

Description of a new species of *Homonota* (Reptilia, Squamata, Phyllodactylidae) from the central region of northern Paraguay

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Appendix S1

PCR mix for amplification

Following we present the list of reagents and amounts for preparation of the master-mix for sequence amplification.

Amounts for 25µl of PCR reaction mix for 16S

Reagent	Concentration	Volume (µl)
Water		14
dNTPs	2.5 mM	4
Reaction Buffer Y	10×	2.5
MgCl ₂	25 mM	1
Primer 1	10 µM	1
Primer 2	10 µM	1
TaqPolymerase	5 U/µl	0.5
DNA	25 ng/ µl	1

Amounts for 25µl of PCR reaction mix for Cytb

Reagent	Concentration	Volume (µl)
Water		11.8
dNTPs	2.5 mM	3.5
Reaction Buffer Y	10×	3.5
MgCl ₂	25 mM	1.5
Primer 1	10 µM	1.5
Primer 2	10 µM	1.5
TaqPolymerase	5 U/µl	0.2
DNA	25 ng/ µl	1.5

Amounts for 20µl of PCR reaction mix for PRLR

Reagent	Concentration	Volume (µl)
Water		8
dNTPs	2.5 mM	3.2
Reaction Buffer Y	10×	2
MgCl ₂	25 mM	1.4
Primer 1	10 µM	1.5
Primer 2	10 µM	1.5
TaqPolymerase	5 U/µl	0.4
DNA	25 ng/ µl	2

Appendix S2

Primers and PCR conditions

Following we detail the primers used for gene amplifications and the conditions for the thermocycler.

16S	L2510 (F)	CGCCTGTTTAACAAAAACAT	Miya & Nishida 1996
	H3056 (R)	CGGTCTGAACTCAGATCACGT	
Cytb	IguaF2	CCACCGTTGTTATTCAACTAC	Corl et al. 2010
	IguaR2	GGTTTACAAGACCAATGCTTT	
PRLR	PRLR_f1	GACARYGARGACCAGCAACTRATGCC	Townsend et al. 2008
	PRLR_r3	GACYTTGTGRACTTCYACRTAATCCAT	

Primers	PCR conditions					Reference
	Den	Den	Ann	Ext	Ext	
L2510 (F) H3056 (R)	94.0°	94.0°	48.5°	72.0°	72.0°	Lotzkat et al. 2013
	02:00	00:35	00:35	01:00	10:00	
			×40			
		95.0°	63.0°	72.0°		Noonan & Yoder 2009
			↓ (*)			
		00:35	00:35	02:00		
		×10				
PRLR_f1	95.0°	95.0°	58.0°	72.0°	72.0°	
PRLR_r3	01:30	00:35	00:35	01:00	10:00	
		×10				
		94.0°	52.0°	72.0°		
		00:35	00:35	01:00		
		×15				
IguaF2 IguaR2	94.0°	94.0°	50.0°	72.0°	72.0°	Corl et al. 2010
	04:00	00:30	00:35	00:50	07:00	
		×25				

References

- Corl et al. 2010. *Evolution* 64: 79–96.
- Lotzkat et al. 2013. *Zootaxa*, 3626: 1–54.
- Miya & Nishida 1996. *Ichthyological Research*, 43: 375–398.
- Noonan & Yoder 2009 *Molecular Ecology Resources*, 9: 402–404.
- Townsend et al. 2008. *Molecular Phylogenetics and Evolution*, 47: 129–42.

Appendix S3

Table of localities

List of localities included in the text, with geographic coordinates (DD format).
Abbreviations: RP (Provincial Route), RN (National Route), PN (National Park).

Country	Division	Locality	Latitude	Longitude
Argentina	La Pampa	RP 1, 23.6 km W RN151	-37.075°	-67.785°
		RP 27, 37.7 km S RN 14	-36.668°	-68.022°
	Mendoza	1 km S Punta de Agua	-35.541°	-68.079°
	Neuquén	41 km NW Punta Carranza	-37.656°	-69.472°
		6 km SW Picun Leufu	-39.555°	-69.301°
		RP 5, 10 km N RP 7	-37.906°	-69.174°
		Mina La Casualidad	-37.904°	-68.488°
		Villa El Chocón	-39.261°	-68.779°
	Río Negro	Avellaneda	-39.145°	-66.145°
		Villa Regina	-39.101°	-67.091°
Paraguay	Boquerón	Comunidad Ayoreo Jesudi	-59.924°	-21.841°
		Comunidad Ayoreo Tunucojai	-59.772°	-22.050°
		Cruce San Miguel	-21.203°	-61.662°
		Estancia Amistad	-22.406°	-60.728°
		Estancia Jabalí	-61.424°	-22.611
		Filadelfia	-22.352°	-60.041°
		31.5 km S Filadelfia	-22.644°	-60.031
		Fortín Mayor Infante Rivarola	-21.679°	-62.401°
PN Teniente Enciso	-21.209°	-61.655°		

Appendix S4

Best substitution models

List of all the models considered by PartitionFinder2 and scores of AICc.

16S		Cytb						PRLR			
		1 st Pos		2 nd Pos		3 rd Pos		1 st Pos		2 nd + 3 rd Pos	
Model	AICc	Model	AICc	Model	AICc	Model	AICc	Model	AICc	Model	AICc
GTR+G	2212.76	TVM+I	1469.37	TIM+G	6064.01	SYM+G	2538.22	K81	1184.44	GTR+G	1869.65
GTR+I	2213.46	GTR+I	1471.43	TIM+I+G	6066.16	TVMEF+G	2538.25	K80	1184.97	TIM+G	1870.24
GTR	2213.55	TVM+I+G	1471.51	GTR+G	6068.27	GTR+G	2538.6	K81+I	1185.49	GTR+I	1871.76
GTR+I+G	2214.82	HKY+I	1471.99	GTR+I+G	6070.44	TVM+G	2539.41	K81+G	1185.8	GTR+I+G	1871.86
TVM+G	2215.11	HKY+I+G	1472.73	TRN+G	6072.19	TVMEF+I+G	2539.9	TIMEF	1185.84	SYM+G	1872.12
TVM	2215.65	GTR+I+G	1473.58	TRN+I+G	6073.92	SYM+I+G	2540.14	K80+I	1186.0	TVMEF+G	1872.19
TVM+I	2215.74	K81UF+I	1473.97	TIM	6075.59	GTR+I+G	2540.44	K80+G	1186.33	TIM+I+G	1872.35
TVM+I+G	2217.17	TRN+I	1474.05	K81UF+G	6077.49	TVM+I+G	2540.84	TRNEF	1186.34	TIM+I	1872.43
TIM+G	2218.12	K81UF+I+G	1474.6	TIM+I	6077.72	TIM+G	2540.86	K81UF	1186.98	TVM+G	1873.86
TIM+I	2218.75	TRN+I+G	1474.91	K81UF+I+G	6079.6	K81UF+G	2541.95	TIMEF+I	1187.06	SYM+I	1874.02
TRN+G	2219.28	TIM+I	1476.06	GTR	6079.74	TIMEF+G	2542.88	TIMEF+G	1187.31	TRN+G	1874.04
TRN+I	2219.85	TIM+I+G	1476.72	TVM+G	6081.2	TIM+I+G	2542.88	HKY	1187.49	TVMEF+I	1874.04
TIM	2219.89	TVM+G	1477.03	TRN	6081.69	K81+G	2543.2	TRNEF+I	1187.55	SYM+I+G	1874.28
TIM+I+G	2220.13	GTR+G	1479.17	GTR+I	6081.9	K81UF+I+G	2543.57	K81+I+G	1187.61	TVMEF+I+G	1874.34
K81UF+G	2220.32	HKY+G	1480.14	TVM+I+G	6083.37	TRN+G	2544.43	TRNEF+G	1187.81	TIMEF+G	1874.59
K81UF+I	2220.85	K81UF+G	1482.11	TRN+I	6083.78	TIMEF+I+G	2544.86	K80+I+G	1188.09	K81UF+G	1874.77
TRN+I+G	2221.26	TRN+G	1482.23	HKY+G	6084.6	K81+I+G	2544.95	TVMEF	1188.32	K81+G	1874.81
HKY+G	2221.28	TIM+G	1484.21	HKY+I+G	6086.71	HKY+G	2545.65	K81UF+I	1188.52	TVM+I	1875.84
HKY+I	2221.84	TRNEF+I+G	1506.38	K81UF	6091.5	TRN+I+G	2546.25	TIM	1188.67	TVM+I+G	1876.06
TRN	2221.88	SYM+I+G	1506.44	K81UF+I	6093.63	HKY+I+G	2546.96	K81UF+G	1188.79	TRN+I+G	1876.21
K81UF	2221.98	SYM+I	1506.96	TVM	6095.55	SYM+I	2547.66	HKY+I	1188.98	TRN+I	1876.23
K81UF+I+G	2222.33	TIMEF+I+G	1507.67	HKY	6097.28	TRNEF+G	2548.1	TRN	1189.15	GTR	1876.29
HKY+I+G	2223.26	TVMEF+I+G	1508.83	TVM+I	6097.7	TVMEF+I	2548.16	TIMEF+I+G	1189.22	TIMEF+I	1876.6
HKY	2223.89	TRNEF+I	1509.23	HKY+I	6099.38	K80+G	2548.52	HKY+G	1189.27	TIMEF+I+G	1876.65
SYM+G	2229.99	K80+I+G	1509.59	SYM+G	6517.49	GTR+I	2548.56	TVMEF+I	1189.49	TIM	1876.67
SYM	2230.24	TVMEF+I	1509.98	SYM+I+G	6519.62	TIM+I	2549.77	TRNEF+I+G	1189.68	K81+I	1876.73
SYM+I	2230.65	TIMEF+I	1510.45	TVMEF+G	6526.45	TRNEF+I+G	2549.91	SYM	1189.78	K81UF+I	1876.74
TVMEF+G	2231.1	K81+I+G	1510.92	TVMEF+I+G	6528.55	K80+I+G	2549.97	TVMEF+G	1189.8	K81UF+I+G	1876.9
TVMEF	2231.23	K80+I	1512.73	TIMEF+G	6541.13	TVM+I	2549.98	TIM+I	1190.38	K81+I+G	1876.96

