

Supplementary document S1. GenBank accession numbers for gene sequences and respective samples employed in our study. Cells in bold correspond to new sequences produced for our study. ND1 = 16S - tRNA^{LEU} - NADH dehydrogenase subunit 1 - tRNA^{LEU}.

Species	Voucher	Observations	12S – tRNA ^{VAL} – 16S	ND1	Cytochrome oxidase c I	Rhodopsin exon 1	Recombination activating gene 1	Tyrosinase	Seven in absentia homologue 1	Tensine 3	Country: State, Municipality, Locality
<i>Aplastodiscus albofrenatus</i>	CFBHt 5051		KU184021		KU184058	KU184111	KU184083	KU184246	KU184149		Brazil: Rio de Janeiro, Rio de Janeiro, Tijuca
<i>Aplastodiscus albosignatus</i>	MZUSPfield 1451		KU184037		KU184064	KU184117	KU184086	KU184252	KU184155	KU184198	Brazil: São Paulo, Santo André, Paranapiacaba
<i>Aplastodiscus arildae</i>	USNM 303022		AY843604		KU184042	AY844578	AY844392	AY844049	AY844803	KU184173	Brazil: São Paulo, Near Salesópolis, Estação Biológica de Boracéia
<i>Aplastodiscus cavicola</i>	FSFL 848		KU184023		KU184044	KU184095		KU184232	KU184134	KU184179	Brazil: Minas Gerais, Congonhas
<i>Aplastodiscus cavicola</i>	MNRJ 63689		KU184029			KU184121	KU184089	KU184255	KU184159	KU184201	Brazil: Rio de Janeiro, Duas Barras, Nascente de Rio
<i>Aplastodiscus cavicola</i>	UFMG 13126	topotype	MT683338	MT683351	MT671499	MT683358	MT683355	MT683369	MT683362	MT683365	Brazil: Espírito Santo, Santa Teresa
<i>Aplastodiscus cavicola</i>	UFMG 13127	topotype	MT683339	MT683352	MT671500	MT683359	MT683356		MT683363	MT683366	Brazil: Espírito Santo, Santa Teresa
<i>Aplastodiscus cavicola</i>	UFMG 13128	topotype	MT683340		MT671501						Brazil: Espírito Santo, Santa Teresa
<i>Aplastodiscus cochranae</i>	CFBH 3001		AY843568	KU184220	KU184043	AY844542	AY844365	AY844024	AY844770	KU184174	Brazil: Santa Catarina, Rancho Queimado
<i>Aplastodiscus ehrhardti</i>	CFBHt 11191		KU184017	KU184225	KU184050	KU184103		KU184239	KU184141	KU184186	Brazil: Paraná, São José dos Pinhais
<i>Aplastodiscus eugenioi</i>	MNRJ 63936		KU184030		KU184066	KU184119	KU184088	KU184254	KU184157	KU184200	Brazil: Rio de Janeiro, Angra dos Reis, Ilha Grande
<i>Aplastodiscus flumineus</i>	CFBH 30832		KU184013		KU184072	KU184127	KU184092	KU184260	KU184164	KU184207	Brazil: Rio de Janeiro, Teresópolis
<i>Aplastodiscus heterophonicus</i>	PCAG n/a		KU184038		KU184073	KU184128			KU184165	KU184208	Brazil: Minas Gerais, Santana do Riacho, Serra do Cipó
<i>Aplastodiscus heterophonicus</i>	UFMGt 1901		KU184039		KU184074	KU184131	KU184093	KU184262	KU184168	KU184211	Brazil: Minas Gerais, Santana do Riacho, Fazenda do Chiquito
<i>Aplastodiscus heterophonicus</i>	UFMG-G 2455a I	paratype (tadpole)	MT683341		MT671502						Brazil: Minas Gerais, Santana do Riacho, Serra do Intendente
