcus</i> sp.	
Fish Species 2	4	<i>Gymnogeophagus</i> sp.	
Fish Species 2 Larval	1	<i>Gymnogeophagus</i> sp.	
Fish Species 3	1	<i>Steindachnerina biornata</i>	<i>Steindachnerina elegans</i> Genus Confirmed COI
Fish Species 3 Larval	1	<i>Steindachnerina biornata</i>	<i>Steindachnerina elegans</i> Genus Confirmed COI
Fish Species 4	5	<i>Steindachnerina biornata</i>	<i>Steindachnerina elegans</i> Genus Confirmed COI
Fish Species 5	5	<i>Charax stenopterus</i>	<i>Charax stenopterus</i> Confirmed COI
Fish Species 6	5	<i>Bryconamericus iheringii</i>	<i>Bryconamericus</i> sp. Confirmed COI
Fish Species 7	1	<i>Australoheros fascetus</i>	
Fish Species 8	2	<i>Gymnogeophagus</i> sp.	
Fish Species 9	1	<i>Microglanis</i> sp.	<i>Microglanis cottoides</i> Confirmed COI
Larval Fish	5	Unidentified Larval Fish	<i>Astyanax</i> sp. COI

Lake Dario Maldonado, Uruguay

Two (2) arachnid species (both terrestrial) were collected from Lake Dario in Maldonado, Uruguay. These arachnid species were identified to the lowest taxonomical level possible (ideally family, genus, species, respectively) via COI (cytochrome oxidase subunit-I) sequencing data and comparisons made with available barcode databases (e.g., NCBI). Aside from arachnids, fifty-seven (57) individual (non-arachnid) macroinvertebrates, representing nine (9) distinct species, were collected from Lake Dario in Maldonado, Uruguay. Only one (1) of these (non-arachnid) macroinvertebrate species, the invasive apple snail (*Pomacea canaliculata*), was identified via COI (cytochrome oxidase subunit-I) sequencing data and comparisons to available barcode databases (e.g., NCBI). Aside from invasive apple snails, Hemiptera species numbers three and four were determined to belong to the insect families Belostomatidae and Corixidae, respectively, based on observed morphological characteristics. All remaining (non-arachnid) macroinvertebrate species were insects and were identified only to their respective orders as a result.

Thirty-one (31) adult fish were collected and categorized into what were thought to be seven (7) distinct fish species by collaborators. Preliminary species identifications for these seven (7) fish species were made by Dr. Marianna Meerhoff (of the CURE Institute in Maldonado, Uruguay). Subsequently, three (3) of these seven (7) total fish species were identified via COI (cytochrome oxidase subunit-I) sequencing data and comparisons to available barcode databases (e.g., NCBI). All species identifications from Lake Dario are listed below, and the means by which these identifications were made, are listed below; corresponding sequence data is available in **Section S.4**.

<u>Arachnids</u>	<u>Sample Size (n)</u>	<u>Species Identification</u>	<u>Means of ID</u>
Arachnid Species 1	2	<i>Eustala</i> sp.	COI
Arachnid Species 2	6		
<u>Other Macroinvertebrates</u>	<u>Sample Size (n)</u>	<u>Species Identification</u>	<u>Means of ID</u>
Hemiptera Species 1	2		
Hemiptera Species 2	5		
Hemiptera Species 3	3	Family Belostomatidae	Field Identification
Hemiptera Species 4	9	Family Corixidae	Field Identification
<i>Odonata</i> Larvae Species 1	5		
<i>Odonata</i> Larvae Species 2	3		
<i>Odonata</i> Larvae Species 3	9		
<i>Odonata</i> Larvae Species 4	3		
Apple Snails	32	<i>Pomacea canaliculata</i>	COI
<u>Fish</u>	<u>Sample Size (n)</u>	<u>Field ID</u>	<u>Means of ID</u>
Fish Species 1	4	<i>Steindachnerina biornata</i>	<i>Steindachnerina elegans</i> Genus Confirmed COI
Fish Species 2	2	<i>Characidium rachovii</i>	Confirmed COI
Fish Species 3	2	<i>Hyphessobrycon luetkenii</i>	
Fish Species 4	7	<i>Oligosarcus</i> sp.	
Fish Species 5	5	<i>Jenynsia multidentata</i>	Confirmed COI
Fish Species 6	4	<i>Australoheros fascetus</i>	
Fish Species 7	4	<i>Gymnogeophagus</i> sp.	
Fish Species 7 Larval	3	<i>Gymnogeophagus</i> sp.	

Xi Xi National Park (Lake Site) Hangzhou, China

Five (5) arachnid species (all terrestrial species) were collected from a Lake Site in Xi Xi National Park Hangzhou, China. However, none (0) of these arachnids were identified via COI (cytochrome oxidase subunit-I) sequencing data and comparisons to available barcode databases (e.g., NCBI). Aside from arachnids, one hundred and eleven (111) individual (non-arachnid) macroinvertebrates, representing thirty (30) distinct (non-arachnid) macroinvertebrate species, were collected from the Lake Site in Xi Xi National Park Hangzhou, China. Altogether, twelve (12) of these (non-arachnid) macroinvertebrate species were identified at least to the taxonomical level of family via COI (cytochrome oxidase subunit-I) sequencing data and comparisons to available barcode databases (e.g., NCBI), including invasive apple snails (*Pomacea canaliculata*). Additionally, one (1) other (non-arachnid) macroinvertebrate species was determined to belong to the family Astacidae based on observed morphological characteristics.

Two (2) adult fish were collected and categorized into what were thought to be two (2) distinct fish species, along with a single (1) larval fish species, by collaborators in China. Subsequently, these two (2) fish species, as well as the single (1) larval fish species, were identified via COI (cytochrome oxidase subunit-I) sequencing data and comparisons made to available barcode databases (e.g., NCBI). All species identifications from the Lake Site in Xi Xi National Park, and the means by which these identifications were made, are listed below; corresponding sequence data is available in **Section S.4**.

List of all animals collected from the Lake Site in Xi Xi National Park

<u>Arachnids</u>	<u>Sample Size (n)</u>	<u>Species Identification</u>	<u>Means of ID</u>
Arachnid Species 1	3		
Arachnid Species 2	1		
Arachnid Species 3	2		
Arachnid Species 4	1		
Arachnid Species 5	2		
<u>Other Macroinvertebrates</u>	<u>Sample Size (n)</u>	<u>Species Identification</u>	<u>Means of ID</u>
Crayfish Species 1	3	Family Astacidae	Field Identification
Coleoptera Species 1	1		
Coleoptera Species 2	1		
Diptera Species 1	1		
Hemiptera Species 1	1	<i>Platypleura kaempferi</i>	COI
Hemiptera Species 2	1	<i>Cryptotympana atrata</i>	COI
Hymenoptera Species 1	1		
Hymenoptera Species 2	2		
Hymenoptera Species 3	2		
Hymenoptera Species 4	3		
Lepidoptera Species 1	1	<i>Gonepteryx rhamni</i>	COI
Lepidoptera Species 2	2	<i>Tongeia filicaudis</i>	COI
Lepidoptera Species 3	1	<i>Papilio polytes</i>	COI
Mantidae Species 1	1	<i>Statilia maculata</i>	COI
<i>Odonata</i> Species 1	7	<i>Nannophya fygmaea</i>	COI
<i>Odonata</i> Species 2	18		
<i>Odonata</i> Species 3	3	<i>Acisoma panorpoides</i>	COI

<i>Odonata</i> Species 4	5		
<i>Odonata</i> Species 5	2		
<i>Odonata</i> Species 6	1		
<i>Odonata</i> Species 7	1		
<i>Odonata</i> Species 8	2		
<i>Odonata</i> Species 9	3	<i>Zygonyx annika</i>	COI
Orthoptera Species 1	2	<i>Atractomorpha sinensis</i>	COI
Orthoptera Species 2	1		
Orthoptera Species 3	6		
Shrimp Species 1	6		
Slug Species 1	7	<i>Philomycus bilineatus</i>	bOI
Apple Snails (<i>Pomacea</i> spp.)	25	<i>Pomacea canaliculata</i>	COI
<u>Fish</u>	<u>Sample Size (n)</u>	<u>Species Identification</u>	<u>Means of ID</u>
Fish Species 1	1	<i>Carassius gibelio</i>	COI
Fish Species 2	1	<i>Acanthorhodeus chankaensis</i>	COI
Larval Fish Species	35	<i>Gambusia</i> sp.	COI

Xi Xi National Park (Creek Site) Hangzhou, China

Three (3) arachnid species (all terrestrial species) were collected from a Creek Site in Xi Xi National Park Hangzhou, China. Two (2) of these arachnid species were identified as two species via COI (cytochrome oxidase subunit-I) sequencing data and comparisons to available barcode databases (e.g., NCBI). Aside from arachnids, seventy (70) individual (non-arachnid) macroinvertebrates, representing fifteen (15) distinct (non-arachnid) macroinvertebrate species, were collected from the Creek Site in Xi Xi National Park Hangzhou, China. Altogether, seven (7) of these (non-arachnid) macroinvertebrate species were identified at least to the taxonomical level of family via COI (cytochrome oxidase subunit-I) sequencing data and comparisons to available barcode (e.g., NCBI), including invasive apple snails (*Pomacea canaliculata*).

Two (2) larval fish were collected and categorized into what were thought to be two (2) distinct fish species. Subsequently, both larval fish species were identified via COI (cytochrome oxidase subunit-I) sequencing data and comparisons to available barcode databases (e.g., NCBI). All species identifications from the Creek Site in Xi Xi National Park are listed below, which these identifications were made, are listed below; corresponding sequence data is available in **Section S.4**.

List of all animals collected from the Creek Site in Xi Xi National Park

<u>Macroinvertebrates</u>	<u>Sample Size (n)</u>	<u>Species</u>	<u>Means of ID</u>
Astacidae Species 1	3	<i>Procambarus clarkia</i>	COI
Blattodea Species 1	2		
Hemiptera Species 1	1	<i>Meimuna</i> sp.	COI
Lepidoptera Larvae Species 1	1	Family Noctuidae	COI
Lepidoptera Species 1	2		
Mantidae species 1	2	<i>Statilia maculata</i>	COI
Slug Species 1	1	<i>Philomycus bilineatus</i>	COI
<i>Odonata</i> Larvae Species 1	1		
<i>Odonata</i> Species 1	2		
<i>Odonata</i> Species 2	1		
Orthoptera Species 1	2		
Orthoptera Species 2	1		
Apple Snail	7	<i>Pomacea canaliculata</i>	COI
Egg Clutches	16	<i>P. canaliculata</i>	
Shrimp Species 1	28	<i>Neocaridina denticulate</i>	COI
<u>Fish</u>	<u>Sample Size (n)</u>	<u>Species Identification</u>	<u>Means of ID</u>
Larval Fish Species 1	1	<i>Odontobutis</i> sp.	COI
Larval Fish Species 2	5	<i>Gambusia affinis</i>	COI

Kawainui Marsh Oahu, Hawaii, USA

No (0) arachnid species were collected from Kawainui Marsh in Oahu, Hawaii, USA. Though no arachnids were collected, two hundred and ten (210) individual (non-arachnid) macroinvertebrates were, representing eleven (11) distinct (non-arachnid) macroinvertebrate species. Altogether, eight (8) of these (non-arachnid) macroinvertebrate species were identified at least to the taxonomical level of family via COI (cytochrome oxidase subunit-I) sequencing data and comparisons to available barcode databases (e.g., NCBI); including invasive apple snails (*Pomacea canaliculata*). All species identifications from Kawainui Marsh, and the means by which these identifications were made, are listed below; corresponding sequence data is available in **Section S.4**.

List of all animals collected in Kawainui Marsh

<u>Macroinvertebrates</u>	<u>Sample Size (n)</u>	<u>Species</u>	<u>Means of ID</u>
Astacidae Species 1	3	Family Astacidae	Field Identification
Diptera Species 1	27	Family Tachinidae	COI
Diptera Species 2	7	<i>Stegana</i> sp.	COI
Hemiptera Species 2	81		
Hemiptera Species 3	37	<i>Rhyparochromidae</i> sp.	COI
Lepidoptera Species 1	3	<i>Herpetogramma licarsisalis</i>	COI
<i>Odonata</i> Species 2	5	<i>Ischnura ramburii</i>	COI
<i>Odonata</i> Species 3	15	<i>Ischnura ramburii</i>	COI
Orthoptera Species 1	2	<i>Svercacheta siamensis</i>	COI
Orthoptera Species 2	13		
(Apple Snails)	17	<i>Pomacea canaliculata</i>	COI

Section S.4: Identified species and respective COI consensus and reference sequences (NCBI)

Apple snails (*Pomacea canaliculata*) COI sequence

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                250      260      270      280      290      300
Consensus  -----|-----|-----|-----|-----|-----|
AB433757   GAGCTAAATTACCAGCTAAAGGTGGRTATACTGTTTCATCCAGTTCAGCACCACCTTTCAA
                .....g.....