16S		Cytb						PRLR			
Model	AICc	1st Pos		2nd Pos		3rd Pos		1st Pos		2nd + 3rd Pos	
Model	AICc	Model	AICc	Model	AICc	Model	AICc	Model	AICc	Model	AICc
TVMEF+I	2231.71	SYM+G	1513.35	TIMEF+I+G	6543.22	TIMEF+I	2551.19	TIM+G	1190.57	HKY+G	1878.67
SYM+I+G	2232.07	K81+I	1513.9	SYM+I	6544.96	K81UF+I	2551.93	K81UF+I+G	1190.73	TVMEF	1878.78
TVMEF+I+G	2233.18	TRNEF+G	1515.95	SYM	6548.26	K81+I	2552.45	TVM	1190.73	TRNEF+G	1878.88
TIMEF+G	2240.34	TVMEF+G	1516.93	K81+G	6548.36	TRN+I	2554.46	TRN+I	1190.81	SYM	1879.1
TIMEF+I	2241.06	TIMEF+G	1517.2	K81+I+G	6550.42	HKY+I	2556.7	TRN+G	1191.02	K80+G	1879.14
K81+G	2241.19	F81+I+G	1517.89	TVMEF+I	6553.21	TRNEF+I	2557.6	SYM+I	1191.13	TVM	1880.25
TIMEF	2241.21	F81+I	1519.47	TVMEF	6558.81	K80+I	2558.83	HKY+I+G	1191.17	TRN	1880.42
K81+I	2241.83	K80+G	1520.15	TRNEF+G	6564.37	JC+G	2638.64	SYM+G	1191.36	HKY+I	1880.64
TRNEF+G	2241.85	K81+G	1521.36	TIMEF+I	6566.35	JC+I+G	2640.53	TVMEF+I+G	1191.67	HKY+I+G	1880.75
K81	2242.07	F81+G	1526.44	TRNEF+I+G	6566.44	F81+G	2641.42	TVM+I	1192.45	K81UF	1880.77
TIMEF+I+G	2242.36	JC+I+G	1562.69	TIMEF	6568.68	F81+I+G	2643.34	GTR	1192.47	TRNEF+I	1880.85
TRNEF+I	2242.49	JC+I	1564.8	K81+I	6571.22	JC+I	2646.64	TIM+I+G	1192.6	TRNEF+I+G	1880.93
K80+G	2242.73	TVM	1570.35	K80+G	6571.36	F81+I	2649.46	TVM+G	1192.68	K81	1880.98
K81+I+G	2243.2	JC+G	1571.36	K80+I+G	6573.41	TVMEF	2654.35	TRN+I+G	1193.01	K80+I	1881.01
K80+I	2243.23	GTR	1572.45	K81	6575.21	SYM	2655.95	SYM+I+G	1193.34	K80+I+G	1881.18
TRNEF	2243.69	HKY	1574.2	TRNEF+I	6587.94	TVM	2664.82	GTR+I	1194.35	TIMEF	1881.19
TRNEF+I+G	2243.82	K81UF	1575.99	TRNEF	6590.54	GTR	2665.83	GTR+G	1194.5	HKY	1884.6
K80	2244.57	TRN	1576.26	K80+I	6592.79	K81	2672.8	TVM+I+G	1194.71	K80	1885.22
K80+I+G	2244.69	TIM	1578.06	K80	6597.1	TIMEF	2674.38	GTR+I+G	1196.62	TRNEF	1885.39
F81+G	2251.17	SYM	1601.48	F81+G	6874.54	K80	2678.52	JC	1205.04	F81+G	1918.24
F81+I	2251.73	TVMEF	1603.19	F81+I+G	6876.24	K81UF	2679.36	JC+I	1206.2	F81+I	1920.12
F81	2251.85	TRNEF	1606.23	F81+I	6892.42	TRNEF	2680.07	JC+G	1206.5	F81+I+G	1920.31
F81+I+G	2253.2	TIMEF	1607.66	F81	6880.59	TIM	2680.36	F81	1207.63	JC+G	1920.9
JC+G	2270.67	K80	1607.97	JC+G	6991.31	HKY	2684.82	JC+I+G	1208.27	JC+I	1922.72
JC	2271.2	K81	1609.38	JC+I+G	6993.34	TRN	2685.77	F81+I	1209.06	JC+I+G	1922.93
JC+I	2271.21	F81	1613.94	JC+I	7000.12	JC	2758.33	F81+G	1209.35	F81	1923.01
JC+I+G	2272.68	JC	1655.85	JC	7001.24	F81	2765.66	F81+I+G	1211.21	JC	1925.8

Appendix S5

Results of the Species Delimitation test with ABGD.

At the end, the group for the new species is highlighted in bold.