<i>Aplastodiscus heterophonicus</i>	UFMG-G 2455a II	paratype (tadpole)	MT683345		MT671503						Brazil: Minas Gerais, Santana do Riacho, Serra do Intendente
<i>Aplastodiscus heterophonicus</i>	UFMG-G 2455a III	paratype (tadpole)	MT683342		MT671504						Brazil: Minas Gerais, Santana do Riacho, Serra do Intendente
<i>Aplastodiscus heterophonicus</i>	MZUSP 159199	paratype	MT683343		MT671505						Brazil: Minas Gerais, Santana do Riacho, Serra do Intendente
<i>Aplastodiscus heterophonicus</i>	MZUSP 159200	paratype	MT683346		MT671507						Brazil: Minas Gerais, Santana do Riacho, Serra do Intendente
<i>Aplastodiscus heterophonicus</i>	MZUSP 159201	paratype	MT683344								Brazil: Minas Gerais, Morro do Pilar
<i>Aplastodiscus heterophonicus</i>	MZUSP 159202	paratype	MT683348		MT671508						Brazil: Minas Gerais, Conceição do Mato Dentro
<i>Aplastodiscus heterophonicus</i>	MZUSP 159203	paratype	MT683349		MT671510						Brazil: Minas Gerais, Dom Joaquim, Fazenda Estiva
<i>Aplastodiscus heterophonicus</i>	MZUSP 159204	paratype	MT683347	MT683353	MT671506	MT683360	MT683357	MT683370		MT683367	Brazil: Minas Gerais, Dom Joaquim, Fazenda Estiva

Species	Voucher	Observations	12S – tRNA ^{VAL} – 16S	ND1	Cytochrome oxidase c I	Rhodopsin exon 1	Recombination activating gene 1	Tyrosinase	Seven in absentia homologue 1	Tensine 3	Country: State, Municipality, Locality
<i>Aplastodiscus heterophonicus</i>	UFMG 21556	holotype	MT683350	MT683354	MT671509	MT683361		MT683371	MT683364	MT683368	Brazil: Minas Gerais, Dom Joaquim, Fazenda Estiva
<i>Aplastodiscus ibirapitanga</i>	MNRJ 51863		KU184025	KU184228	KU184046	KU184099		KU184236	KU184138	KU184183	Brazil: Bahia, Amargosa, Serra do Timbó
<i>Aplastodiscus leucopygius</i>	MTR-StoAn 53		KU184033		KU184055	KU184108	KU184080	KU184243	KU184146	KU184190	Brazil: São Paulo, Santo André
<i>Aplastodiscus lutzorum</i>	BB49		KU184003	KU184217	KU184054	KU184107		KU184242	KU184145		Brazil: Distrito Federal, Brasília, Fazenda Água Limpa
<i>Aplastodiscus musicus</i>	ZUFJRJ 15549		MH754953/ MH754954	MH754954							Brazil: Rio de Janeiro, Teresópolis, Parque Nacional da Serra dos Órgãos
<i>Aplastodiscus perviridis</i>	CFBHt 270		KU184020		KU184057	KU184110	KU184082	KU184245	KU184148	KU184192	Brazil: Santa Catarina, São Bento do Sul, Rio Vermelho
<i>Aplastodiscus sibilatus</i>	CFBH32528		KU184014			KU184133	KU184094	KU184264	KU184170	KU184213	Brazil: Bahia, Ibirapitanga, Fazenda Pedra Formosa
<i>Aplastodiscus weygoldti</i>	MNRJ 51867		KU184026		KU184069	KU184124	KU184090	KU184257	KU184161	KU184204	Brazil: Espírito Santo, Santa Teresa, Santa Lucia