                310      320      330      340      350      360
Consensus  -----|-----|-----|-----|-----|-----|
AB433757   CAGCAGCAGAAGACAATAAYAGTAATAGAGAAGGTGGTAATAACCAAAATCTTATATTAT
                .....t.....

                370      380      390      400      410      420
Consensus  -----|-----|-----|-----|-----|-----|
AB433757   TAAGACGCGGAAAAGCCATGTCAGGAGCTCCTAAYATTARTGGTACTAGTCAGTTACCAA
                .....t....a.....

                430      440      450      460      470      480
Consensus  -----|-----|-----|-----|-----|-----|
AB433757   ATCCACCAATCATTATAGGTATAACTAAGAAAAAATTATGACAAAAGCATGAGCTGTAA
                .....

                490      500      510      520      530      540
Consensus  -----|-----|-----|-----|-----|-----|
AB433757   CAATAACATTATAAAGCTGATCATCTCCTAGTAAAGCACCAGGTTGTCCTAATTCAGCAC
                .....

                550      560      570      580      590      600
Consensus  -----|-----|-----|-----|-----|-----|
AB433757   GAATAAGTAACTTAGACCAGCCCAACTAGGCCTGATCATACCCCAAATAAAATATAAA
                .....

Consensus  -----:
AB433757   GAGTA
                ....
```

Lake Sauce Arachnid Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT383737   GCACCKGCTAAAACKGGTAAAGATAAYAATAATARWACAGCAGTAATYAAAACAGATCAT
          70          80          90          100         110         120
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT383737   ACAAATAAAGGMACYTTTTCTATMGTYATYCCATRAAATCGTATATTAATAATAGTWGAA
          130         140         150         160         170         180
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT383737   ATAAARTTAATWGCCCCYATAATAGAAGAAGCCCCAGCTAAATGTARAGARAAAATAGCA
          190         200         210         220         230         240
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT383737   AARTCTACTGATCTYCCWGCATGMCCCTCTARYCYKGCTARAGGGGGRTATACTGTTTAY
          250         260         270         280         290         300
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT383737   CCAGCWCCRACCCCTATYTCTACTATKGAMGAARTAATTAAYAAAAATAAMGAAGGRGGT
          310         320         330         340         350         360
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT383737   AATAATCARAACTCAAATTATTTATYCGMGGAAAWGCTATRTCWGGAGCWCCTAATATT
          370         380         390         400         410         420
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT383737   AARGGTACCAAYCAATTYCCAAAYCCWCCAATTAATWGGTATTACYATAAAAAAATT
          430         440         450         460         470         480
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT383737   ATWACAAAAGCATGAGCMGTAACWAYMACATTATAYAATTGATCATCYCCAATAAAYCTY
          490         500         510         520
Consensus  ----:----|----:----|----:----|----:----|----:----|
KT383737   CCTGGYTGWCCCTAAYTCWAYYCGAATYAAAACTCTYATWGCTGTTC
```

Lake Sauce Diptera Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
KM243546   TCAAAAAATGARGTATTTAAATTTTCGATCAGTTAAAAGTATAGTAATAGCTCCAGCTAAT
          .....g.....

          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
KM243546   ACTGGTAATGARAGTAATAAAAGAATAGCAGTAATTACTACAGCTCATACAAATAAWGGT
          .....g.....a...

          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
KM243546   ATTCGRTCAAAAGTAATTCCTGTTGATCGTATATTAATTACTGTAGTAATAAAATTAACT
          .....g.....

          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
KM243546   GCYCCTAAAATTGAAGARATTCCTGCTAAATGTAATGAAAAAATTGCTAAATCTACTGAT
          ..t.....g.....

          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
KM243546   CCTCCTCCATGGGCAATTGCTGCAGATAGRGGTGGRTAAACAGTTCATCCAGTTCAGCY
          .....g.....a.....t

          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
KM243546   CCGTTTTCTACTATACTACTGGCTAATAGWAGGGTTAAAGATGGKGGTAATARTCAAAAA
          .....t.....g.....g.....

          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
KM243546   CTTATATTATTTATTCGAGGAAATGCTATATCAGGAGCTCCTAATATTAAAGGAAGTAGT
          .....

          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
KM243546   CAATTTCCAAATCCTCCAATTATAATAGGTAWNACTATAAAGAAAATTATTACRMAGGCN
          .....tT.....ga....A

          490         500         510         520
Consensus  -----|-----|-----|-----|
KM243546   TGTGCTGTTACAATTACATTATAAATTTGGTNATCACCAA
          .....C.....
```

Lake Sauce Diptera Species 2 COI sequence

```

          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
JF869006    TTCCTGTAGATCGTATATTAATTACTGTWGTAATAAMATTAAACWGCWCCTAAAATAGAWG
          .....t.....a.....a..a.....a.

          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
JF869006    AAATTCCTGCTAAATGTAATGAAAAAATTGCTAAATCWACTGATCCTCCWCCATGTGCAA
          .....a.....a.....

          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
JF869006    TTGCTGCAGATAGAGGTGGGNTAAACWGTTTCATCCAG-TTCCAGCTC-CATTTTCTACTA
          .....TA..CTGT.CATC.AGTTCCAGCT.CATTT.C.A...TAC

          80          190         200         210         220         230         240
Consensus  -|-----|-----|-----|-----|-----|-----|
JF869006    TACTACTGGCTNAATAAAAGGGTTAAWGA-AGGNGGTAATAATCAAAAACCTTATATTATT
          ....GGCTAA.A..AGGGTTAA.G..G..GGTAATAATCA..AACTT.TA....T.AT.C

          240         250         260
Consensus  --|-----|-----|-----|
JF869006    TATTCGAGGAAANGCTATGTCAGGAG
          G.GGAA.T.CT.T.TC.G.AG-----
```

Lake Sauce *Odonata* Species 2 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
AB709128    .....a.....t.....T...CG.TCTGT.A.TAGCATAGTA.TAgCTC.TGCT

          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
AB709128    TARGACGGGTAGAGATAATAAKAGKARTAYTGCTGTAATTACTACWGCTCATACAAATAA
          AGgACG..TAGAGATA.TA.TAG.AGTACtGCTGTA.T.ACTACTGCTCATACA..TA.T

          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
AB709128    TGGTATTTGATCTAKYTTTATWCCAGGKGATTTTATATTAATTACRGTAGTAATAAAATT
          G.TAT..GATCTAGCt..ATAC.AG..gAT...ATAT.A.T.ACAgTAGTA.TA...T.G

          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
AB709128    GATTGCACCTAAAATWGAAGATACWCCTGCAAGRTGTAAWGAGAAAATAGTTAAATCTAC
          AT.GCAC.TA...T.GA.GATACTC.TGCA.GATGTA..GAGA...TAGT.A..TCTACG

          ---
Consensus  GGA
AB709128    .A-
```

Lake Sauce *Odonata* Species 7 COI sequence

```

          10          20          30          40          50          60
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MF174519   .....a.....a....T.A.TA.TATG.TAaTAGCTC.TGCTA.TACAG.T

          70          80          90          100         110         120
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MF174519   a.TGATA.TA.TA.TA.GAC.GCAGTAATTACTACTGCT.AT.C.A.T.A.GGTA.T.GA

          130         140         150         160         170         180
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MF174519   GATCTAWYTTTATWCCAGGKGAYTTTATATTRATTACWGTTGTAATAAAATTRATTGCYC
TC.AACtt.A.TCCAGGT.ACTt.A...TGATTACTGtTG.AAT.A..TTAATTGCT.cT

          190         200         210         220         230         240
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MF174519   CTAAAATWGAAGATACACCTGCAARATGWAGTGAAAAAATTGTTAARTCTACTGAKGCYC
AA..T.GaAG.T.C..CTGCAAG.TG.AGT.AA...TTG.TAAGTC.ACTGATGCT.cT

Consensus  ----:
MF174519   CTGCA
GCA--
```


Lake Sauce *Odonata* Species 8 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
JF839359  .....a.....t.....a.....g.....g.....t.....

          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
JF839359  ..a.....a.....a.....a.....a.....a.....

          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
JF839359  GGTATTTGATCTATYTTTATTCCTGGTGACTTTATATTAATWGTTGTAGTAATAAAATTA
          .....c.....t.....

          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
JF839359  ATAGCYCCTARAATTGAAGATACWCCAGCMAGRTGTARWGAAAAAATAGTTAAATCTACT
          .....c.....a.....t.....c..a....aa.....

          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
JF839359  GATGTCYCCWGCRTGAGCAATTGCACCAGCYARRGGTGGATAWACAGTTCAWCCWGTTCR
          .....t..t..a.....t.ga.....t.....a..t....g

          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
JF839359  GCTCCTCTTTCAACTATACTTCCTGCTAATAAWAGTGTTAATGAWGGAGGTAATAATCAA
          .....t.....a.....

          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
JF839359  AATCTTATATTATTTAAACGTGGGAAAGCTATATCAGGAGCTCCTAATATTAGTGGTACT
          .....

          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
JF839359  AACCAATTYCCRAATCCTCCAATTATAATAGGTATYACTATAAAGAAAATTATAACAAAA
          .....c..g.....c.....

          490         500         510         520         530         540
Consensus  -----|-----|-----|
JF839359  -|-----|-----|-----|
Consensus  GCATGTGCTGTTACAATTACATTATAAATYTGATCATCTCCAATTAATGATCCNTGGTTG
JF839359  .....t.....TG.T.GT