Results are shown for our dataset, according to the following parameters:

Pmin: 0.001 Pmax: 0.1 Steps: 10

X (relative gap width): 0.5

Nb bins (for distance distribution): 20

Simple Distance

Partition 1 : found 12 groups (prior maximal distance P= 0.001000)

Partition 2 : found 12 groups (prior maximal distance P= 0.001668)

Partition 3 : found 12 groups (prior maximal distance P= 0.002783)

Partition 4 : found 12 groups (prior maximal distance P= 0.004642)

Partition 5 : found 12 groups (prior maximal distance P= 0.007743)

Partition 6 : found 12 groups (prior maximal distance P= 0.012915)

Partition 7 : found 12 groups (prior maximal distance P= 0.021544)

Partition 8 : found 12 groups (prior maximal distance P= 0.035938)

Partition 9 : found 12 groups (prior maximal distance P= 0.059948)

Initial Partition with prior maximal distance P=5.99e-02

Distance Simple Dist MinSlope=0.500000

Group[1] n: 2 ;id: *H_whitii*_LJAMM-CNP_14387 *H_whitii*_LJAMM-CNP_14388

Group[2] n: 2 ;id: *H_andicola*_LJAMM-CNP_12493 *H_andicola*_LJAMM-CNP_12495

Group[3] n: 2 ;id: *H_darwini*_LJAMM-CNP_11424 *H_darwini*_LJAMM-CNP_9266

Group[4] n: 2 ;id: *H_williamsii*_LJAMM-CNP-4467 *H_williamsii*_LJAMM-CNP-6517

Group[5] n: 3 ;id: *H_borellii*_LJAMM-CNP_12116 *H_borellii*_LJAMM-CNP_12125

*H_borellii*_LJAMM_CNP_12119

Group[6] n: 3 ;id: *H_uruguayensis*_UFRGS-5769 *H_uruguayensis*_UFRGS-5770

*H_uruguayensis*_UFRGS-5771

Group[7] n: 2 ;id: *H_rupicola*_MNHNP-2 *H_rupicola*_MNHNP-1

Group[8] n: 2 ;id: *H_taragui*_LJAMM-CNP_14419 *H_taragui*_LJAMM-CNP_14420

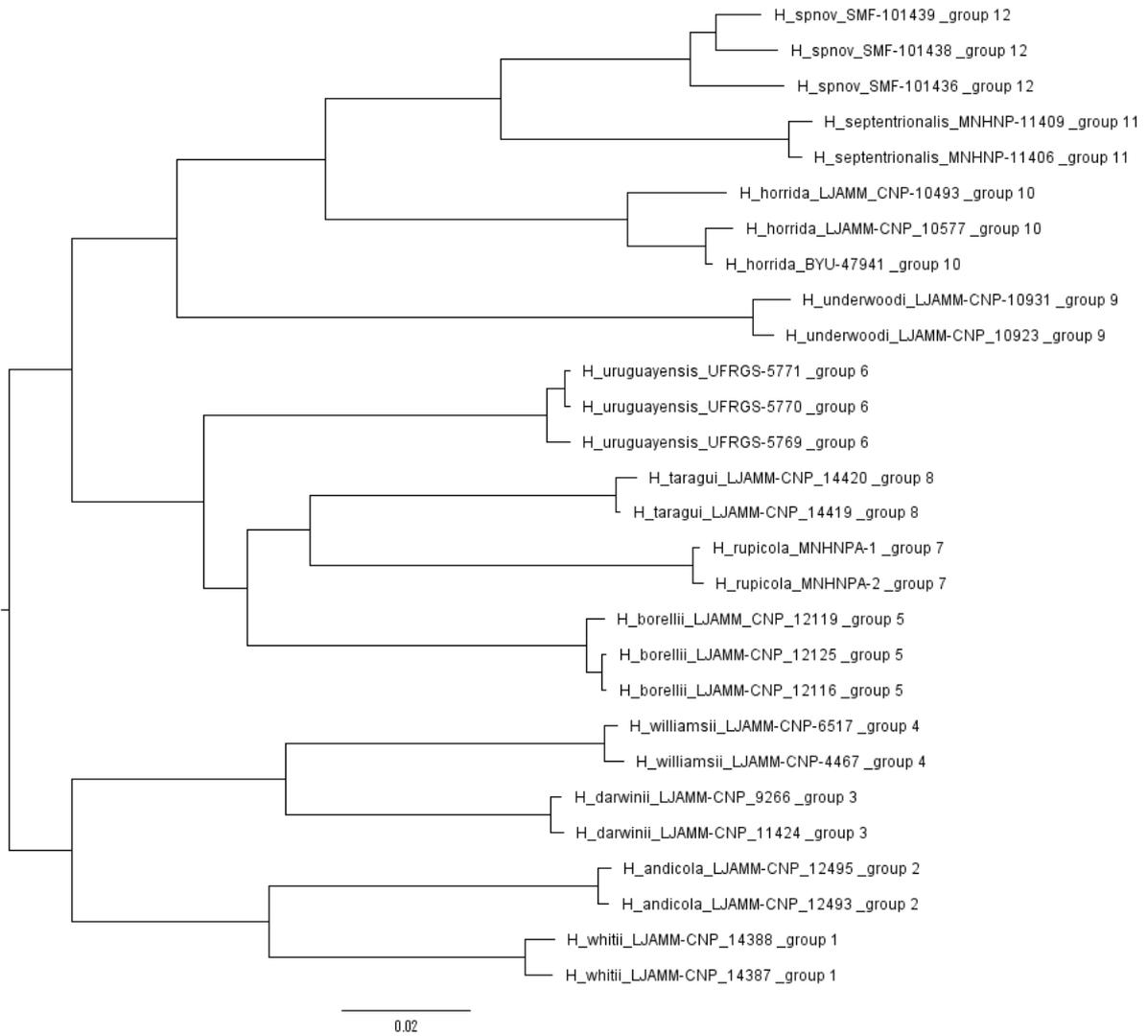
Group[9] n: 2 ;id: *H_underwoodi*_LJAMM-CNP_10923 *H_underwoodi*_LJAMM-CNP-10931

Group[10] n: 3 ;id: *H_horrida*_BYU-47941 *H_horrida*_LJAMM-CNP_10577

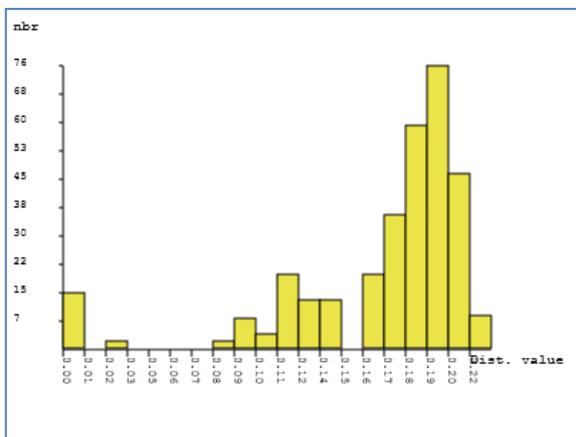
*H_horrida*_LJAMM_CNP-10493

Group[11] n: 2 ;id: *H_septentrionalis*_MNHNP-11406 *H_septentrionalis*_MNHNP-11409

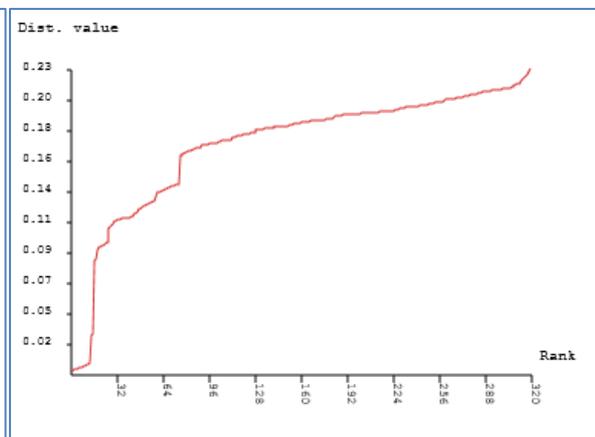
Group[12] n: 3 ;id: **H_spnov_SMF-101436 H_spnov_SMF-101438 H_spnov_SMF-101439**



Tree corresponding to the partition listed above.



