

COI 2 groups

Group 1	Group 2	Dist	Std. Err
Nagano Clade	Osaka Clade	0.19450	0.01859
Nagano Clade	Outgroup	0.37969	0.03546
Osaka Clade	Outgroup	0.32660	0.02954

Table: Estimates of Evolutionary Divergence over Sequence Pairs between 2 groups Nagano group and Osaka group, for COI gene. The number of base substitutions per site from averaging overall sequence pairs between groups that contain *C. sowerbii* of Nagano and Osaka are shown. The Nagano group contains *C. sowerbii* from Nagano, Italy, Germany, Chile, Singapore, Greece, Czech Republic and one from unknown location. The Osaka group is made up of *C. sowerbii* from Osaka, Switzerland, Germany (from two different studies), Morocco, and China. The standard error estimates between the groups can be seen in the last column. Estimated mean divergence between Osaka and Nagano groups is 0.19450.

Nagano Clade	OK037605-037607 Nagano	MH230079	MZ508276	MF177101-177133	JN593332	OK037612	KP231217	MZ508275
Osaka Clade	MZ508274	MZ508273	MK600508-600509	KF510026	FJ423613-423620	MZ326744	MF000493	
Outgroup	OK037611 A.japonica	MH700550 O.phosphorica						

Supplementary Data Ia. Analyses were conducted using the Jukes-Cantor model [1]. The rate variation among sites was modeled with a gamma distribution (shape parameter = 1). This analysis involved 17 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 1566 positions in the final dataset. Evolutionary analyses were conducted in MEGA11 [2][3]”

[1]Jukes T.H. and Cantor C.R. (1969). Evolution of protein molecules. In Munro HN, editor, Mammalian Protein Metabolism, pp. 21-132, Academic Press, New York.

[2]Tamura K., Stecher G., and Kumar S. (2021). MEGA 11: Molecular Evolutionary Genetics Analysis Version 11. Molecular Biology and Evolution <https://doi.org/10.1093/molbev/msab120>.

[3]Stecher G., Tamura K., and Kumar S. (2020). Molecular Evolutionary Genetics Analysis (MEGA) for macOS. Molecular Biology and Evolution 37:1237-1239.

COI 3 groups

Group 1	Group 2	Dist	Std. Err
Nagano Clade	Osaka Clade	0.20025	0.02244
Nagano Clade	Others	0.19221	0.02036
Others	Osaka Clade	0.14995	0.01824
Nagano Clade	Outgroup	0.37969	0.03645
Osaka Clade	Outgroup	0.34157	0.03218
Others	Outgroup	0.32061	0.02993

Table: Estimates of Evolutionary Divergence over Sequence Pairs between 3 groups including Nagano group and Osaka group, for COI gene.

The number of base substitutions per site from averaging overall sequence pairs between groups that contain *C. sowerbii* of Nagano and Osaka are shown. The Nagano group contains *C. sowerbii* from Nagano, Italy, Germany, Chile, Singapore, Greece, Czech Republic and one from unknown location. The Osaka group is made up of *C. sowerbii* from Osaka and Switzerland. A third separate group containing Germany (from two different studies), Morocco, and China was compared as well. The standard error estimates between the groups can be seen in the last column. Estimated mean divergence between Osaka and Nagano groups is 0.20025.

Nagano Clade	OK037605-037607 Nagano	MH230079	MZ508276	MF177101-177133	JN593332	OK037612	KP231217	MZ508275
Osaka Clade	MZ326744 Osaka	MF000493						
Others	MZ508274	MZ508273	MK600508-600509	KF510026	FJ423613-423620			
Outgroup	OK037611 A.japonica	MH700550 O.phosphorica						

Supplementary Data Ib. Analyses were conducted using the Jukes-Cantor model [1]. The rate variation among sites was modeled with a gamma distribution (shape parameter = 1). This analysis involved 17 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 1566 positions in the final dataset. Evolutionary analyses were conducted in MEGA11 [2][3]

Group 1	Group 2	Dist	Std. Err
Nagano Clade	Osaka Clade	0.0587	0.0081
Outgroup	Nagano Clade	0.2653	0.0276
Outgroup	Osaka Clade	0.2520	0.0255
China	Nagano Clade	0.0926	0.0141
China	Osaka Clade	0.0870	0.0132
Outgroup	China	0.2875	0.0301

Table. Estimates of Evolutionary Divergence over Sequence Pairs between groups with *C. sowerbii* from Nagano and Osaka and outgroups, for 16S gene

The number of base substitutions per site from averaging over all sequence pairs between groups *C. sowerbii* of Nagano and Osaka are shown. The Nagano group contains *C. sowerbii* from Germany, Czech Republic, Singapore and from unknown locations. Standard error estimates are shown in the last column. The estimated mean divergence between Osaka and Nagano groups is 0.0587.

Nagano Clade	OK037602-037604 Nagano	EU293971	KX267739	LN901194	MZ508275	JN593332	OK037610 Singapore
Osaka Clade	MK600506	MZ508273	MZ508274	MZ326744			
China	AY512507 C.sinesis	EU293974 C.ziguiensis					
Outgroup	OK037609 A.japonica	OK037608 A.japonica	EU293975	LC508964 O.formosus			

Supplementary Data Ic. Analyses were conducted using the Jukes-Cantor model [1]. The rate variation among sites was modeled with a gamma distribution (shape parameter = 1). This analysis involved 20 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair (pairwise deletion option). There were a total of 1823 positions in the final dataset. Evolutionary analyses were conducted in MEGA11 [2][3]