<i>Aplastodiscus</i> sp. 1	MNRJ50124		KU184024	KU184227	KU184047	KU184100	KU184079		KU184139	KU184184	Brazil: Alagoas, Murici, Fazenda Bananeira
<i>Aplastodiscus</i> sp. 2	MNRJ 73089		KU184032		KU184068	KU184123			KU184160	KU184203	Brazil: Rio de Janeiro, Maricá, Espiraído
<i>Aplastodiscus</i> sp. 5	CFBH 11183		KU184004		KU184060	KU184113		KU184248	KU184151	KU184194	Brazil: São Paulo, São Paulo, Parque Estadual da Serra do Mar-Curucutu
<i>Aplastodiscus</i> sp. 6	CFBH 27269		KU184011		KU184065	KU184118	KU184087	KU184253	KU184156	KU184199	Brazil: Minas Gerais, Carangola
<i>Boana albopunctata</i>	ZUEC12053		AY549317			AY844569		AY844041	AY844795		Brazil: São Paulo, Campinas
<i>Boana faber</i>	MACN 37000/ CFBH 27825		AY549334	KF794124	KU184075	AY844607			AY844825		Argentina: Misiones, Guarani, San Vicente/Brazil: Bahia, Camamu
<i>Boana pellucens</i>	KU 202734		AY326058								Ecuador: Pichincha, 1.8kmSSE, San Juan
<i>Boana prasina</i>	CFBH 3388		AY549347		KU184076	AY844642		AY844100	AY844860		Brazil: Santa Catarina, São Bento do Sul, Rio Vermelho
<i>Boana punctata</i>	MACN 37792		AY549353	KF794139	KU184077	AY844645					Argentina: Chaco: Resistencia: Camino a Isla del Cerrito
<i>Boana semilineata</i>	CFBH 5424		AY843778/ AY843779			AY844656	AY844453	AY844108	AY844871		Brazil: Rio de Janeiro: Duque de Caxias
<i>Boana tepuiana</i>	USNM 302435		AY843606	KF794117		AY844583	AY844396				Brazil: Roraima, Villa Pacaraima
<i>Bokermannohyla hylax</i>	USNM 303036		AY549338			AY844614	AY844419	AY844077	AY844832		Brazil: São Paulo: Near Salesópolis, Estação Biológica de Boracéia
<i>Bokermannohyla martinsi</i>	AF 414		AY843641			AY844626		AY844086	AY844844		Brazil: Minas Gerais, Santa Barbara
<i>Bokermannohyla oxente</i>	CFBH 5642		AY843676	KU184222		AY844667	AY844460	AY844118	AY844879		Brazil: Bahia, Lençóis, Rio Grisante
<i>Hyloscirtus armatus</i>	AMNH-A 165163		AY549321	KF794111		AY844579	AY844393	AY844050	AY844804		Bolivia: Santa Cruz, Caballero, Canton San Juan, Amoro National Park
<i>Hyloscirtus palmeri</i>	SIUC-H 6924		AY843650			AY844636	AY844439	AY844095	AY844854		Panama: El Copé Parque Nacional “Omar Torrijos”
<i>Hyloscirtus tapichalaca</i>	QCAZ 16704		AY563625	KF794114		AY844672		AY844121			Ecuador: Zamora-Chinchiipe, Reserva Tapichalaca
<i>Nesorohyla kanaima</i>	ROM 39582		AY843634	GQ366307		AY844617	AY844422	AY844079	AY844835		Guyana: Mount Ayanganna

Supplementary document S2. Primers used to amplify the mitochondrial and nuclear gene fragments.

Gene region	Primer name	Direction	Primer sequence (5' to 3')	Reference
	MVZ59	Forward	ATAGCACGTA AAAAYGCTDAGATG	GRAYBEAL (1997)
	tRNA-VAL	Reverse	GGTGTAAAGCGARAGGCTTTKGTAAAG	GOEBEL et al. (1999)
12S – tRNA ^{VAL} – 16S	12S-L13	Forward	TTAGAAGAGGCAAGTCGTAACATGGTA	FELLER & HEDGES (1998)