          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
JF839359  TCCTAATTCAATNTCRAATTAAGCTCTTAARGMANTTCCTAYTATTCCTGATCATGCCC
          C.TA.T.CA.T.CGAaTTAA..CT..TAA.GCAGTTCCTACTA.TCCTGATCATGCC..A
```

	10	20	30	40	50	60
Consensus	----- ----- ----- ----- ----- -----					
KF919537	AAAAAWGAWGTATTAATATTACGATCWGTWARYAATATTGTRATWGCTCCTGCGYAGWACA					
a..t.....t..t.at.....g..a.....t..t...					
	70	80	90	100	110	120
Consensus	----- ----- ----- ----- ----- -----					
KF919537	GGTAARGATAATAAAAGWARAATKGCTGTAATTAAACTGAYCAAACAAATARAGGAGTA					
a.....t.a...t.....c.....g.....					
	130	140	150	160	170	180
Consensus	----- ----- ----- ----- ----- -----					
KF919537	CGRTCAAAATYTTATACCAATASYTCGTATATTAATTACAGTAGTAATAAAGTTAACWGCM					
	..g.....t.....ct.....a..c					
	190	200	210	220	230	240
Consensus	----- ----- ----- ----- ----- -----					
KF919537	CCTAAATAGATGAWAYACCTGCTAARTGTAAWGAAAAATWGCWARATCAACTCTWGSW					
a.t.....a.....t.....t..t.a.....a.gt					
	250	260	270	280		
Consensus	----- ----- ----- -----					
KF919537	CCAGAATGTGCTAMATTAKAAGAKAGWGGRGGATAAACAGTT					
a....g....t..a.a.....					

Lake Sauce Orthoptera Species 3 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
KF670968  CCTACKGCTCAWACAAATAARGGWGTTTGTATCTAAAGTTATKCCTGGTGCYCGTATATTA
          .....t.....a.....a.....t.....t.....

          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
KF670968  ATTATAGTAGARATAAAATTAATTGCWCCWARAATWGARGAAATTCCAGCTAAATGAAGA
          .....a.....t..t.a...t..a.....

          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
KF670968  GAGAAAATKGCWAKATCAACWGAWMWCCWCTRTGRGCAATAAGAGATGAKANAGGGRRGG
          .....g..a.g.....a..t.ca..t..g..g.....t.AG..Ag.A

          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
KF670968  NTAAACTGTTTCATCCWGTWCCTGCACCRYTTTCTACYAWTCTTCTWGATAAYAGAAGAGT
          TA..CTGT.CATC.TGT.C.TGCAC.GTt..CTAC.ATtCT.CTAGATA.TAGA.GAGT.

          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
KF670968  TAATGAAGGWGGWARKARTCARAATCTTATATTATTTATTCGGGGRAAWGCTATATCTGG
          A.TGA.G.AG.Ta.TA.TCA.a.TCT.ATAT.AT..AT.CG...Aa..GCTATATCTG.A

          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
KF670968  AGCTCTTAATATTARWGGGRAYTARTCAATTTCCAAKCCWCCAATTATAATTGGTATYAC
          GCTCT.A.TAT.A.TG.AaCtA.TCA.T..C.A..TC.TC.A.T.ATA.T.G.TAT.ACT

          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
KF670968  TATAAARAAAATTATTACAAAAGCATGKGCAGTYACAAYTACRTTATAAATTTGATCRTC
          ATA...a...T.AT.ACA...GCATGTgCAGTCACA.TtACAT.ATA..T..GATCGTCT

          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
KF670968  YCCAATTAAWGAYCCTGGTTGRCCTAATTCAGTWCGAATTAAATTCTTAGWGAKGTWCC
          c.A.T.A.TGATc.TG.T.GAC.TA.T.CAGT.CGA.T.A...T.CT.AGAGATgT.C.T

          490         500         510         520
Consensus  -----|-----|-----|-----|
KF670968  WACTATAGCWGATCAAGCTCCRAAAATRAAATATAAWGTT
          aCTATAGCAGATCA.GCTC.Aa...TAa..TATA.TGT.-
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Lake Sauce Shrimp Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
AB250504    TTTTCGRCTCTGTTAGWAGTATGGTAATRGCTCCWGCTARRACTGGWAGAGAKAGTARKAGN
          .....g.....t.....g.....t....ag.....a.....t....gg..A

          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
AB250504    AAGNATRGCWGTTAGAAAWACRGMTACACAAATARTGGGAKTCGATCTATWGTTATTCC
          .GAATGgCTGT.AGA...aCGgATCACACA..TAGTG..ATtCGATCTAT.GT.AT.C.T

          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
AB250504    TGGKGMTCGTATGTTAATCACTGTRGTGATAAARTTTACWGCTCCTARAATTGAAGARAC
          G.TgATCGTATGT.A.TCACTGTGgTGATA...T..ACAGCTC.TA.a.T.GA.GAGaCT

          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
AB250504    TCCTGCTAAGTGGAGRGAGAAAATTCCTAGRTCTACTGAKGCTCCTGCATGAGCAGTWYY
          C.TGCTA.GTG.AGAgAGA...T.C.TAG.TCTACTGAGgCTC.TGCATGAGCAGT.Cct

          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
AB250504    WGCWGCTAGTGGWGGGTAWACAGTTCATCCTGTKCCYACYCCACTTTCTACTATWCCTCT
          GCTGCTAGTG.TG..TATaCAGT.CATC.TGTGC.TACTc.ACT..CTACTAT.C.TCT.

          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
AB250504    TGATAARAGKAGWGTTARTGATGGWGGWARWAGTCARAATCTTATGTTATTTATTCGTGG
          GATA.GaGTAGAGT.AGTGATG.TG.AaGaaGTCA.a.TCT.ATGT.AT..AT.CGTG..

          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
AB250504    GAAWGCTATRTCTGGKGCTCCWAGTATKAGGGGRACTAGTCARTTACCAAATCCKCCRAT
          A.TGCTATGTCTG.TgCTC.TaGTATGAG...AaCTAGTCAGT.AC.A..TC.GC.GaT.

          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
AB250504    TATRATKGGTATAACTATRAARAAATTATTACRAAWGCATGRGCRGTRACAATAACRTT
          ATAaT.g.TATA.CTATGa.Ga...T.AT.ACGa.TGCATGAgCAgTGaCA.TA.CAT.G

          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
AB250504    RTAGATTTGRTCATTTCCAATTAAKCTTCCTGGTTGACCKAGYTCTGCYCGGATTARWAG
          TAGAT..G.TCAT..C.A.T.A.TCT.C.TG.T.GAC.TAGTtCTGC.cG.AT.AGTaGT

          550         560         570         580         590
Consensus  -----|-----|-----|-----|-----|
AB250504    TCTTAAAGATGTRCCSACTATTCCYGCTCAAGCTCCGAAAATAAAATATAAGGTT
          CT.A..GATGTGC..ACTAT.C.TGCTCA.GCTC.GA...TA...TATA.G.T.-
```

Lake Sauce Fish Species 2 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
KU288892   CCCCCGAATAAATAANATAAGCTTCTGACTTCTTCCTCCNTCTTTCCTCCTNCNTTTNGC
          .....T.....A.....A.T...A..

          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
KU288892   CTCATCNGGCGTTGAAGCCGGGNCGGCACAGGATGTRACTGTTTATCCCCCTCTTGCAGG
          .....A.....C.....g.....

          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
KU288892   CAATCTCGCNCACGCTGGGGCTTCTGTAGANTTAACCATCTTCTCACTTCATTTGGCCGG
          .....G.....T.....

          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
KU288892   AGTTTCTTCTANTTTAGGGGCAATTAATTTTATTACAACCTATTATTAATATGAAACCCCC
          .....T.....

          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
KU288892   AGCTATTTTACAATATCAAACCCCCCTATTTGTTTGAGCNNNNTTANTAACAGCTGTTCT
          .....CGTC...G.....

          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
KU288892   CCTCCTCCTCTCTCTGCCAGTCCTAGCAGCCGGAATCACAATGCTANTAACAGACCGAAA
          .....T.....

          370         380
Consensus  -----|-----|-----|
KU288892   TCTAAATACCACATTCTTTGACCCGGCAG
          .....

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Lake Sauce Fish Species 3 COI sequence

```

          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
HM405101   CGGTATAGTTGGTACCGCCCTAAGTCTCNCTAATTGAGCAGAGCTTAGCCAACCCGGAG
          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
HM405101   ..TACT.G.TGACGATCAGAT..ATA.TGTCATCGT.ACTGCACACGC.T.CGTA.TA.T
          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
HM405101   TCTTCTTTATAGTAATGCCAATTATGATTGGAGGTTTCGGAAACTGATTAATTCCCCTAA
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
HM405101   CT.CT..ATAGTA.TGC.A.T.ATGAT.G.AG.T..CG.A..CTGAT.A.T.C...TA.T
          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
HM405101   TGATTGGAGCCCCGATATGGCATTCCCTCGAATAAATAACATRAGTTTTTGACTRCTAC
          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
HM405101   GAT.G.AGC....GATATG.CAT.C..TCGA.TA..TA.CATGaGT....GACTGCTAC.
          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
HM405101   .c..TCAT.C.T.CT.CTAT.ATC.TC.TCTG.TGT.GA.GC.G..gTAG.AaCAG.CTG
          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
HM405101   GAACTGTATATCCGCCTCTAGCTGGTAATCTCGCCCATGCAGGMGCTTCTGTTGATTTAG
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
HM405101   A.CTGTATATC.GC.TCTAGCTG.TA.TCTCGC..ATGCAG.AGCT.CTGT.GAT..AGC
          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
HM405101   CCATTTTTCCTTCATCTCGCYGGGGTTTCCTCAATCCTTGGGGCAATTAATTTTATTA
          610         620
Consensus  -----|-----|
HM405101   .AT...CtC..T.CATCTCGC.G...T..C.TCA.TC.T.G...CA.T.A.T...AT.AC
          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
HM405101   CAACCATTATTAAYATGAAACCCCCAGCAATTTACARTACCAAACACCCCTATTTGTAT
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
HM405101   A.C.AT.AT.A.TATGA..C....AGCA.T..CACA.TAC.A..CAC...TAT..GTATG
          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
HM405101   GAGCYACTCTAATTACAGCTGTACTTCTTCTTCTATCYCTTCCAGTCCTAGCTGCTGGAA
          610         620
Consensus  -----|-----|
HM405101   AGCTACTCTA.T.ACAGCTGTACT.CT.CT.CTATCTcT.C.AGTC.TAGCTGCTG.A.T
          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
HM405101   TTACTATRCTRCTCACAGACCGAAATATYAATACCACATTCTTTGAYCCTGCGYGGMGAG
          610         620
Consensus  -----|-----|
HM405101   .ACTATGCTGCTCACAGAC.GA..TAT.A.TAC.ACAT.CT..GATc.TGC.G.CG.AG.
          610         620
Consensus  -----|-----|
HM405101   GAGACCCAATTCTATACCAACA
```

Lake Sauce Fish Species 5 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
KF210147  CTTCTCATCCGGGCAGAACTAAGCCAACCCGGATCATTACTGGGCGATGACCAAATTTAY
          .....t

          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
KF210147  AATGTTATCGTAACTGCACACGCATTYGTAAATAATYTTCTTTATAGTAATGCCTGTWATA
          .....c.....t.....a...

          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
KF210147  ATTGGGGGTTTGGCAACTGACTTTRTWCCAYTAATGATYGGCGCCCCAGATATAGCCTTC
          .....t.....a.t...c.....c.....

          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
KF210147  CCCCWATAAATAATATAAGCTTCTGACTTCTTCCTCCATCTTTCCTCCTRCTTYTRGCC
          .....t.....g...c.g...

          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
KF210147  TCATCAGGYGTTGAAGCCGGRGCGYGGYACAGGATGRACTGTTTAYCCCCCTCTTGCCAGGC
          .....t.....a..t..t.....a.....c.....

          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
KF210147  AATCTCGCRCACGCTGGGGCTTCTGTAGATTTAACCATCTTCTCACTTCATTTGGCCGGA
          .....a.....

          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
KF210147  RTTTCTTCTATTTTAGGGGCAATTAAYTTTATTACAACCTATTATTAATATGAAACCCCCCA
          a.....c.....

          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
KF210147  GCTATTTACAAATATCAAACCCCYTATTTGTYTGAGCYGTYTTAGTAACAGCTGTYCTC
          .....t.....c.....t..t.....c...

          490         500         510         520
Consensus  -----|-----|-----|-----|
KF210147  CTYCTCCTCTCYCTRCCAGTYCTAGCAGCCGGAATCACAAT
          ..t.....c..a.....t.....
```

Lake Sauce Fish Species 6 COI sequence

```

          10          20          30          40          50          60
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ749041    ATCCGAGCGGAATTAAGTCAACCTGGMTCCCTGCTAGGTGATGATCAAATYTACAACGTT
          .....c.....c.....

          70          80          90          100         110         120
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ749041    ATCGTAACTGCACACGCATTTGTGATAATTTTCTTTATAGTAATACCAGTTATAATTGGG
          .....

          130         140         150         160         170         180
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ749041    GGCTTCGGAAACTGACTTATTCCCCTAATRATCGGTGTCYCCAGACATAGCCTTCCCCCGA
          .....a.....t.....

          190         200         210         220         230         240
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ749041    ATAAATAACATAAGCTTCTGACTATTACCRCCATCTTTCCTTCTCCTATTAGCCTCATCT
          .....g.....

          250         260         270         280         290         300
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ749041    GGAGTTGAAGCCGGRGCAGGTACAGGTTGAACTGTTTATCCYCCMCTTGCTGGGAATCTA
          .....a.....c..a.....

          310         320         330         340         350         360
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ749041    GCACATGCGGGAGCTTCTGTAGACCTAACAATTTTCTCACTTCATTTAGCCGGGGTGTCA
          .....

          370         380         390         400         410         420
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ749041    TCTATYCTAGGRGCAATCAATTTTATTACCACTATTATTAATATAAAACCTCCAGCCATC
          .....c.....a.....

          430         440         450         460         470         480
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ749041    TCACAATACCARACACCTTTATTTGTTTGAGCTGTTTAAATTACTGCCGTCTCCTTCTA
          .....a.....

          490         500         510         520         530         540
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ749041    CTATCACTCCCTGTACTAGCAGCCGGAATTACAATGCTACTAACAGATCGAAACCTTAAT
          .....