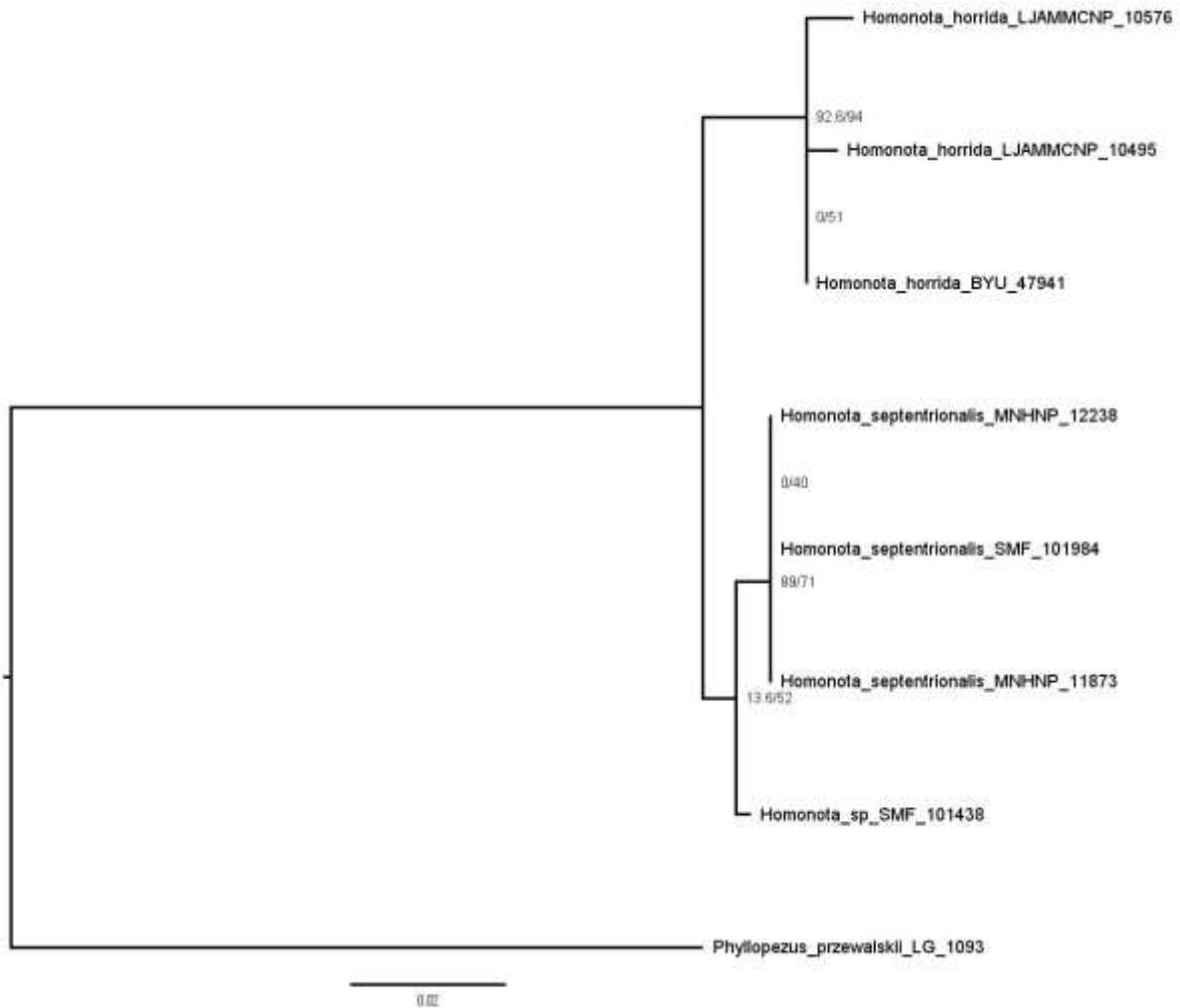
Histogram of distances



Ranked distances

Figure S1

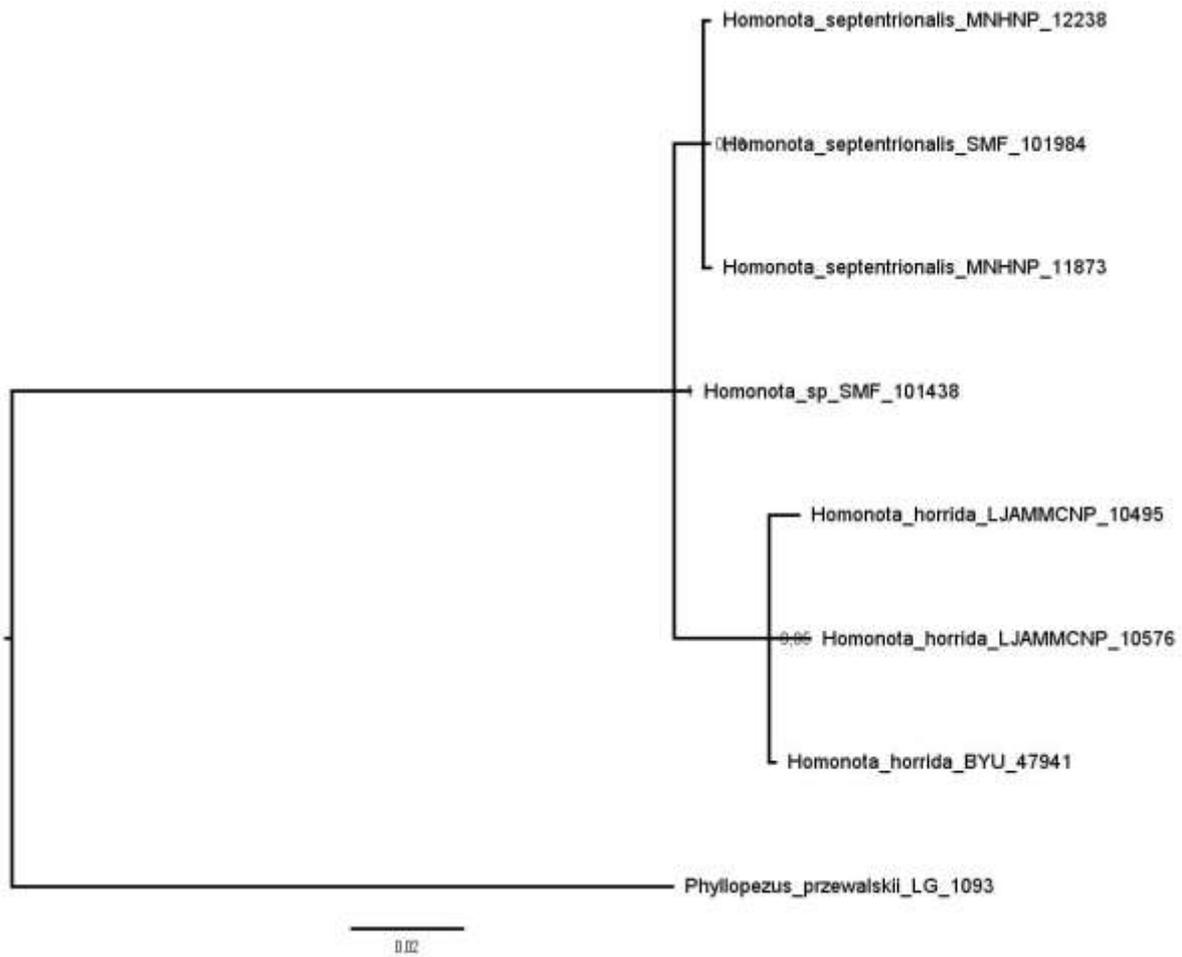
Maximum likelihood tree of 16S



Maximum Likelihood clusters of samples of *Homonota*, based on the rRNA gene 16S. Support values on nodes represent SH-aLRT/UFBboot (in percentages). Scale bar represents substitutions per site.