	16S-H10	Reverse	TGCTTACGCTACCTTTGCACGGT	HEDGES (1994)
	16Sa-L	Forward	CGCCTGTTTATCAAAAACAT	PALUMBI et al. (1991)
	16Sb-H	Reverse	CCCGTCTGAACTCAGATCACGT	PALUMBI et al. (1991)
16S – tRNA ^{LEU} – NADH dehydrogenase subunit 1 – tRNA ^{ILE}	16S-frog	Forward	TTACCCTRGGGATAACAGCGCAA	WIENS et al. (2005)
	tMET-Frog	Reverse	TTGGGGTATGGGCCCAAAAGCT	WIENS et al. (2005)
Cytochrome oxidase c subunit I (COI)	AnF1	Forward	ACHAAYCAYAAAGAYATYGG	LYRA et al. (2017)
	AnR1	Reverse	CCRAARAATCARAADARRTGTTG	LYRA et al. (2017)
Rhodopsin exon 1	Rhod1A	Forward	ACCATGAACGGAACAGAAGGYCC	BOSSUYT & MILINKOVITCH (2000)
	Rhod1D	Reverse	GTAGCGGAAGAARCTTCAAMGTA	BOSSUYT & MILINKOVITCH (2000)
Tyrosinase	Tyr1C	Forward	GGCAGAGGAWCRTGCCAAGATGT	BOSSUYT & MILINKOVITCH (2000)
	Tyr1G	Reverse	TGCTGGCRTCTCTCCARTCCCA	BOSSUYT & MILINKOVITCH (2000)
Recombination activating gene 1	R1-GFF	Forward	GAGAAGTCTACAAAAVGGCAAAG	FAIVOVICH et al. (2005)
	R1-GFR	Reverse	GAAGCGCCTGAACAGTTTATTAC	FAIVOVICH et al. (2005)
Seven in absentia homologue 1	SIA1	Forward	TCGAGTGCCCCGTGTGYTTYGAYTA	BONACUM et al. (2001)
	SIA2	Reverse	GAAGTGGAAGCCGAAAGCAGSWYTGATCAT	BONACUM et al. (2001)
Tensine 3	WL421	Reverse	CAGTGTGGAGAAGATGGTATGTC	SMITH et al. (2007)
	WL423	Forward	CAGCATAGGTACTTTATCATCATCAG	SMITH et al. (2007)

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Supplementary document S3. Table showing uncorrected p-distances among *Aplastodiscus* samples employed on our study. Lower diagonal corresponds to percentual differences between sequence fragments of the final ~590 bp of the mitochondrial ribosomal gene 16S. Upper diagonal corresponds to percentual differences between sequence fragments of ~650 bp of the mitochondrial gene cytochrome oxidase c subunit I (COI). An asterisk indicates the holotype of *A. heterophonicus* sp. n. Cells highlighted in light grey point distances between sequences of *A. heterophonicus* sp. nv. (upper, left) and *A. cavicola* (center of the table). The 16S fragment of *A. sibilatus* CFBH 32528 contains only 97 bp, though values for this species must be looked cautiously. We were not able to acquire COI sequences for *A. heterophonicus* MZUSP 159201, *A. cavicola* MNRJ 63689, *A. musicus* ZUFRI 15549, and *A. sibilatus* CFBH 32528.

		COI																																		
		<i>A. albosignatus</i> group																							<i>A. perviridis</i> group			<i>A. albofrenatus</i> group					<i>A. sibilatus</i> group			
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
16S	<i>A. albosignatus</i> group	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35
		–	0.0	0.0	3.8	1.2	1.2	1.2	1.2	1.2	1.2	n/a	1.2	8.9	12.1	13.0	13.7	12.1	12.7	n/a	12.9	13.1	12.9	12.9	14.3	14.6	14.9	n/a	18.9	17.9	17.8	19.0	20.3	19.8	20.3	n/a