          550         560         570         580         590
Consensus  ----:----|----:----|----:----|----:----|----:----|----:--
FJ749041    ACCTCTTTCTTTGACCCGGCAGGCGGRGGAGACCCAATCCTWTATCAACATTTATT
          .....g.....t.....
```


Lake Sauce Fish Species 9 COI sequence

```

          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
EU179805   CCGGTCCTTCTTAGGCGACGATCAAATTTATAATGTTATCGTTACTGCTCACGCCTTC
          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
EU179805   GTAATAATTTTCTTTATAGTAATACCCATTATGATYGGGGGCTTTGGAACTGACTTATC
          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
EU179805   CCACTAATAATYGGTGCACCAGATATAGCATTCCRCGAATAAATAATATAAGCTTCTGR
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
EU179805   STACTCCCCCYTCATTCTACTAMTACTCGCCTCCTCTGGTGTTGAAGCGGGAGTGGGG
          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
EU179805   ACAGGATGAACTGTCTATCCGCCCCTTGCGGAACTTAGCACATGCAGGAGCCTCCGTA
          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
EU179805   GATCTAGCTATTTTCTCCCTGCACCTTGSTGGTGTGTCCTCCATCTTGGGTGCCATCAAC
          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
EU179805   TTTATTACAACTATTATTAATATGAAACCCCGAGCTATTTTACAATACCARACACCTCTC
          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
EU179805   TTTGTATGGGCAACTCTAATTACAGCAGTACTACTACTATTATCGCTTCCAGTCCTAGCC
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
EU179805   GCCGGTATTACAATACTACTAACAGACCGAACTTAAACACCACATTCTTTGACCCGCA
          550         560         570         580
Consensus  -----|-----|-----|-----|-----|
EU179805   GGAGGAGGRGACCCAATTCTCTATCAACACCTATTCTGATTCTTCGG
          .....a.....
```

Lake Dario Arachnid Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ525320   .....g.....a..T..t.....a.....a.....t

          70          80          90          100         110         120
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ525320   ..c..t.....a.....a..c..c.....a..t..t....a.....

          130         140         150         160         170         180
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ525320   .....a.....c..t.....t.....ac

          190         200         210         220         230         240
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ525320   ..a.....a.....a.....a..c..t.....t....a.....a...a..a

          250         260         270         280         290         300
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ525320   ..a..a..c..t..t..c..c..t.....c.....a.g.....t.....

          310         320         330         340         350         360
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ525320   .gc.....a..t..t.....t..a.....a.....

          370         380         390         400         410         420
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ525320   ..t.....g.....t..t.....g.....a..t

          430         440         450         460         470         480
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
FJ525320   .....t.....c.....t..a.ta.....t.....a

          490
Consensus  ----:----|----
FJ525320   .....

```

Lake Dario Fish Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
HM405101   GAGCAGAGCTTAGCCAACCCGGAGCCCTACTYGGTGACGATCAGATTTATAATGTYATCG
          .....t.....c....

          70          80          90          100         110         120
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
HM405101   TTACTGCACACGCCTTCGTAATAATCTTCTTTATAGTAATGCCAATTATGATTGGAGGTT
          .....

          130         140         150         160         170         180
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
HM405101   TCGGAAACTGATTAATTCCCCTAATGATTGGAGCCCCGATATGGCATTCCCTCGAATAA
          .....

          190         200         210         220         230         240
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
HM405101   ATAACATRAGTTTTTGACTRCTACCYCCCTCATTCTTCTTCTATTTRCCTCCTCTGGTG
          .....g.....g.....c.....a.....

          250         260         270         280         290         300
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
HM405101   TTGAAGCCGGRGTAGGRACAGGCTGAACTGTATATCCGCCTCTAGCTGGTAATCTCGCCC
          .....g.....a.....

          310         320         330         340         350         360
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
HM405101   ATGCAGGMGCTTCTGTTGATTTAGCCATTTTTCCTTCATCTCGCYGGGGTTTCCTCAA
          .....a.....c.....c.....

          370         380         390         400         410         420
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
HM405101   TCCTTGGGGCAATTAATTTTATTACAACCATTATTAAYATGAAACCCCCAGCAATTTAC
          .....t.....

          430         440         450         460         470         480
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
HM405101   ARTACCAAACACCCCTATTTGTATGAGCYACTCTAATTACAGCTGTACTTCTTCTTCTAT
          .a.....t.....

          490         500         510         520         530         540
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
HM405101   CYCTTCCAGTCCTAGCTGCTGGAATTACTATRCTRCTCACAGACCGAAATATYAATACCA
          .t.....g..g.....t.....

          550
Consensus  ----:----|----:--
HM405101   CATTCTTTGAYCCTGC
          .....t.....
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Lake Dario Fish Species 2 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
JX111702   TTGGTACGGCCCTTAGCCTTCTAATTCGAGCAGAACTTAGTCAACCCGGCTCCCTTTTAG
          70          80          90          100         110         120
Consensus  GRGACGATCAAATTTATAATGTGATCGTTACCGCACACGCTTTTATTATAATCTTCTTCA
JX111702   .a-----|-----|-----|-----|-----|-----|
          130         140         150         160         170         180
Consensus  TAGTAATACCAATTATAATTGGGGGCTTTGGAAATTGATTAATTCCTTAATAATTGGAG
JX111702   -----|-----|-----|-----|-----|-----|
          190         200         210         220         230         240
Consensus  CACCTGATATAGCATTCCCCGAATAAATAACATAAGTTTTTGAATTCTCCCACCCTCCT
JX111702   -----|-----|-----|-----|-----|-----|
          250         260         270         280         290         300
Consensus  TTCTTCTCCTATTAGCCTCTTCCGGAGTTGAGGCCGAGCCGGGACAGGGTGGACTGTAT
JX111702   -----|-----|-----|-----|-----|-----|
          310         320         330         340         350         360
Consensus  ATCCTCCCCTCGCTGGAAATCTTGCCACGCAGGCGCATCGGTGACCTTACTATTTTCT
JX111702   -----|-----|-----|-----|-----|-----|
          370         380         390         400         410         420
Consensus  CTCTTCACTTAGCAGGCGTATCTTCAATTCTAGGTGCAATCAACTTTATTACTACTATTA
JX111702   -----|-----|-----|-----|-----|-----|
          430         440         450         460         470         480
Consensus  TTAATATAAAACCTCCTGCTATTTCCCAATATCAGACACCTTTATTCGTATGAGCAGTTT
JX111702   -----|-----|-----|-----|-----|-----|
          490         500         510         520         530         540
Consensus  TAGTAACAGCTGTCCTTTTACTGCTATCTCTTCCCGTTTTAGCCGCCGGTATTACGATAC
JX111702   -----|-----|-----|-----|-----|-----|
          550         560         570         580         590         600
Consensus  TACTCACAGATCGAAATTTAAACACAACCTTCTTTGACCCAGCAGGAGGCGGAGACCCGA
JX111702   -----|-----|-----|-----|-----|-----|
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Lake Dario Fish Species 5 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
JX111778   GTCGGAACGGCCCTAAGCCTTTTAATCCGAGCTGAACTTAGCCAGCCGGGGTCCCTATTA
          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
JX111778   GGGGACGACCAGATCTACAATGTAATCGTTACAGCCCATGCTTTTGTAATAATCTTTTTT
          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
JX111778   ATAGTCATACCCATCATAATTGGGGGCTTCGGAAATTGACTGGTCCCATTAATAATTGGC
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
JX111778   GCTCCAGACATGGCTTTTCCTCGAATAAATAATATGAGCTTCTGACTACTCCCCCTTCT
          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
JX111778   TTCCTCTTACTCCTGGCTTCCTCAGGCGTGGAAGCAGGCGCAGGGACAGGGTGGACCGTT
          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
JX111778   TACCCACCCCTATCGAGCAATCTAGCACACGCAGGAGCGTCCGTTGACCTAACTATTTTT
          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
JX111778   TCACTTCATCTGGCAGGTATCTCTTCTATTCTTGGGGCAATCAATTTTATTACCACAATT
          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
JX111778   ATTAACATAAAACCCCCAGCAATTTACAATACCAAACACCTTTATTCATCTGATCTGTT
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
JX111778   CTCATCACTGCTATCCTTCTTCTCCTCTCCCTTCCTGTCCTTGCCGCGGGTATCACTATA
          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
JX111778   CTTCTAACCGACCGAAACTTAAATACCACATTCTTCGACCCTGCAGGAGGGGGCGACCCA
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Lake Site Xi Xi National Park Coleoptera Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
FJ859903    TGAAGTATTAATATTTTCGRTCWGTAAGWARTATRGTAATWGCYCCWGCNAAGNACTGGTA
          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
FJ859903    .GATAGTA.a.GTA.TAGAGCAGTTa.GGCTaCTG.TCA.A...T..GGGTaTTCGG..
          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
FJ859903    GRTCRAARGTTATYCCAGTWGAYCGTATGTTAATTACAGTAGTAATAAAATTTACTGCMC
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
FJ859903    AaAaGtTaT.CCAGTAGA.C.TAT..TAA...CAGTAGTA.TA..ATTT.C.GCACCTaG
          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
FJ859903    CTCTATGGGCAATATTTRGCWGAAAGWGGGGGRTAWACWGTTTAYCCAGTKCCWGCWCCTC
          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
FJ859903    A.GGGCAATATTAGC.gAAa.TGG.G.ATAAaCTGTTCA.C..GTTCCAg.ACCTCTT..
          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
FJ859903    TTTTCTACTAATCTTCTTATTATAAWARWARAGTTARKGAMGGWGGWAGWARTCARAATCTYA
          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
FJ859903    .ACTa.TCTTCT.AT.A.AAGTa.aGTT.A.G.ag.TG.Ta.AaGTC.aAATCTTATaT
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
FJ859903    TRTTATTTATTTCGAGGAAARGCTATATCYGGRGCWCCTAGTATKARGGGTACTAGTCAAT
          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
FJ859903    AT.....CGAGGA.AAGCTaTA.C.GGGGCTCCTaGTATTA.GgGTACTAGTC.A.TTCC
          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
FJ859903    TTCCRAATCCKCCAATTATAATKGGCATWACTATGAAGAAAATYATYACAAAKGCATGWG
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
FJ859903    AAATCCTC.AATT.TAAT.GGCATTAC.aTGA.GA..ATT.T.ACAA.TGC.t.AGCTGT
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
FJ859903    CTGTRACAATMACRTTATAAATTTGATCGTCMCCAATTAARGTTCCWGGGYTACCWARTT
          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
FJ859903    GACAaT..CGTTATAA..TTGA.C.TC.CCAaTT..AGTTCC.GGGCTACcA.GTtCaGC
          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
FJ859903    CWGCTCGAATTAGGAGWCTAAGAGAAGTTCCYACTATWCCWGCTCAACTWCCAAATAGRA
          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
FJ859903    TC.AATT.GGAGACTAaGAG.AGTTCC.A.TATTCC.G.TCAACTTC.AaAT.G.A.AT.
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Lake Site Xi Xi National Park Hemiptera Species 1 COI sequence

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              10      20      30      40      50      60
Consensus    -----|-----|-----|-----|-----|-----|
AB897517     TAATAAAATTTACAGCACCTAAAATAGAAGATACTCCTGCTAAATGAAGTGAAAAAATAG
              70      80      90     100     110     120
Consensus    -----|-----|-----|-----|-----|-----|
AB897517     TTATATCAACACATGAGCCAGAATGATATAAAACTCTTGATAAAGGAGGATAAACAGTTC
              130     140     150     160     170     180
Consensus    -----|-----|-----|-----|-----|-----|
AB897517     ATCCTGTTCCAGCACCTCTATCAATTATACTTCTAAATAATAATAATGTTAAAGAGGGTG
              190     200     210     220     230     240
Consensus    -----|-----|-----|-----|-----|-----|
AB897517     GTAAAAGTCAAAATCTTATATTATTTATTCGAGGAAATGCCATATCAGGGGCACCAATTA
              250     260     270     280     290     300
Consensus    -----|-----|-----|-----|-----|-----|
AB897517     TCAAGGGAACCAGCCAATTCCCAAAACCCCAATTATAATAGGTATAACTATAAAAAAAAA
              310     320     330     340     350     360
Consensus    -----|-----|-----|-----|-----|-----|
AB897517     TCATAATAAATGCATGAGCAGTAACAATTACATTATAAATTTGATCGTCTCCAATAAATG
              370     380     390     400
Consensus    -----|-----|-----|-----|-----|
AB897517     AACCAGGAATTCTTAATTCTACTCGAATTAAAAATCTTAATGCAGTT

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Lake Site Xi Xi National Park Hemiptera Species 2 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
GQ527122    TATAGTAATAGCACCAGCTAAAAGTGGTAAAGATAACAATAATAAGAATGCAGTAATTAA
          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
GQ527122    AACTGATCAAACAAATAATGGAGTTTTATCTAATCTCATACCAGTTGAACGCATATTAAA
          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
GQ527122    AATAGTTCTAATAAAATTTACAGCTCCCAAATGGATGAAACACCTGCTAAATGTAAAGA
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
GQ527122    AAAAATTGTTAAATCAACACAAGAACCAGAATGAAATATAAATCTRGACAAAGGAGGATA
          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
GQ527122    GACAGTTCATCCTGTCCCAGCACCATTGTCTACTAATCTACCAACCAATAATAAAGTTAA
          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
GQ527122    TGAAGGAGGAAGAAGTCAAATCTTATATTATTTATTCGAGGAAATGCTATATCTGGTGC
          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
GQ527122    TCCAATCATTAGAGGAATTAATCAATTCCCAAATCCACCCATTATGATGGGTATAACTAT
          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
GQ527122    AAAAAAAATTATAACAAAAGCGTGAGCTGTAACAATAACATTATAAATCTGATCATCACC
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
GQ527122    AATAAAAGAACCAGGAGTTNCCTAACTCAATTCNGAATTAATGTTCTAAGAGCTGTACCA
          550         560         570
Consensus  -----|-----|-----|-----|
GQ527122    ATTATTCCNTGATCNAATACCGAAAATAAANTATA
          TA.TCCTGA.C.AAT.CCGAAA.T..A.T.TA---
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Lake Site Xi Xi National Park Lepidoptera Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
KF881048  TTTTCGATCWGTTARTARTATAGTAATAGCTCCKGCTAAWACTGGTAATGAKAGAAGTARW
          .....a....g..g.....t.....a.....t.....aa

          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
KF881048  ARWAAWGCTGTAATWCCTACAGCTCAAACAAATAAAGGTATTTGATCAAAAGATATATTA
          .gt..t.....a.....