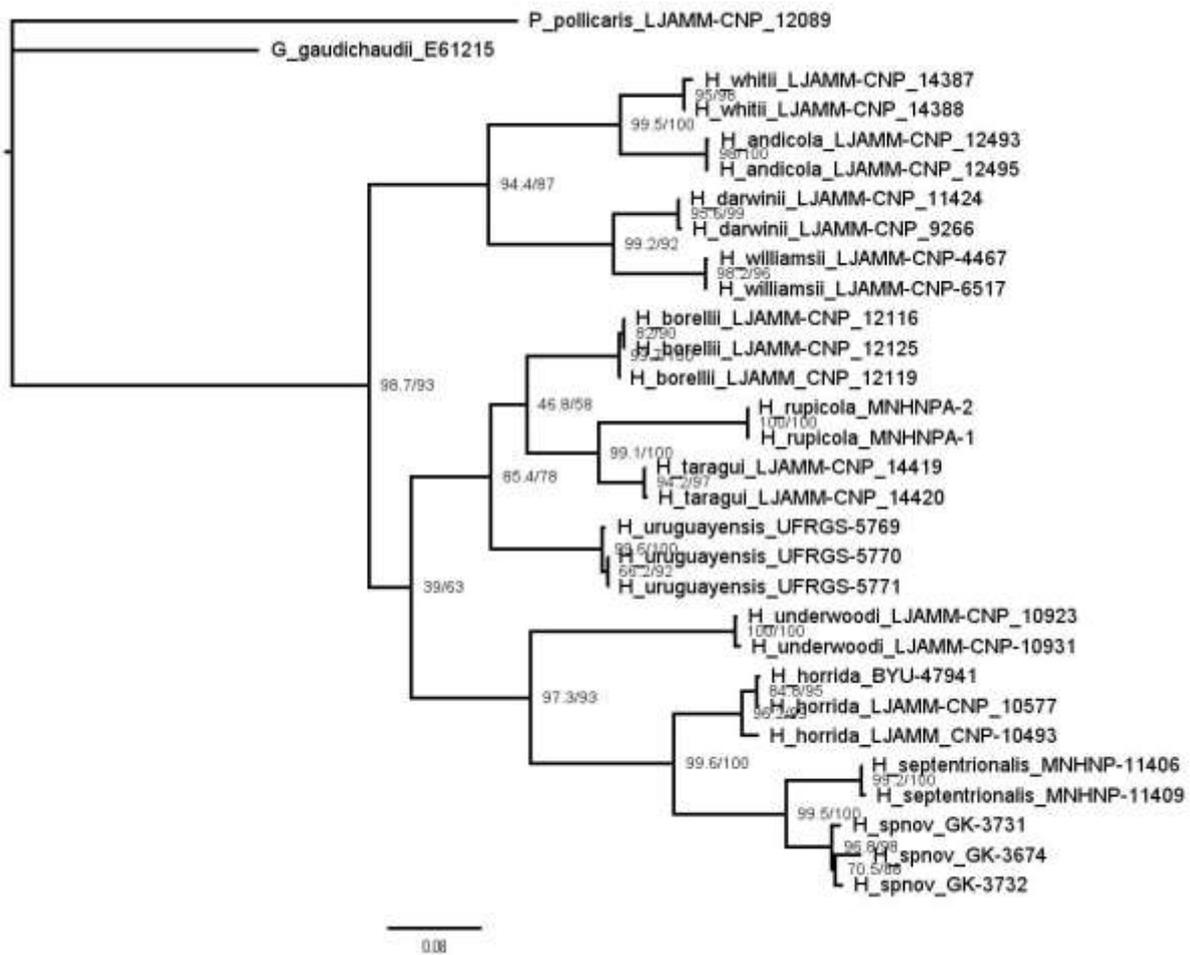
Figure S2

Bayesian tree of 16S

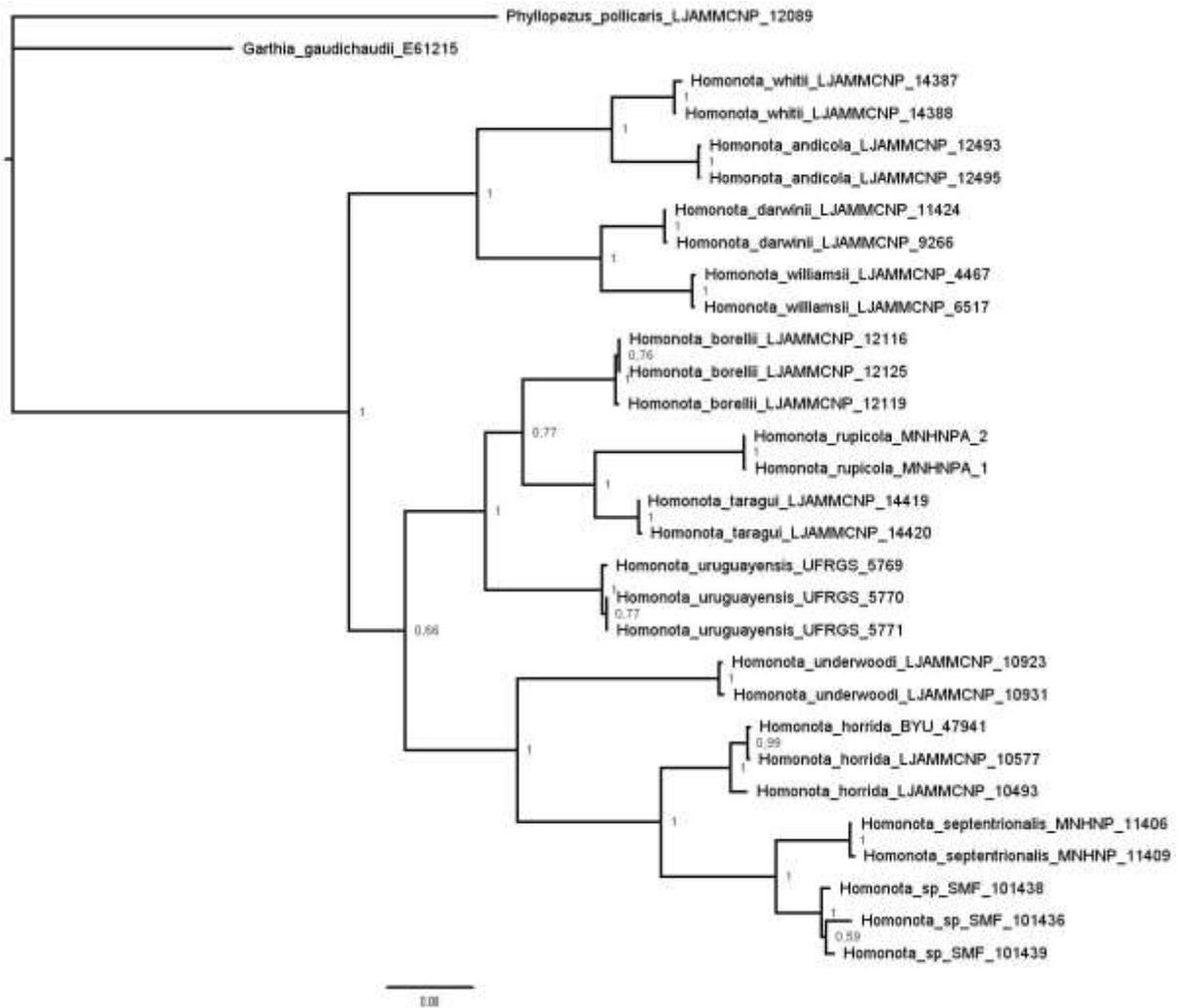


Clusters of the samples of *Homonota* based on a Bayesian inference, using the rRNA gene 16S.

Support values on nodes represent posterior probability. Scale bar represents substitutions per site.