		0.0	–	0.0	3.8	1.2	1.2	1.2	1.2	1.2	1.2	n/a	1.2	8.9	12.1	13.0	13.7	12.1	12.7	n/a	12.9	13.1	12.9	12.9	14.3	14.6	14.9	n/a	18.9	17.9	17.8	19.0	20.3	19.8	20.3	n/a
		0.0	0.0	–	3.8	1.2	1.2	1.2	1.2	1.2	1.2	n/a	1.2	8.9	12.2	13.0	13.7	12.2	12.8	n/a	12.9	13.1	12.9	12.9	14.3	14.6	14.9	n/a	18.9	17.9	17.8	19.1	20.4	19.8	20.3	n/a
		0.7	0.7	0.7	–	2.9	2.9	2.9	2.9	2.9	2.9	n/a	2.9	10.5	13.6	14.5	15.4	13.6	14.6	n/a	15.4	15.4	15.2	15.2	16.5	16.8	17.2	n/a	20.4	19.6	19.3	20.8	21.3	21.9	21.7	n/a
		0.6	0.6	0.6	0.0	–	0.2	0.0	0.0	0.0	0.0	n/a	0.0	8.9	12.3	12.8	13.8	12.5	12.5	n/a	13.5	13.7	13.5	13.5	14.6	14.6	15.2	n/a	19.1	17.7	18.0	19.1	20.4	20.2	20.3	n/a
		0.7	0.7	0.7	0.0	0.0	–	0.2	0.2	0.2	0.2	n/a	0.2	9.2	12.4	12.9	13.8	12.6	12.9	n/a	13.1	13.2	13.1	13.1	15.1	14.9	15.6	n/a	18.8	17.5	18.0	19.0	19.7	19.9	20.4	n/a
		0.7	0.7	0.7	0.0	0.0	0.0	–	0.0	0.0	0.0	n/a	0.0	8.9	12.3	12.8	13.8	12.4	12.4	n/a	13.5	13.7	13.5	13.5	14.6	14.6	15.2	n/a	19.0	17.7	18.0	19.0	20.3	20.1	20.3	n/a
		0.5	0.5	0.5	0.2	0.0	0.2	0.2	–	0.0	0.0	n/a	0.0	8.9	12.3	12.8	13.8	12.4	12.4	n/a	13.5	13.7	13.5	13.5	14.6	14.6	15.2	n/a	19.0	17.7	18.0	19.0	20.3	20.1	20.3	n/a
		0.5	0.5	0.5	0.2	0.0	0.2	0.2	0.0	–	0.0	n/a	0.0	8.9	12.3	12.8	13.8	12.4	12.4	n/a	13.5	13.7	13.5	13.5	14.6	14.6	15.2	n/a	19.0	17.7	18.0	19.0	20.3	20.1	20.3	n/a
		0.5	0.5	0.5	0.2	0.0	0.2	0.2	0.0	0.0	–	n/a	0.0	8.9	12.3	12.8	13.8	12.4	12.4	n/a	13.5	13.7	13.5	13.5	14.6	14.6	15.2	n/a	19.0	17.7	18.0	19.0	20.3	20.1	20.3	n/a
		0.5	0.5	0.5	0.2	0.0	0.2	0.2	0.0	0.0	0.0	–	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
		0.5	0.5	0.5	0.2	0.0	0.2	0.2	0.0	0.0	0.0	0.0	–	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
		3.0	2.9	2.9	2.6	2.9	2.6	2.6	2.7	2.7	2.7	2.7	2.7	–	14.6	13.2	13.8	13.2	13.1	n/a	14.4	14.9	14.8	14.7	16.3	15.5	16.1	n/a	19.8	18.3	18.9	19.0	19.8	20.0	20.3	n/a
		5.2	5.0	5.0	4.6	5.0	4.6	4.6	4.8	4.8	4.8	4.8	4.8	3.8	–	10.5	11.1	11.4	12.1	n/a	12.4	12.3	12.5	12.4	13.7	14.4	15.7	n/a	19.5	19.3	18.9	18.0	18.9	20.3	22.0	n/a
		5.9	5.6	5.7	5.3	5.6	5.3	5.3	5.5	5.5	5.5	5.5	5.5	4.3	2.7	–	5.1	10.1	11.5	n/a	11.9	11.8	11.6	11.6	14.9	14.2	15.9	n/a	20.0	19.1	20.9	18.6	20.7	20.3	19.7	n/a
		5.5	5.3	5.3	5.0	5.4	5.0	5.0	5.1	5.1	5.1	5.1	5.1	4.8	2.6	2.6	–	10.6	11.5	n/a	11.8	12.3	12.2	12.1	14.7	14.1	16.1	n/a	19.8	19.2	19.7	18.4	19.0	19.4	21.2	n/a
		6.0	5.8	5.8	5.3	6.0	5.3	5.3	5.5	5.5	5.5	5.5	5.5	4.3	3.4	4.1	3.7	–	6.9	n/a	9.8	9.7	9.5	9.5	12.0	12.7	13.1	n/a	19.7	19.5	18.1	19.0	19.8	19.0	21.2	n/a
		5.9	5.7	5.7	5.1	5.4	5.1	5.1	5.3	5.3	5.3	5.3	5.3	4.1	3.1	3.6	3.2	2.7	–	n/a	8.3	8.1	8.0	8.0	13.5	13.5	13.4	n/a	19.5	19.0	18.9	18.9	19.5	19.0	20.6	n/a