          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
KF881048  TTAAYTCGTATATTAATAATAGTWGTAATAAAATTAATWGCWCCTAARATWGAWGAAATW
          ....t.....t.....a..t....g..t..t....t

          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
KF881048  CCRGCTAAATGWAGGGAAAAAATAGCTAAATCTACTGATNCTNCCTCTRTGRCGAATATT
          ..a.....a.....G..C.TCTGTG.gCA.TAT.A

          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
KF881048  AGATGARAGTGGGGGTAAACTGTTTCATCCTGTTCCAGCMCCWKTTTCTACAATACTACT
          GATGAGaGTG....TA..CTGT.CATC.TGT.C.AGCac.Att..CTACA.TACTACTA

          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
KF881048  AGAAATTAAAAGWRTTAGTGAGGGGGGTARTAWTCAAATCTTATATTATTTATTCGRGG
          GA..T.A...GAGT.AGTGAG....TA.TA.tCA...TCT.ATAT.AT..AT.CG.g..

          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
KF881048  RAAAGCTATATCWGGGGCTCCTAATATTAAAGGSACTAATCARTTTCCRAATCCTCCAAT
          a..GCTATATCTG...CTC.TA.TAT.A..G.CACTA.TCA.T..C.Ga.TC.TC.A.T.

          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
KF881048  TATAATWGGTATAACTATAAAAAAAATTATAATAAAAGCATGRGCTGTRACAATAGTATT
          ATA.TAG.TATA.CTATA.....T.ATA.TA...GCATGAgCTGTGaCA.TAGTAT.A

          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
KF881048  ATAAATTTGATCATCWCCAATTARTGAMCCTGGATTTCTTAATTCWGYTCGAATTAATAA
          TA..T..GATCATCAC.A.T.A.TGA.c.TG.AT..C.TA.T.CTGTtCGA.T.A.TA..

          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
KF881048  ACTTAAKGAWGTTTCTACTATTTCCTGMTCAAATTCCAAAAATAAARTATAAAGTKCCAAT
          CT.A.TgATGT.C.TACTAT.C.TGATCA..T.C.A....TA...TATA..GTGC.A.TA
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Lake Site Xi Xi National Park Lepidoptera Species 2 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
KT236376   TAAAAGTAATAAAGCTGTAATTCCAACAGCTCAAATAAATAATGATATTTGATCAAAAGA
          70          80          90         100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
KT236376   TAAATTACTTACTCGTATATTAATAATTGTTGTAATAAAATTAATTGCACCTAAAATTGA
          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
KT236376   AGAAATACCAGCTAAGTGTAAGAAAAAATAGCTAAGTCTACAGAAGATCCTCTATGAGC
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
KT236376   AATATTTGATGAAAGTGGGGGTACACAGTTCATCCAGTTCCTGCTCCATTTTCTACAAT
          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
KT236376   TCTTCTAGAAATTAATAATATTAAGATGGAGGTAATAATCAAAATCTTATATTATTTAT
          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
KT236376   TCGTGGAATGCTATATCAGGGGCTCCTAATATTAATGGGACTAATCAATTTCCAAATCC
          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
KT236376   ACCAATTATAATAGGCATAACTATGAAAAAATTATAATAAAAGCATGAGCTGTTACAAT
          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
KT236376   AGTATTATAAATTTGATCATCACCAATTAATGATCCTGGAGTACCTAATTCTATTCTGAAT
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
KT236376   TAAAATTCTTAAGGATGTTCTAATATTCCTGCTCAAATACCAAAAATAAAATATAATGT
          550         560
Consensus  -----|-----|-----
KT236376   TCCAATATCTTTATGATTTGTWGA
          .....a..
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Lake Site Xi Xi National Park Lepidoptera Species 3 COI sequence

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              10      20      30      40      50      60
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KM215138   TAATATAGTAATAGCTCCTGCTAATACAGGTAAAGAAAGGAGTAATAATAAGGCAGTGAT
          .....

              70      80      90     100     110     120
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KM215138   TCCTACAGCTCACACAAATAATGGTATTTGATCAAAAGATATTCTATTAATTCGTATATT
          .....

              130     140     150     160     170     180
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KM215138   AATAATTGTTGTAATAAAGTTAATTGCACCTAAAATTGATGAAATACCAGCTAAATGAAG
          .....

              190     200     210     220     230     240
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KM215138   RGAAAAAATAACTAAATCAACAGATCTTCTCCATGGGCAATATTAGATGAAAGAGGGGG
          g.....

              250     260     270     280     290     300
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KM215138   GTAAACAGTTCAACCAGTTCCAGCTCCATTTTCTACAATTATTCTAGAAATTAAGGGT
          .....

              310     320     330     340     350     360
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KM215138   YAGGGATGGGGGAAGTAATCAAAATCTTATATTATTTATTTCGGGGGAAAGCTATATCAGG
          c.....

              370     380     390     400     410     420
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KM215138   GGCTCCTAATATTAATGGGACTAATCAATTTCCAAATCCTCCAATTATAATAGGTATAAC
          .....

              430     440     450     460     470     480
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KM215138   TATAAAAAAATTATAATAAAGCGTGGGCTGTAACAATAGTATTATAAATTTGATCATC
          .....

              490     500     510     520     530     540
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KM215138   CCCAATTAGAGAACCTGGAGTTCCTAATTCAGTTCGAATTAATAAACTTAATGAAGTTCC
          .....

              550     560     570     580     590     600
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KM215138   TAATATTCTTGCTCAAATACCAAAATAAAATATAATGTTCCAATATCTTTATGATTTGT
          .....
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Lake Site Xi Xi National Park Mantidae Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT036560   AAAGTATTGTGATAGCCCCTGCAAGAACTGGTAAGGAAAGTAGAAGTAAAAGTGCTGTAA
          70          80          90          100         110         120
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT036560   TTCCTACTGATCAAACAAATAAAGGAACTTGAGTTTGATTTATATAAGCTGGTTTTATAT
          130         140         150         160         170         180
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT036560   TAATTATAGTTGTAATAAAATTTACTGTCYCTATAATACTTGATATTCCAGCTAAATGTA
          190         200         210         220         230         240
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT036560   ATGAAAAGATTGTTAAATCAACTGCRGGCCCTGCATGGGCAATTCTTGCTGATAAAGGGG
          250         260         270         280         290         300
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT036560   GATAAACTGTTTCATCCTGTTCCCGCCCCTCTTTCAACTGTTCTTCTAATTAATAAAAGTA
          310         320         330         340         350         360
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT036560   AAATTGAAGGTGGTAAAAGTCAAAATCTTATGTTATTTATACGTGGAAAAGCTATATCAG
          370         380         390         400         410         420
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT036560   GGGCTCCTAATATTAAAGGAACTAATCAATTACCAAATCCCCCAATTATAATTGGTATAA
          430         440         450         460         470         480
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT036560   CTATAAAGAAAATTATAATGAAAGCGTGTGCGGTAACAATAACATTGTARATTTGATCAT
          490         500         510         520         530         540
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT036560   CTCCAATTAAGGATCCTGGTTGACCAAGTTCTGTTCGAATTAAAATTCTTAGTGATGTAC
          550         560         570         580         590         600
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
KT036560   CAAGTATTCTGCTCAAGCACCAAAAATAAAGTARAGTGTTCCAATATCTTTATGATTTG

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Lake Site Xi Xi National Park *Odonata* Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
KT991525   GTATTAATATTTTCGATCWGTTARTAAAYATTGTAATAGCTCCKGCTAGAACKGGTAATGAT
          .....t....g...t.....g.....t.....

          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
KT991525   ARTAAWARTAAWACWGCWGTAATTACTACYGCTCATACAAATAAWGGYATTTGATCTAKT
          .g...a.g...a..a.a.....t.....t..t.....g.

          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
KT991525   TTTATWCCSGGAGATTTTATATTAATTACWGTTAGTAATAAAATTAATAGCTCCTAAATTT
          .....a..g.....a.....

          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
KT991525   GATSWGACACCTGCTARATGWARGGARAAGATTGTTAAATCWACTGAWGCWCCAGCATGA
          ...ga.....a...t.a...a.....t....t..a.....

          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
KT991525   GCRATWGCTCCTGCMARAGGAGGATAAACWGTTTCATCCTGTTCCAGCMCCWCTTTCWACT
          ..a..t.....a.g.....t.....c..t.....a...

          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
KT991525   ATNCTTCTTGCAAGAARTAAWGTRAAAGAKGGAGGRAGWARTCARAATCTTATGTTATTW
          ..A.....g...a..g.....g.....a..t.a...g.....t

          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
KT991525   ARTCGTGGGAAWGCTATATCTGGTGCKCCTARTATWARTGGWACTARTCAATTWCCGAAW
          .a.....a.....g....g...t.a...t...a.....t....t

          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
KT991525   CCYCCAATTATAATWGGTATWACTATAAARAAAATTATKACAAAWGCATGKGCWGTYACA
          ..t.....t.....a.....g.....t.....t.....t..t..c...

          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
KT991525   ATWACATTAWAAATTTGATCRTCWCCAATTARAGATCCAGGTTGTCCTAATTCAATWCGA
          ..t.....t.....g..t.....a.....t...

          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
KT991525   ATTAAWACWCTTAAWGCWGTTCCAATTATTCCTGTCYAYGCWCCRAAGATYAAGTATAAR
          .....a..a.....a..a.....c..c..a..a.....t.....g

          610
Consensus  -----|-----
KT991525   GTTCCAATATCTTT
```

Lake Site Xi Xi National Park *Odonata* Species 3 COI sequence

```

          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
KT957514    ATAGAATAGGATCTCCCCCTCCGGCAGGGTCSAAGAATGATGTATTGATATTTTCGATCAG
          .....g.....

          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
KT957514    TCAATAACATTGTAATTGCTCCAGCCAATACAGGTAAAGATAATAAAAGAAGGACAGCAG
          .....

          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
KT957514    TAATTACTACTGCTCATACAAAAGAGGTATTTGATCTAGCTTTATTCCAGGTGATTTTA
          .....

          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
KT957514    TATTAATTACTGTTGTAATAAAATTAATAGCTCCTAGAATTGAGGAAACCCAGCTAAAT
          .....

          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
KT957514    GAAGTGAGAAAATCGTTAGATCTACTGATGCACCTGCATGAGCAATTGCACCTGCTAATG
          .....

          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
KT957514    GTGGATAAACAGTTCAACCTGTTCCCTGCCCTCTTTCTACTATACTACTAGATAAAAGTA
          .....

          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
KT957514    ATGTAAAAGAAGGTGGTAATAATCAAAATCTTATATTATTTAATCGTGGGAACGCTATAT
          .....

          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
KT957514    CTGGAGCTCCTAGTATTAGAGGTACAAGTCAATTACCAAACCTCCAATTATAATAGGTA
          .....

          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
KT957514    TAACTATAAAAAAATTATTACAAAAGCATGTGCAGTAACAATTACATTATAAATTTGAT
          .....

          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
KT957514    CATCTCCAATTAAAGATCCGGGTTGACCTAATTCAATTCGAATTARAACACTTAGAGCTG
          .....g.....
```

Lake Site Xi Xi National Park *Odonata* Species 9 COI sequence

```

          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
KU566470  ...G.....g..g..a..t..t.a...a.....a.....aa.....a..t.