Figure S3Maximum likelihood tree of *Cytb*

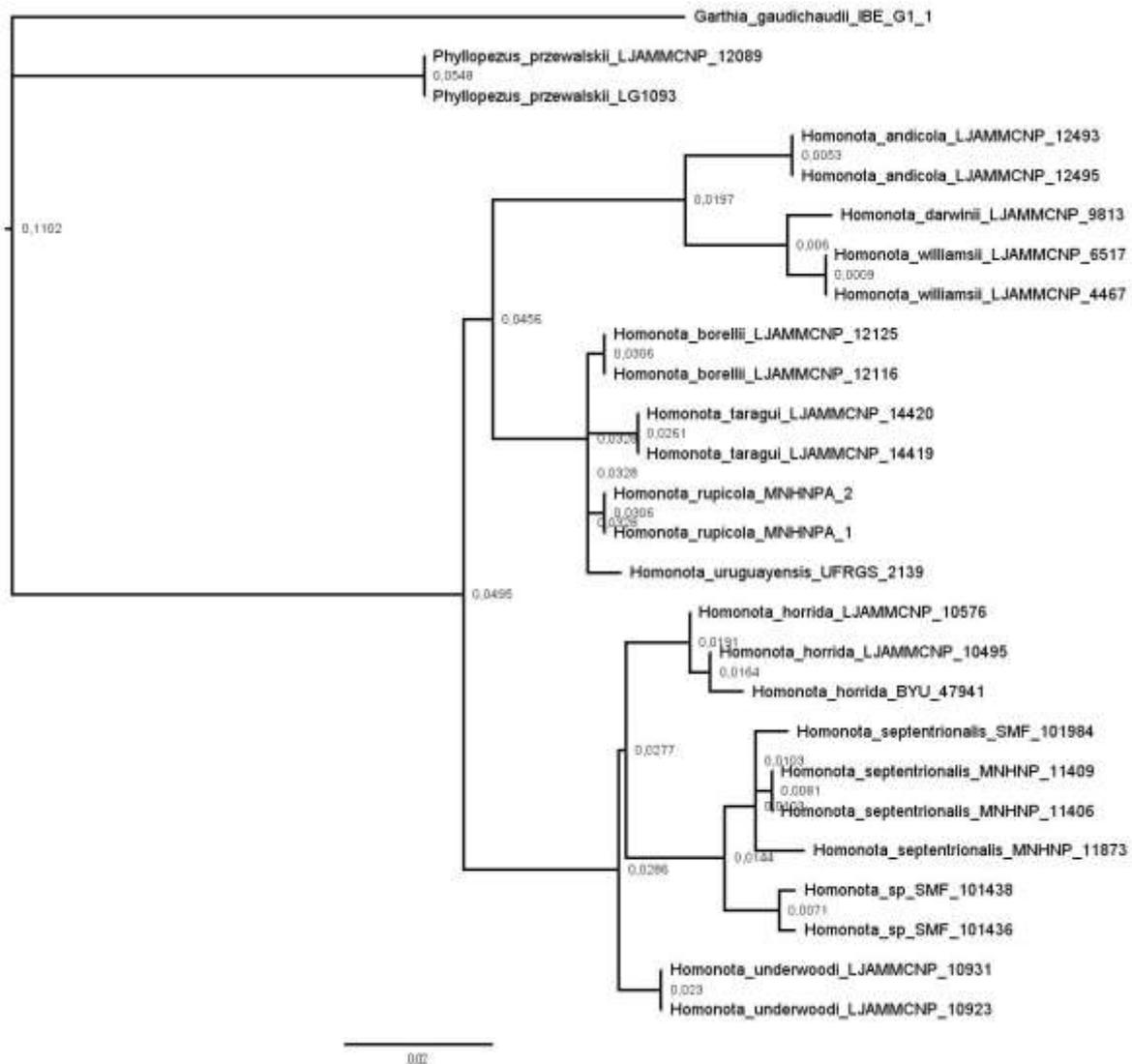
Maximum Likelihood gene tree of *Homonota*, based on the mitochondrial gene *Cytb*. Support values on nodes represent SH-aLRT/UFBoot (in percentages). Scale bar represents substitutions per site.

Figure S4Bayesian tree of *Cytb*

Clusters of the samples of *Homonota* based on a Bayesian inference, using the mitochondrial gene *Cytb*. Support values on nodes represent posterior probability. Scale bar represents substitutions per site.

Figure S5

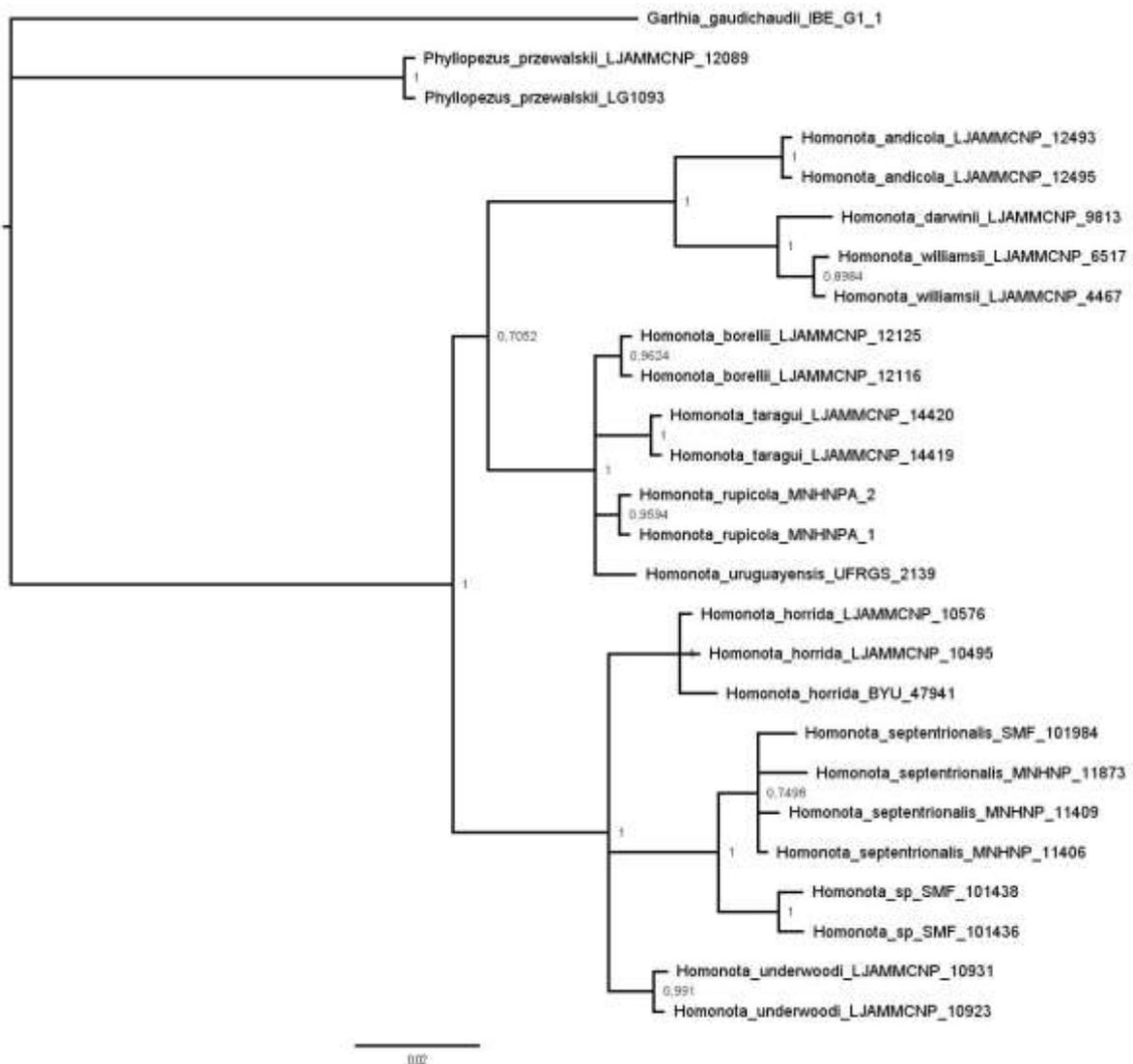
Maximum likelihood tree of PRLR



Maximum Likelihood gene tree of *Homonota*, based on the nuclear gene PRLR. Support values on nodes represent SH-aLRT/UFBoot (in percentages). Scale bar represents substitutions per site.

