

Table S5 Estimates of average K2P distances over sequence pairs within family Agalmatidae, based on mtCOI, 16S rRNA and 18S rRNA gene data.

Taxonomic group	mtCOI			16S rRNA			18S rRNA		
	N	Min–Max (Average)	Standard deviation	N	Min–Max (Average)	Standard deviation	N	Min–Max (Average)	Standard deviation
Intraspecies	35	0.000–0.022 (0.005)	0.006	16	0.000–0.480 (0.080)	0.152	11	0.000–0.005 (0.001)	0.002
Interspecies	36	0.098–0.212 (0.176)	0.025	19	0.059–0.510 (0.179)	0.100	13	0.001–0.008 (0.003)	0.002
Instragenus	36	0.098–0.172 (0.147)	0.019	14	0.059–0.149 (0.116)	0.019	10	0.001–0.002 (0.002)	0.001
<i>Halistemma</i>	9	0.098–0.131 (0.119)	0.014	10	0.108–0.149 (0.121)	0.013	6	0.002–0.002 (0.002)	0.000
<i>Agalma</i>	15	0.138–0.150 (0.144)	0.004	4	0.059–0.108 (0.088)	0.021	4	0.001–0.001 (0.001)	0.000
<i>Nanomia</i>	12	0.168–0.172 (0.169)	0.002	-	-	-	-	-	-
Intergenue	36	0.134–0.212 (0.183)	0.021	19	0.083–0.510 (0.198)	0.106	13	0.001–0.008 (0.004)	0.002