          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
KU566470  .....c.....a...c.....GTt.CATAC.Ag.TGaTt..A

          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
KU566470  ATATTAAATTRYTGTAAGTAATAAAATTAATWGCTCCGAGRATTGAWGATACWCCTGCIYARR
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
KU566470  TGTAARGARAARATAGNTAAGNTCWACWGAYSTCCWGCRTGAGCRATWGCTCCWGCWAR
          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
KU566470  .A.GAT.A.C.GTTCATCCTG.TCCTGCT.CT..T.CAACTA..CTTC.AGCTAG.AGTA

          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
KU566470  TAAWRTKAAWGAAGGAGGTAAWARTCAAATCTTATRTTATTTAWTCGTGGRATGCIYAT
          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
KU566470  C.GGT.CT.CTAGTA.TAATGGAATAATCAATT.CCGAATCtT.CAATTA..AC.GGTA

          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
KU566470  TATWACTATAAAAAAATTATTACAAARGCRTGGGCAGTWACAATAACRTTATAGATTG
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
KU566470  RTCATCTCCAATWARAGATCCWGGYTGTCTAGTTCAATTCGAATTAAACTCTTARWGC
          550         560         570         580
Consensus  -----|-----|-----|-----|-----|
KU566470  TGTTCCAAYTATACCTGCTCASGCYCCAAAAATTAAGTATAAAGTA
          590
Consensus  .TCCAATTA..CCTGCT.AGGcC.cAA...TTAAGTA..A.GTA--

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Lake Site Xi Xi National Park Orthoptera Species 1 COI sequence

```

          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
EU263919   TTAATAGTATTGTAATTGCTCCTGCTAATACAGGTAATGATAGTAGTAATAATAATGCAG
          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
EU263919   TAATTGCTACTGATCAAACAAATAAAGGTGTTTGATCTAGTGATATATTTTTGGACCGTA
          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
EU263919   TATTGATTCTAGTTGTAATGAAGTTTACTGCCCTAAAATWGAAGATACACCTGCTAAAT
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
EU263919   GGAGTGAAAAAATTGCAAGATCTACTGATGATCCTCTATGCGCAATAGTTCTTGCTAATG
          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
EU263919   GTGGATAAACTGTTTCATCCTGTWCCTACTCCCGTWTTCACTAACGATGATCTAATTAATA
          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
EU263919   GGGTTAGTGAAGGTGGTAAWARTCAGAATCTTATATTATTTATTCGRGGAAARGCTATAT
          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
EU263919   CTGGWGCYCCRATTATWARWGGTACTAATCAATTTCCAAATCCTCCAATTATAATTGGTA
          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
EU263919   TWACTATAAAGAAAATTATRATRAATGCSTGKGMTGTAAWGATTACATTWTWAATTTGWT
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
EU263919   CATCWYYAATTAWKKTCYKGGTTGACCYAWTTTCWGCTCGGATWATTATTCTYATWGAWG
          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
EU263919   TTCCTAYTATTCCTGMTCAYGCTCCAAAYAWRARRTAYAAGWGTGCCAATATCYTTATGRT
          .....c.....c...c.....t.ta.gg..c..t..t.....c.....g.
```


Lake Site Xi Xi National Park Slug Species 1 COI sequence

```

          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  CAAAAAATGATGTGTGTTAAAATTACGGTCTGTTAATAACATAGTAATAGCCCCTGCTAGAA
          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  CTGGTAATGATAATAGCAATAAAAAATACAGTAATWAAGATAGATCAAACAAATAAGCTAA
          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  CTCGCTCTCATGAAATAATTGGTGAACGTATATTAATAAATGGTTGAAATAAAATTGATTG
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  CCCCTAAAATAGAAGAAATTCCTGCTAAATGTAAAGAAAAAATAGCTAGATCTACAGAAG
          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  CATTATTATGCCCTAATCTCCCTCTTAAAGGTGGGTAAACTGTCCACCCAGTTCCTGCAC
          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  CACCTTCTACTATACTACTACAAATTAATAAAGTTAATGATGGTGGTAAAAGTCAGAATC
          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  TTATATTGTTTATTTCGTGGGAAGCTTATGTCTAGGTGCTCCGATTAATAACGGAACCTATTC
          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  AATTACCAAATCCACCAATTATAAGGGGTATAACTATAAAAAAATTATAATAAAAGCAT
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  GTGCTGTTACAATTACATTAATAAATGATCATCAGTAAGAGAACCTGTTGTCCCTAACT
          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  CTAATCGAATTAACAATGAAAGAGCGGTTCCAATTAAACCTCTTCAAATCCCAAAAATTA

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Lake Site Xi Xi National Park Fish Species 1 COI sequence

```

          10          20          30          40          50          60
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB379922    .....A.....

          70          80          90          100         110         120
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB379922    ATCACTTCTAGGTGATGACCAAATTTACAATGTAATTGTTACGCCCACGCCTTCGTAAT
          .....

          130         140         150         160         170         180
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB379922    AATTTTCTTTATAGTAATGCCTATCCTCATTGGAGGATTTCGAAACTGACTTGTACCCCT
          .....

          190         200         210         220         230         240
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB379922    GATAATYGGAGCCCCAGACATGGCATTCCCACGAATAAATAATATAAGCTTCTGACTTCT
          .....c.....

          250         260         270         280         290         300
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB379922    TCCCCCATCATTCTGTTACTACTAGCTTCTCTGGTGTTGAAGCCGGAGCTGGCACCGG
          .....

          310         320         330         340         350         360
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB379922    ATGGACAGTATACCCCCCTCTTGCAGGGAACCTGGCCCACGCAGGAGCATCAGTAGACCT
          .....

          370         380         390         400         410         420
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB379922    AACCAATTTTCTCACTACATTTAGCAGGTGTTTCATCAATCCTGGGGGCAATCAACTTCAT
          .....

          430         440         450         460         470         480
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB379922    TACTACAACCATTAACATAAAACCTCCAGCCATTTCCAATACCAAACACCCCTATTTGT
          .....

          490         500         510         520         530         540
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB379922    TTGATCCGTACTTGTAACCGCYGTCCTCCTTCTCCTATCACTACCTGTTCTAGCTGCCGG
          .....c.....

          550         560         570         580         590         600
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB379922    TATTACAATGCTTTTAACAGATCGAAATCTTAACACCACATTCTTTGATCCCGCAGGCGG
          .....
```

Lake Site Xi Xi National Park Fish Species 2 COI sequence

```

          10          20          30          40          50          60
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AP012986    AGTTGGAACCGCCCTAAGCCTCCTTATTCGAGCTGAGCTAAGCCAGCCCGGCTCGCTCCT
          70          80          90          100         110         120
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AP012986    AGGAGATGATCAAATCTACAATGTAATTGTTACTGCCCATGCCTTCGTAATAATTTTCTT
          130         140         150         160         170         180
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AP012986    TATAGTTATGCCCATCCTCATCGGCGGATTTGGAAACTGACTTGTTCTCTTATAATTGG
          190         200         210         220         230         240
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AP012986    GGCCCCCGATATGGCCTTCCCACGAATRAACAACATGAGCTTCTGACTCCTTCCCCCATC
          250         260         270         280         290         300
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AP012986    CTTTCTACTTTTACTAGCCTCCTCTGGGGTAGAAGCCGGGGCCGGGACAGGCTGAACAGT
          310         320         330         340         350         360
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AP012986    TTACCCGCCTCTTGCGGGCAACTTAGCCACGCAGGAGCATCCGTAGATCTCACGATCTT
          370         380         390         400         410         420
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AP012986    TTCACTACACCTAGCAGGTGTATCCTCAATCCTAGGGGCAATTAACCTTTATTACGACAAT
          430         440         450         460         470         480
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AP012986    TATTAATATAAAACCCCCAGCCATCTCCAGTACCAAACACCTCTATTTGTTTGAGCTGT
          490         500         510         520         530         540
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AP012986    ACTCGTTACAGCCGTTCTTCTACTTCTATCTCTACCAGTCCTAGCCGCCGGGATTACAAT
          550         560         570         580         590         600
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AP012986    ACTACTTACAGATCGTAACCTTAAATACCACATTCTTTGACCCGGCAGGGGGAGGTGACCC
```

Lake Site Xi Xi National Park Larval Fish Species COI sequence

```

          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
AP004422  AACAACATAAGCTTTTGATTACTTCCCCCCTCATTNTNCTNSTCCTTGNANNWTCTNGG
          .....C.C..Cc.....C.TCt...G..

          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
AP004422  GTYGAAGCAGGGGNNNGGAACANGCTGAACTGTCTACCCCCCTCTCRCAGGTAACCTASCC
          ..t.....CA.....G.....g.....g..

          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
AP004422  CATGCCGGASCTTCTGTAGACTTAACCATCTTTTCCCTTCNCCTANCGNNNTCTCCTCN
          .....c.....A....G...GCA.....T
Continued

          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
AP004422  ATTCTGGGAGCTATTAATTTTATTANCACCATTATTAATATAAAACCTCCCGCAGCCTNC
          .....C.....C..

          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
AP004422  CAGTACCAAACACCATTGTTTGTGTGANNAGNCCTAATTACAGCTGTCCTCCNTCTKCTT
          .....GC..T.....T...t...

          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
AP004422  TCCCTKCCAGTTCTTGCNGNAGGCRTTACAATACTTCWWACAGATCGAAACCTANMCWCC
          .....t.....C.C....a.....tt.....Aa.a..

          370         380         390         400
Consensus  -----|-----|-----|-----|
AP004422  WCYTTCYTTGATCCGGCGGGGGCGGNAGACCCANATCCTCTNATCA
          a.t...t.....AGAC..A.TCCT..A.C.---
```

Creek Site Xi Xi National Park Arachnid Species 1 COI sequence

```

          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
JN817157    AGCAGTGATTAATACAGATCATACAAACAAAGGGATTTTTCTATAGTTACCCCATAAAA
          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
JN817157    TCGTATATTAATAATAGTCGAGATAAAATTAATTGCGCCTATAATAGAAGAGGCACCCGC
          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
JN817157    TAAATGAAGAGAAAAAATAGCAAAATCGACGGATCTCCAGCATGTCCTTCTAATCCAGC
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
JN817157    CAAAGGAGGGTAAATAGTTCACCCTGCACCTACCCCTATTTCTACTATAGAAGAAACAAT
          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
JN817157    TAAAAGAAATAATGAAGGAGGTAATAATCAAAAACCTCAAATTATTTATTCGTGGAAACGC
          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
JN817157    CATATCTGGAGCCCCTAATATTAGAGGCACTAACCAATTCCCAAACCTCCAATTAAAAT
          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
JN817157    TGGTATAACTATAAAAAAAATTATAACAAAAGCATGAGCTGTAACAATTACATTATATAA
          430         440
Consensus  -----|-----|-----|
JN817157    TTGATCATCTCCTATAAATCTCCCAGGT
```

Creek Site Xi Xi National Park Arachnid Species 2 COI sequence

```

              10      20      30      40      50      60
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB374052  AAATTTTCGATCTGTTTRATNATRTAGNAANMGCACCTGNNAATACNGGTAAAGACAATANT
          .....a..A..a...T..Ta.....CT.....A.....A.

              70      80      90      100     110     120
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB374052  AATAAAATAGCAGTAATAANAACNGATCAAACAAATAAAGGAACCTTCTCTATAGTTATT
          .....A...A.....

              130     140     150     160     170     180
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB374052  CCCACTAAACGTATRTTAATAATAGTAGAAATAAAATTTACTGCTCCTATAATAGAAGAA
          .....g.....

              190     200     210     220     230     240
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB374052  GCCCCAGCTAAATGTAAAGAAAAAATAGCAAATCTATAGATCTTCCTATATGACCAACT
          .....

              250     260     270     280     290     300
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB374052  CTAGAAGCTAAAGGAGGATAAACAGTTCATCCTGCACCCACTCCTATTTCAACCATAGAT
          .....

              310     320     330     340     350     360
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB374052  GATATAAATAATAAAAATAANGAAGGAGGNAACAATCAAAAAGACAAATTATTTATTCGA
          .....A.....T.....

              370     380     390     400     410     420
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB374052  GGAAATGATATRTCAGGAGCACCTAATATTAAAGGAACCTAATCAATTACCAAAACCACCA
          .....g.....

              430     440     450     460     470     480
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB374052  ATTAAAATTGGTATTACTATAAAAAAATCATAACARAAGCATGAGCAGTAACTATAACA
          .....a.....

              490     500     510     520     530     540
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AB374052  TTATATAAGTGATCATCACCTAAAAGACTTCCAGGATTACCTAATTCTATTTCGAATTAAT
          .....