Figure S6

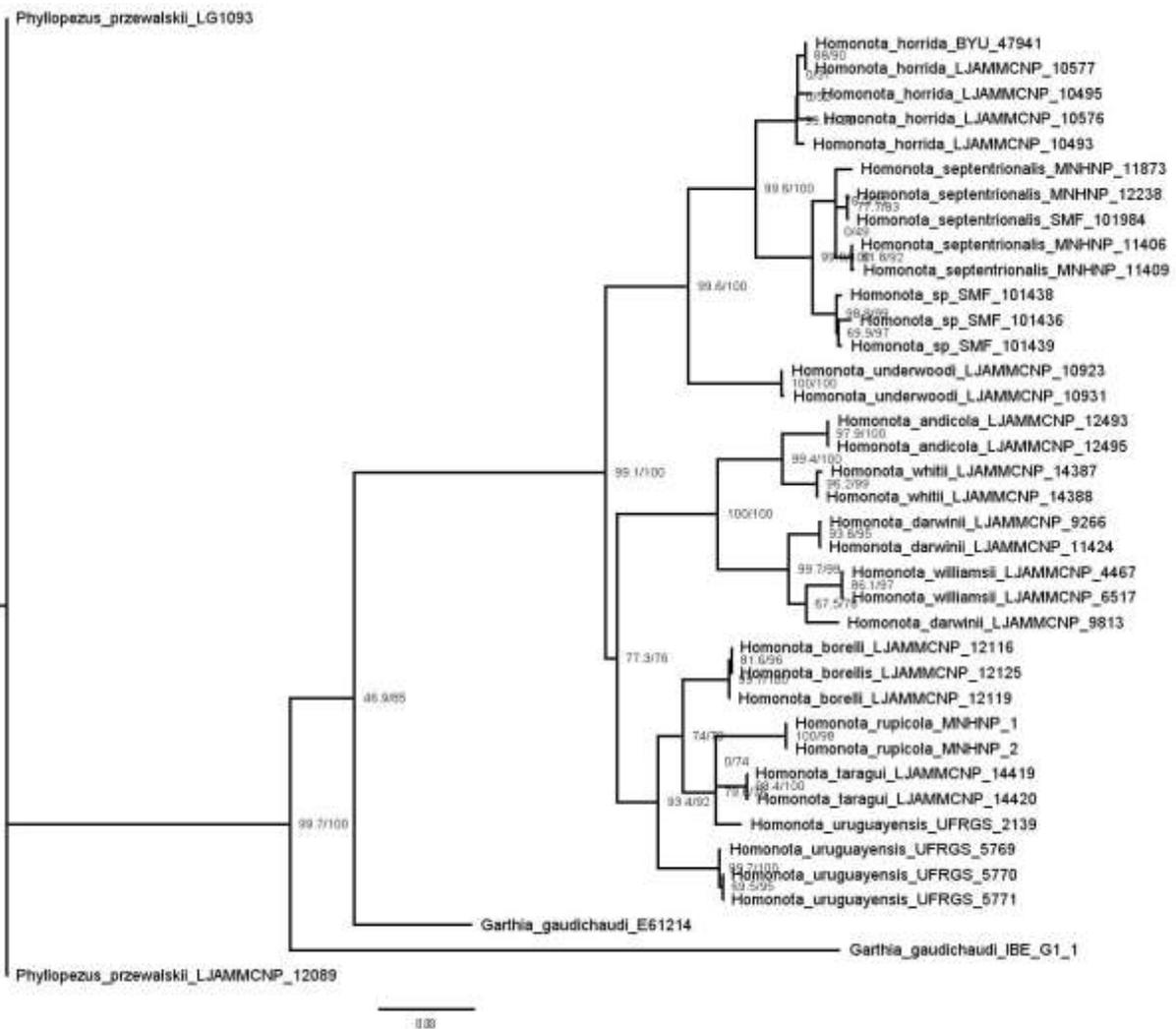
Bayesian tree of PRLR



Clusters of the samples of *Homonota* based on a Bayesian inference, using the nuclear gene PRLR. Support values on nodes represent posterior probability. Scale bar represents substitutions per site.

Figure S7

Maximum likelihood tree of concatenated genes

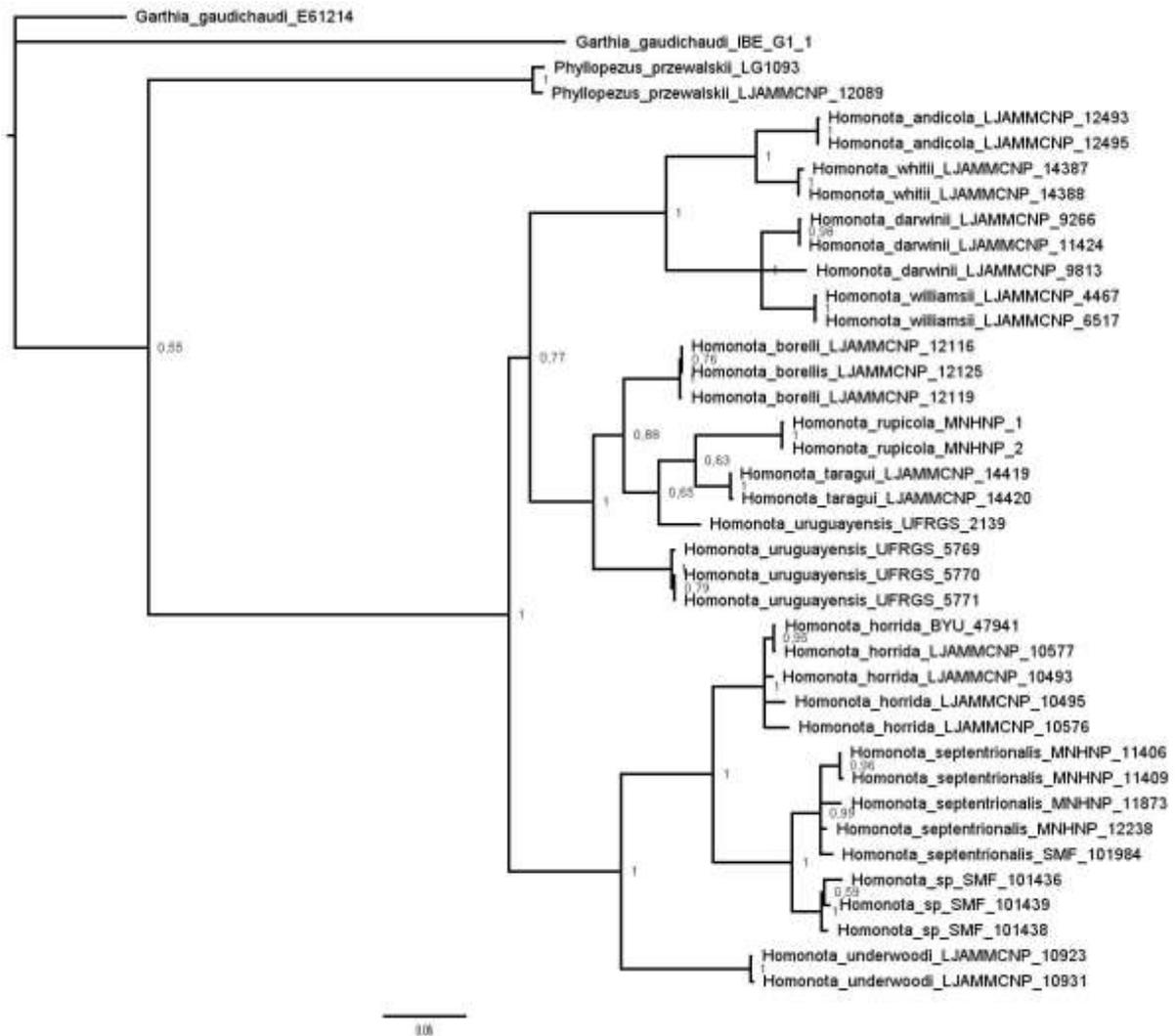


Maximum Likelihood gene tree of *Homonota*, based on concatenated genes (16S+Cytb+PRLR).