		6.7	6.5	6.5	6.0	6.6	6.0	6.0	6.2	6.2	6.2	6.2	6.2	5.7	5.0	5.5	4.6	3.9	3.9	–	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
		6.7	6.5	6.5	6.3	6.8	6.3	6.5	6.5	6.5	6.5	6.5	6.5	5.8	4.8	5.3	4.6	4.6	4.3	4.9	–	1.8	1.7	1.7	13.5	14.3	13.8	n/a	18.1	20.3	19.5	18.7	20.5	20.0	21.0	n/a
		7.1	6.8	6.9	6.7	7.2	6.7	6.7	6.8	6.8	6.9	6.8	6.8	6.0	4.6	5.1	4.4	4.8	4.4	4.8	1.2	–	0.2	0.2	14.3	14.1	14.4	n/a	17.4	19.8	19.0	18.4	19.8	19.5	21.5	n/a
		7.3	7.3	7.3	7.1	7.4	7.1	7.1	7.3	7.3	7.3	7.3	7.3	6.4	4.9	5.4	4.7	5.1	4.7	5.1	1.1	0.0	–	0.0	14.2	14.0	14.3	n/a	17.5	19.7	19.1	18.3	20.0	19.4	21.4	n/a
	7.0	7.0	7.0	7.0	7.2	7.0	7.0	7.0	7.0	7.0	7.0	7.0	6.2	4.5	5.1	4.3	4.9	4.5	4.7	1.3	0.0	0.0	–	14.1	14.0	14.3	n/a	17.5	19.7	19.0	18.3	20.0	19.4	21.3	n/a	
<i>A. perviridis</i> group	24	8.2	7.9	7.9	7.5	8.1	7.5	7.5	7.7	7.7	7.7	7.7	6.7	5.0	5.0	5.3	6.5	6.3	7.2	7.0	6.8	7.3	6.8	–	8.9	9.1	n/a	20.0	19.0	18.1	19.5	20.5	21.2	21.5	n/a	
	25	8.0	7.7	7.7	7.4	7.9	7.4	7.4	7.5	7.5	7.5	7.5	6.5	5.3	6.2	6.2	6.7	6.2	6.5	6.2	6.3	6.7	6.2	2.1	–	9.1	n/a	18.1	17.7	17.4	18.6	18.7	19.0	21.8	n/a	
	26	9.6	9.2	9.3	8.9	9.7	8.9	8.9	9.1	9.1	9.1	9.1	9.1	7.9	5.8	6.2	6.8	7.2	7.0	7.0	8.7	8.6	9.1	8.7	3.9	4.5	–	n/a	18.4	18.5	17.8	19.7	19.7	20.1	21.5	n/a
<i>A. albofrenatus</i> group	27	10.8	10.4	10.4	10.4	11.4	10.4	10.4	10.5	10.5	10.6	10.5	10.2	9.5	11.0	9.5	10.0	9.5	9.8	10.4	10.0	10.6	10.3	10.9	10.4	12.0	–	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	
	28	12.7	12.3	12.3	12.3	13.3	12.3	12.3	12.4	12.4	12.5	12.4	12.4	11.7	10.7	11.5	11.0	11.7	11.4	12.4	11.9	11.5	12.2	12.0	11.8	12.1	11.9	9.5	–	17.2	15.2	15.7	15.5	16.9	22.7	n/a
	29	12.1	11.7	11.7	11.7	13.0	11.7	11.7	11.8	11.8	11.9	11.8	11.3	11.3	12.2	11.8	11.8	11.5	11.5	12.3	12.3	13.1	13.1	12.2	11.8	12.9	7.7	10.7	–	12.9	15.7	12.4	14.2	22.0	n/a	
	30	13.4	12.9	12.9	12.7	14.1	12.7	12.7	12.9	12.9	12.9	12.9	12.0	11.7	12.7	11.7	12.5	12.0	12.2	13.1	12.9	13.7	13.5	12.9	13.1	13.5	8.9	9.3	7.2	–	12.0	11.8	12.4	21.7	n/a	
	31	12.3	11.8	11.8	11.6	12.6	11.6	11.6	11.8	11.8	11.8	11.8	11.3	10.2	11.6	10.9	10.9	10.9	11.3	11.8	11.8	12.5	12.5	12.2	12.0	12.5	8.2	8.9	7.0	6.6	–	11.5	12.0	21.0	n/a	
	32	11.3	10.9	10.9	10.7	11.4	10.7	10.7	10.9	10.9	10.9	10.9	10.2	9.3	9.8	9.8	10.2	9.8	10.9	11.1	10.9	11.6	11.3	11.3	11.4	11.8	9.4	8.7	6.8	6.6	6.0	–	7.6	22.3	n/a	
33	12.4	11.9	11.9	11.7	12.7	11.7	11.7	11.9	11.9	11.9	11.9	11.6	10.3	11.5	10.6	11.2	11.0	11.7	11.5	11.7	12.4	12.4	11.4	11.9	12.1	8.6	8.6	7.9	6.6	6.5	3.0	–	22.2	n/a		
<i>A. sibilatus</i> group	34	13.0	12.5	12.5	12.5	13.8	12.5	12.5	12.7	12.7	12.7	12.7	12.0	11.8	12.3	12.3	12.7	13.2	12.8	11.8	11.6	12.3	12.3	12.7	12.7	13.7	10.5	11.9	12.7	13.1	12.0	10.0	10.7	–	n/a	
	35	7.4	7.4	7.4	6.3	7.3	6.3	6.3	7.4	7.4	7.4	7.4	5.3	9.3	9.3	9.3	8.2	9.3	8.2	6.2	6.2	6.0	5.0	8.4	8.4	9.5	6.2	7.2	7.3	7.2	7.2	8.3	8.3	1.0	–	