              550
Consensus  ----:----|
AB374052  ACTCTTATAGC
          .....
```

Creek Site Xi Xi National Park Astacidae Species 1 COI sequence

```
          10          20          30          40          50          60
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AY701195   AAGTATTTAGATTACGATCTGTTAATAATATAGTAATAGCTCCTGCCAACACAGGTAAAG
          .....
```

```
          70          80          90          100         110         120
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AY701195   ATAATAATAATAAAACAGTAGTAATAAAACACTGATCAAACAAATAACGGYATTTCGATCCA
          .....t.....
```

```
          130         140         150         160         170         180
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AY701195   TGGTTATCCCTACTGTTTCGTATATTAATAGCAGTTGTTATAAAATTTACTGAACCTAAAA
          .....
```

Continued

```
          190         200         210         220         230         240
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AY701195   TAGAAGATACACCTGCTAAATGTAGAGAAAAAATACCTAAATCTACAGATGCTCCCGCAT
          .....
```

```
          250         260         270         280         290         300
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AY701195   GAGCAATAGCAGAAGCTAAAGGAGGATAAACAGTCCAYCCTGTTCCAACCTCTCTCAA
          .....t.....
```

```
          310         320         330         340         350         360
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AY701195   CTATACCCCTAGTTAATAATAAAGTCAAAGAAAAGGAAGTAATCAAAACCTTATATTAT
          .....
```

```
          370         380         390         400         410         420
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AY701195   TTATTTCGAGGAAAAGCCATATCTGGAGCACCTAATATTAAAGGAATTAATCAATTTCCAA
          .....
```

```
          430         440         450         460         470         480
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AY701195   ACCCACCAATTATAATAGGTATTACTATAAAAAAATTATTACAAAAGCATGAGCTGTAA
          .....
```

```
          490         500         510         520         530         540
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AY701195   CTACCACATTATAGATCTGATCATCCCCAATTAATCTTCCTGGTTGACCTAACTCCACCC
          .....
```

```
          550         560         570         580         590         600
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
AY701195   GAATAATCATTCTTAATGAAGTTCCTACTATACCAGCTCAAGTACCAAAAACAAAATATA
          .....
```

Creek Site Xi Xi National Park Hemiptera Species 1 COI sequence

```

          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
GQ527080    TCAAAAAAAGAAGTATTTAAATTTGATCTGTYAATAATATAGTAATYGCACCAGCYARC
          .....t.....c.....c.g.

          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
GQ527080    ACYGGTAATGATAATAATAAAAGAAAAGCTGTAATTAACAGCTCAAACAAAYAATGGW
          ..t.....c.....a

          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
GQ527080    GTYCGATCAAGAAATATYCCAAYTGTTTCGTATATTAATAATTGTTCTAATAAAATTTACA
          ..t.....t....c.....

          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
GQ527080    GCTCCYAAAATTGATGAAGCWCAGCYAAATGTAAAGAAAAAATTGTTAAATCAACACAA
          .....c.....a....c.....

          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
GQ527080    GCACCAGAATGWGATATAATTCTAGATAAAGGAGGATATACTGTTCAACCAGTACCTGCA
          .....a.....

          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
GQ527080    CCTCTATCCACTATTCTMCCAAYTAATARTAAARTTAARGAAGGAGGAAGYAAYCAAAAA
          .....a....t....g....a....a.....c..t.....

          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
GQ527080    CTTATATTATTYAATCGAGGRAAMGCTATATCYGGAGCTCCAATTATYAATGGWACAAGT
          .....t.....a..c.....t.....c.....a.....

          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
GQ527080    CAATTTCCAAWCCACCAATTATAATTGGYATAACTATAAAAAAATTATAATAAAYGCA
          .....a.....t.....t.....

          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
GQ527080    TGRGCAGTYACAATAACRTTATAAATYTGATCATTTCCAATAAAAGAACCAGGAGTWCCW
          ..g.....t.....g.....c.....a..a

          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
GQ527080    ARTTCAAYACGAATYAATATTCTTAARGAAGTTCCAATTATTCCAGATCAAATRCCAAAA
          .g.....c.....t.....a.....g.....
```


Creek Site Xi Xi National Park Lepidoptera Larvae Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
KX862509    AGAAGTATTTAAATTACGGTCAGTTAAAAGTATAGTAATTGCTCCAGCTAAACAGGTAG
          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
KX862509    AGATAATAATAAAAGGAAAGCTGTAATACCTACAGCTCAAATAAATAAAGGTATCTGATC
          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
KX862509    AAAAGATAAATTATTTAATCGTATATTAATAATTGTTGTAATGAAATTAATTGCTCCTAA
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
KX862509    AATTGATGAAATTCCAGCTAAATGAAGGGAGAAAATAGCTAAATCTACTGAACTACCTCC
          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
KX862509    ATGGGCAATATTAGATGAAAGTGGGGGATAAACTGTTTCATCCGGTACCTGCTCCATTTTC
          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
KX862509    TACAATTCTTCTAGAAATTAATAAAGTTAATGATGGGGGAAGAAGTCAAAAATTATATT
          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
KX862509    ATTTATTTCGAGGAAAAGCTATATCAGGAGCTCCTAATATAAGAGGTACTAATCAATTACC
          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
KX862509    AAATCCTCCAATTATAATAGGTATTACTATAAAAAAATTATGATAAATGCATGTGCTGT
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
KX862509    TACAATAGTATTATAAATTTGATCATCACCAATTAAAGATCCGGGGGTACCTAATTCTGC
          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
KX862509    TCGAATTAATAATCTTAAAGATGTTCCAACCTATTCCAGCTCAAATACCAAAAATAAAATA
```

[illegible]

Creek Site Xi Xi National Park Slug Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  CCTNCCAGCAGGGTCAAAAAATGATGTGTTAAAAATTACGGTCTGTTAATAACATAGTAAT
          ...C.AGCAG..TCA.....TGATGTGT.A...T.ACG.TCTGT.A.TA.CATAGTA.TA

          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  AGCCCCCTGCTAGAACTGGTAATGATAATAGCAATAAAAAATACAGTAATWAAGATAGATCA
          GC...TGCTAGA.CTG.TA.TGATA.TAGCA.TA...TACAGTA.TAa.GATAGATCA.

          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  AACAAATAAGCTAACTCGCTCTCATGAAATAATTGGTGAACGTATATTA AAAAATGGTTGA
          .CA..TA.GCTA.CTCGCTCTCATGA..TA.T.G.TGA.CGTATAT.A...TG.T.GA.

          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  AATAAAATTGATTGCCCTAAAATAGAAGAAATTCCTGCTAAATGTAAAGAAAAAATAGC
          .TA...T.GAT.GC...TA...TAGA.GA..T.C.TGCTA..TGTA..GA....TAGCT

          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  TAGATCTACAGAAGCATTATTATGCCCTAATCTCCCTCTTAAAGGTGGGTAAACTGTCCA
          AGATCTACAGA.GCAT.AT.ATGC..TA.TCTC..TCT.A..G.TG..TA..CTGTC.AC

          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  CCCAGTTCTGTCACACCTTCTACTATWCTACTACAAATTAATAAAGTTAATGATGGTGG
          ..AGT.C.TGCAC.AC.T.CTACTATACTACTACA..T.A.TA..GT.A.TGATG.TG.T

          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  TAAAAGTCAGAATCTTATATTGTTTATTCGTGGGAAGCTTATGTCAGGTGCTCCGATTAA
          A...GTCAGA.TCT.ATAT.GT..AT.CGTG..A.GCT.ATGTCAG.TGCTC.GAT.A.T

          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  TAACGGAAGTATTCAATTACCAAATCCACCAATTATAAGGGGTATAACTATAAAAAAAT
          A.CG.A.CTAT.CA.T.AC.A..TC.AC.A.T.ATA.G...TATA.CTATA.....T.

          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  TATAATAAAAGCATGTGCTGTTACAATTACATTA AAAAATGATCATCAGTAAGAGAACC
          ATA.TA...GCATGTGCTGT.ACA.T.ACAT.A.....TGATCATCAGTA.GAGA.C.T

          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
MG722906  TGTGTGTCCTAACTCTAATCGAATTAACAATGAAAGAGCGGTTCCAATTAAACCTCTTCA
          GT.GTC..TA.CTCTA.TCGA.T.A.CA.TGA..GAGCG.T.C.A.T.A..C.TCT.CA.
```

Creek Site Xi Xi National Park Shrimp Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
LC324767    TGACGTGTTTAGGTTTCGATCTGTAAGAAGTATAGTAATAGCTCCTGCTAAAACTGGAAG
          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
LC324767    GGAAAGAAGTAGAAGAACCGCGGTTAAGAAAAGTATGATCAAACGAATAGAGGTATTTCGATC
          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
LC324767    TCTTAGTATCCCCGTCGTGCGCATATTAATTACTGTAGATATAAAATTAGCGGCWCCTAG
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
LC324767    AATTGAAGAAATACCGGCTARATGTAGGGAGAAAATTCCCATATCTACTGAGGCCCTGC
          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
LC324767    GTGGGCAATTCTCTTGCTAATGGGGGTAAACGGTTCAGCCAGTGCCGACTCTCTCTC
          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
LC324767    TACCATTCTCTGGAAAGTAGTAATGTTAAAGCCGGGGTAAAAGTCAAACCTTATATT
          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
LC324767    GTTCATTCTGTGGGAACGCTATATCTGGGGCACCTAGTATTAAAGGTACTAATCAATTCCC
          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
LC324767    AAATCCTCCAATTATAATAGGCATAACTATAAAAAAATTATTACAAAGGCGTGAGCAGT
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
LC324767    AACAATTACATTATAAATTTGGTCATTTCCAATTAATCTACCTGGTTGCCCAATTCTGC
          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
LC324767    TCGGATTAAAAGTCTTAGAGCAGTACCTACTATTCCAGCTCAGGCTCCTAATATAAAATA
```

Creek Site Xi Xi National Park Larval Fish Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
KF305680  TTTTCTCTTTCACCTGGCAGGAGTTTCTTCCATCCTTGGCGCCATTAACTTCATCACCAC
          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
KF305680  AATTATTAATATAAAGCCCCCGCCATCTCCCAATACCAAACACCATTATTTATCTGGGC
          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
KF305680  TCTTTTAATCACAGCAGTCCTCCTCCTCCTATCCCTYCCCGTGCTTGCCGCCGGCATTAC
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
KF305680  AATACTCCTAACAGACCGAACTTAAATACCACATTTTTTGACCCCGCGGGAGGAGGAGA
          250         260
Consensus  -----|-----|-----
KF305680  CCCCATTTCTTTACCAACACCTCTT

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Creek Site Xi Xi National Park Larval Fish Species 2 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
AP004422  CCCCACATGGCCTTTCCACGAATAAACACATAAGCTTTTGATTACTTCCCCCCTCATT
          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
AP004422  TCTCCTCCTCCTTGTCATCTTCTGGGGTTGAAGCAGGGGCAGGAACAGGCTGAACTGTCTA
          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
AP004422  CCCCCCTCTCGCAGGTAACCTAGCCCATGCCGGACCTTCTGTAGACTTAACCATCTTTTC
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
AP004422  CCTTCACCTAGCGGGCATCTCCTCTATTCTGGGAGCTATTAATTTTATTACCACCATTAT
          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
AP004422  TAATATAAAACCTCCCGCAGCCTCCAGTACCAAACACCATTGTTTGTGTGAGCAGTCCT
          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
AP004422  AATTACAGCTGTCCTCCTTCTTCTTTCCCTTCCAGTTCTTGCCGCAGGCATTACAATACT
          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
AP004422  TCTTACAGATCGAAACCTAAACACCACTTTCTTTGATCCGGCGGGGGGCGGAGACCCAAT
          430         440         450
Consensus  -----|-----|-----|
AP004422  CCTCTATCAACACCTGTTCTGRTTYTTTCGG
          .....g..t.....
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Kawainui Marsh Astacidae Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
JN000903  AAGTATTTAGATTACGATCTGTTAATAATATAGTAATAGCTCCTGCCAACACAGGTAAAG
          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
JN000903  ATAATAATAATAAAACAGTAGTAATAAAACACTGATCAAACAAATAACGGCATTTCGATCCA
          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
JN000903  TGGTTATCCCTACTGTTTCGTATATTAATAGCAGTTGTTATAAAATTTACTGAACCTAAAA
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
JN000903  TAGAAGATACACCTGCTAAATGTAGAGAAAAAATACCTAAATCTACAGATGCTCCCGCAT
          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
JN000903  GAGCAATAGCAGAAGCTAAAGGAGGATAAACAGTCCACCCTGTTCCAACCTCTCTCTCAA
          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
JN000903  CTATACCCCTAGTTAATAATAAAGTCAAAGAAAAAGGAAGTAATCAAACCTTATATTAT
          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
JN000903  TTATTTCGAGGAAAAGCCATATCTGGAGCACCTAATATTAAAGGAATTAATCAATTTCCAA
          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
JN000903  ACCCACCAATTATAATAGGTATTACTATAAAAAAATTATTACAAAAGCATGAGCTGTAA
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
JN000903  CTACCACATTATAGATCTGATCATCCCCAATTAATCTTCCTGGTTGACCTAACTCCACCC
          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
JN000903  GAATAATCATTCTTAATGAAGTTCCTACTATACCAGCTCAAGTACCAAAAACAAAATATA
```

Kawainui Marsh Diptera Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MG167579   AAAATWGGATCTCCTCCTCCWGCTGGGTCAAARAARGAAGTATTTAAATTTTCGRTCTGTT
          70          80          90          100         110         120
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MG167579   AATAATATAGTAATWGCTCCAGCTAAACTGGTAAAGATAAWARAAGTAATAAWGCTGTA
          130         140         150         160         170         180
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MG167579   ATWGCWACTGATCAWACAAATARAGGTATTCGATCAAATGTAATTCCTSTAGAWCGTATA
          190         200         210         220         230         240
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MG167579   TTAATWACAGTWGTAATAAAATTWACTGCTCCTAAAATAGAAGARATTCMGCTAAATGT
          250         260         270         280         290         300
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MG167579   AAAGAAAAAATAGCTAAATCWACWGAAGMTCTCCATGAGCAATAATAGAAGATAAAGGA
          310         320         330         340         350         360
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MG167579   GGGTAAACTGTTTCATCCTGTTCCAGCTCCAYTTTCYACTATACTACTTTRTYAATAAAAGT
          370         380         390         400         410         420
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MG167579   RTTAAWGCAGGTGGAAGRAGTCAAAACTTATATTATTTATTCGWGGRAAAGCTATATCT
          430         440         450         460         470         480
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MG167579   GGKGCTCCTAATATTAAAGGRACTAATCAATTTCAAATCCWCCAATTATAATTGGTATT
          490         500         510         520         530         540
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MG167579   ACTATAAAAAAATTATAATRAATGCATGAGCWGTTACAATTACATTATAAATTTGATCA
          550         560         570         580         590         600
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MG167579   TTTCCAATTAAWGAACCAGGATGWCCTAATTCAATTCGAATTARTATACTTAAAGAAGTT
```


	10	20	30	40	50	60
Consensus	----- ----- ----- ----- ----- -----					
MH550566	AAAATTGGATCTCCTCCTCTCGCNGGATCRAAAAAKGAWGTATTTAAATTTTCGATCWGTT					
A.....t..a.....t...					
	70	80	90	100	110	120
Consensus	----:---- ----:---- ----:---- ----:---- ----:---- ----:----					
MH550566	AAWARTATAGTAATAGCTCCWGCTAAAACWGGTARRGATAAWARAAGTAATARAGCAGTA					
	..t.a.....a.....t...aa.....t.a.....a.....					
	130	140	150	160	170	180
Consensus	----:---- ----:---- ----:---- ----:---- ----:---- ----:----					
MH550566	ATWRCTACWGATCATACAAATAAAGGTATTCGATCTAAAGAAATTCRGAWGCTCGTATR					
	..ta....a.....a.....a..t.....a					
	190	200	210	220	230	240
Consensus	----:---- ----:---- ----:---- ----:---- ----:---- ----:----					
MH550566	TTAATTACGWGTGTAATAAAATTWACTGCACCTAAAATTGAAGAAATTCRGCTAAATGT					
t..t.....t.....g.....					
	250	260	270	280	290	300
Consensus	----:---- ----:---- ----:---- ----:---- ----:---- ----:----					
MH550566	AAWSWAAAAATAGCTAAATCTACAGAAGCTCCTCCATGAGCRATTMCKGMWGAAAGYGGK					
	..tga.....a...c.g.ca....c..t					
	310	320	330	340	350	360
Consensus	----:---- ----:---- ----:---- ----:---- ----:---- ----:----					
MH550566	GGATAMACAGTTTCATCCWGTMCAGCTCCGTTTTCTWACTATTCTACTKACWAGTARTARA					
a.....t..a.....a.....t..t....a..a.					
	370	380	390	400	410	420
Consensus	----:---- ----:---- ----:---- ----:---- ----:---- ----:----					
MH550566	GWTARAGMAGGAGGAAGAAGTCAAAAACTTATATTATTCATTTCGWGGAANGCTATATCM					
	.t..a..c.....t.....a.....c					
	430	440	450	460	470	480
Consensus	----:---- ----:---- ----:---- ----:---- ----:---- ----:----					
MH550566	GGWGCWCCYAAAYATYAAAGGAACCTAAYCAATTTCCAAATCCWCCAATTATAATTGGYATM					
	..t..a..c..t..t.....t.....t.....t..c					
	490	500	510	520	530	540
Consensus	----:---- ----:---- ----:---- ----:---- ----:---- ----:----					
MH550566	ACTATRAAAAAAATTATWAYAAATGCATGAGCAGTTACAATTACATTRTAAATTTGATCA					
a.....a.t.....g.....					
	550	560	570	580	590	600
Consensus	----:---- ----:---- ----:---- ----:---- ----:---- ----:----					
MH550566	TCACCAATTAAWGCWCCWGGATGACCTAATTCAGCTCGAATYAAAATTCTTAAMGAAGTW					
a..t..a.....t.....a.....t					

Kawainui Marsh Hemiptera Species 2 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
MF936456   GTCGGTTAATAGTATGGTAATTGCTCCTGCTAATACGGGTAGTGACAATAATAATAGTAA
          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
MF936456   TGCTGTAATACCTACTGATCATACAAAGAGGGGTACTTGATCTATAGATATACCATATGG
          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
MF936456   GCGTATATTAATAATGGTTGARATAAAGTTAATTGCTCCTAGGATGGAGGATACCCCTGC
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
MF936456   CAAATGAAGGGAGAAAATTGCCAGGTCAACAGATCCTCCTCTGTGGAATAGGTTATTAGA
          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
MF936456   CAAAGGAGGGTAGACGGTCCATCCTGTACCGGCTCCTATTTCTACTATTCTTCTTGTAAT
          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
MF936456   TAATAAAGTTAGAGAGGGGGGAAGTAGTCAGAATCTTATATTATTTATTCGTGGAAATGC
          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
MF936456   TATATCTGGGGCCCCGATCATTAAAGGGACTAATCAATTTCCAAATCCTCCAATTATAAT
          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
MF936456   AGGTATTACTATAAAGAAAATTATGATAAATGCATGTGCTGTTACAATCGTATTATAAAT
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
MF936456   TTGATCATCCCCAATGAATGTRCCTGGTTGTCCTAATTCAACTCGAATGATTCATCTTAA
          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
MF936456   .....g.....N.....N.....
          610         620         630         640         650         660
Consensus  -----|-----|-----|-----|-----|-----|
MF936456   TGATGATCC
          670         680         690         700         710         720
Consensus  -----|-----|-----|-----|-----|-----|
MF936456   .....
```

Kawainui Marsh Lepidoptera Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
HQ953206    GATGTATTTAAATTTTCGGTCAGTTAAAAGTATAGTAATAGCTCCTGCTAAAACTGGTAAT
          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
HQ953206    GAAAGAAGTAATAATAGAGCTGTAATTCCTACAGCTCATACAAATAAAGGTATTTGATCG
          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
HQ953206    AAATTTATACCATTAACTCGTATATTAATAATTGTTGTAATAAAATTAATAGCTCCTAGA
          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
HQ953206    ATAGATGAAATTCCAGCTAAATGTAATGAAAAATAGCTAAATCAACTGATCTTCCTCCA
          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
HQ953206    TGAGCAATATTGGAAGACAGAGGGGGGTATACTGTTTCATCCTGTTCTGCTCCATTTTCT
          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
HQ953206    ACAATTCTTCTAGAAATTAATAATGTTAAAGAAGGTGGAAGTAATCAAATCTTATATTA
          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
HQ953206    TTTATTTCGGGGGAAAGCTATATCAGGGGCTCCAAGTATTAAAGGAACTAATCAATTTCCA
          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
HQ953206    AATCCACCAATTATAATCGGTATAACTATAAAAAAATTATAATAAATGCATGGGCTGTT
          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
HQ953206    ACAATAGTATTATAAATTTGGTCATCTCCAATTAACGATCCTGGATTACCTAATTCAGCT
          550         560         570         580         590         600
Consensus  -----|-----|-----|-----|-----|-----|
HQ953206    CGAATTAATAAACTTAAAGAAGTTCCTACTATTCTGCTCAAATTCCAAAAATAAAATAT
```

Kawainui Marsh *Odonata* Species 2 and 3 COI sequence

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          10          20          30          40          50          60
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MH450004  CCTCCTCCTGCAGGATCAAAAAATGATGTATTAATATTACGATCTGTTAATAATATAGTA
          70          80          90          100         110         120
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MH450004  ATAGCACCAGCTAATACTGGTAAGGATAATAAAAGTAGTACTGCAGTAATAACCACAGCT
          130         140         150         160         170         180
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MH450004  CAGACAAATAGAGGTAAGTATCCATGTTTATCCCGGTGATTTTATATTAATTGTGGTG
          190         200         210         220         230         240
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MH450004  GTAATAAAATTAATTGCCCCTAAGATTGAGGATACCCCGCCAAGTGAATGAAAAAATT
          250         260         270         280         290         300
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MH450004  GTTAAATCAACGGATGCTCCAGCATGTGCAATTACTCCTGCTAATGGAGGATATACTGTT
          310         320         330         340         350         360
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MH450004  CATCCAGTTCCTGCCCCTCTTTCTACTAGTCTTCTTGCTAGAAGAAGAGTTAATGATGGA
          370         380         390         400         410         420
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MH450004  GGTAAGTCAAAATCTTATGTTGTTTAATCGAGGGAAAGCTATATCTGGTGCTCCTAGT
          430         440         450         460         470         480
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MH450004  ATTAATGGTACCAATCAATTTCCAAATCCACCAATTATGATTGGTATTACTATAAAAAAA
          490         500         510         520         530         540
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MH450004  ATCATGACAAAGGCGTGTGCAGTTACTACTACATTATAAATTTGGTCATCTCCAATTAGA
          550         560         570         580         590         600
Consensus  ----:----|----:----|----:----|----:----|----:----|----:----|
MH450004  GATCCAGGCTGTCCTAGTTCAACTCGAATTAATATTCTTAAAGCAGTCCCTACTATTCCC
```

Kawainui Marsh Orthoptera Species 1 COI sequence

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          10          20          30          40          50          60
Consensus  -----|-----|-----|-----|-----|-----|
MH992038    TAATAATATTGTAATTGCACCTGCTAAYACGGGTAATGAAAATAATAATAAARGCAGT
          .....c.....a.....

          70          80          90          100         110         120
Consensus  -----|-----|-----|-----|-----|-----|
MH992038    AATTCCTACTGCTCATACAAATAAGGGTGTTTGATCTAAAGATATTCCTGGGGTTCGTAT
          .....

          130         140         150         160         170         180
Consensus  -----|-----|-----|-----|-----|-----|
MH992038    ATTAATTATTGTAGTAATAAAGTTTACGGCTCCTAAAATTGATGAAATTCCTGCAAGATG
          .....

          190         200         210         220         230         240
Consensus  -----|-----|-----|-----|-----|-----|
MH992038    GAGTGAAAAAATTGCTAAATCTACTGATGCTCCAGCATGTGCAATTCCTGTAGATAAAGG
          .....

          250         260         270         280         290         300
Consensus  -----|-----|-----|-----|-----|-----|
MH992038    TGGGTAGACTGTTTCATCCAGTACCTGCTCCATTTTCGACTATTCTTCTGGTTAGTAGGAG
          .....

          310         320         330         340         350         360
Consensus  -----|-----|-----|-----|-----|-----|
MH992038    AATTAATGATGGTGGTAATAATCAAAAACCTTATGTTATTTATTCGTGGAAATGCTATATC
          .....

          370         380         390         400         410         420
Consensus  -----|-----|-----|-----|-----|-----|
MH992038    AGGAGCTCCTAATATTAAAGGTACAAGTCAATTTCCAAATCCTCCAATTATAATTGGCAT
          .....

          430         440         450         460         470         480
Consensus  -----|-----|-----|-----|-----|-----|
MH992038    AACTATAAAAAAATCATAATAAATGCGTGTGCAGTTACAATTACATTATAGGTTTGATC
          .....

          490         500         510         520         530         540
Consensus  -----|-----|-----|-----|-----|-----|
MH992038    ATCTCCAATTAAATATCCTGGTTGTCCAAGTTCAGTTCGAATTAANATTCTTAAAGATGT
          .....G.....

          550         560         570         580
Consensus  -----|-----|-----|-----|
MH992038    ACCTACTATACCAGCTCATGCTCCAAAAATGAAATATAAAGTT
          .....
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