Support values on nodes represent SH-aLRT/UFBoot (in percentages). Scale bar represents substitutions per site.

Figure S8

Bayesian tree of concatenated genes



Clusters of the samples of *Homonota* based on a Bayesian inference, based on concatenated genes (16S+Cytb+PRLR). Support values on nodes represent posterior probability. Scale bar represents substitutions per site.

Table S1

Raw metric data (in mm) used for statistical analyses. See Materials and Methods section for explanation of the characters. Missing data indicated with “?”. Sex of specimens indicated in

Table S2.

	Voucher	SVL	TrL	FL	TL	AL	HL	HW	HH	END	ESD	EMD	ID	IND
<i>Homonota horrida</i>	LJAMM-CNP 6520	57	24	10	9.2	12.2	12.8	8.6	6.7	4.3	5.3	4.8	3.8	1.7
	LJAMM-CNP 6530	64	29	11	12.5	15.4	14.6	10.4	7.6	4.7	6.3	5.3	4.8	1.7
	LJAMM-CNP 6532	56	23	9	9.6	?	13.5	10.5	6.9	4.6	5.8	5.2	5.2	1.8
	LJAMM-CNP 6533	60	26	?	11.2	13.4	13.9	11.1	7.1	4.8	6.1	4.9	4.9	2.3
	LJAMM-CNP 6535	53	21	11	9.6	?	?	?	?	?	?	?	?	?
	LJAMM-CNP 6967	42	18	7	8.3	11.9	10.5	10.4	5.8	3.5	4.1	4.4	4.5	1.7
	LJAMM-CNP 6968	46	19	10	9.0	13.7	?	8.9	?	?	?	?	4.6	1.6
	LJAMM-CNP 7670	55	23	11	11.3	?	10.5	8.6	5.8	4.2	4.9	4.6	4.5	1.8
	LJAMM-CNP 7674	51	23	10	9.9	11.9	11.8	8.3	6.3	4.1	4.8	4.7	4.5	1.6
	LJAMM-CNP 7804	52	21	12	10.2	12.1	9.8	10.1	6.1	2.9	3.6	4.7	5.3	2.3
	LJAMM-CNP 8713	56	25	9	10.5	?	?	10.6	?	?	?	?	4.8	2.2
	LJAMM-CNP 10493	53	22	11	10.4	14.4	11.7	8.7	?	3.7	4.6	4.5	4.5	2.0
	LJAMM-CNP 10496	51	23	9	9.4	12.9	12.5	9.9	5.5	4.0	4.8	5.1	4.4	1.8
	LJAMM-CNP 10523	58	23	?	10.3	14.5	14.5	12.4	6.7	4.8	6.0	5.9	5.8	1.8
	LJAMM-CNP 10526	65	28	12	12.0	16.8	14.3	10.8	6.3	4.9	6.1	5.5	5.2	1.9
	LJAMM-CNP 10576	51	18	9	10.1	12.7	13.2	10.8	6.1	4.5	5.8	5.3	4.6	1.8
	LJAMM-CNP 10577	42	17	9	8.3	11.8	10.6	8.5	4.9	3.7	4.2	4.2	4.1	1.2
	LJAMM-CNP 10578	47	17	9	9.5	14.2	14.1	9.2	6.7	4.8	6.0	5.5	4.4	2.2
	LJAMM-CNP 10579	53	20	?	10.4	13.1	13.4	9.9	6.4	4.1	5.3	5.3	4.1	2.0
LJAMM-CNP 10584	60	24	9	11.4	14.7	16.1	10.4	7.8	5.0	6.6	6.5	5.1	2.3	
LJAMM-CNP 13948	44	20	10	8.9	12.8	10.7	8.2	5.5	3.2	4.3	4.4	4.1	1.7	
LJAMM-CNP 14551	52	24	9	9.9	12.8	12.0	10.0	?	3.9	5.0	4.7	4.8	1.5	
<i>Homonota septentrionalis</i>	MNHNP 12238	60	26	11	10.8	14.1	14.8	13.3	7.9	4.6	6.6	5.1	5.5	2.5
	MNHNP 11860	51	23	10	9.4	13.1	12.9	9.7	6.8	4.9	5.8	4.6	4.6	1.9
	MNHNP 11850	53	25	9	9.8	12.2	13.3	10.6	7.9	4.7	5.9	4.5	5.1	2.5
	MNHNP 11855	58	28	11	11.1	13.6	13.7	11.2	8.4	4.6	6.4	5.6	5.3	2.3
	MNHNP 2821	61	28	12	9.9	14.6	14.4	11	7.7	4.5	5.9	5.3	4.8	2.4
	MNHNP 11872	48	20	9	8.4	11.8	11.5	8.9	6.4	4.5	4.9	3.8	3.8	1.9
	MNHNP 9038	51	23	9	9.8	13.1	13.1	10.2	7.1	4.3	5.1	4.9	4.4	2.0
	MNHNP 11423	45	19	9	9.1	11.6	11.6	9.0	6.4	3.4	4.5	4.0	4.0	1.6
	MNHNP 9037	65	28	12	11.3	15.0	17.3	12.4	8.6	5.8	6.8	6.0	5.2	2.5
	MNHNP 11421	45	17	9	8.1	11.0	10.9	9.2	6.7	3.7	5.0	3.9	3.8	1.7
	MNHNP 9131	41	20	9	8.4	11.8	11.4	9.5	6.4	3.9	3.6	4.4	4.2	1.4
	MNHNP 11410	39	15	8	7.2	10.2	10.7	8.1	5.8	3.7	4.4	3.6	3.7	1.7
	<i>Homonota</i> sp. nov.	SMF 101441	56	25	11	9.6	13.3	13.6	10.8	8.3	4.2	5.9	4.7	4.6
MNHNP 7832		59	24	11	10.2	14.0	13.5	11.2	7.4	4.5	6.1	5.0	5.4	1.7
MNHNP 2810		53	23	8	9.3	12.7	12.7	10.5	6.7	4.5	5.7	4.3	4.9	1.5
MNHNP 9726		51	23	10	9.8	12.4	12.9	10.3	7.4	4.2	5.2	4.4	5.1	1.8
SMF 101438		45	21	9	8.3	11.4	11.4	9.8	6.9	4.0	5.3	3.9	5.1	1.6
MNHNP 10534		56	26	11	10.1	13.7	13.8	11.2	7.6	4.6	5.8	4.8	5.3	2.1
MNHNP 2795		52	23	9	9.4	11.7	13.1	10.8	6.9	4.6	5.6	4.4	4.8	1.6
MNHNP 11791		54	22	8	8.8	13.3	12.8	10.1	6.9	4.1	5.7	4.7	5.2	1.6
SMF 101442		57	25	9	9.1	12.9	13.1	10.5	8.0	4.4	5.9	4.1	4.7	2.1
MNHNP 10744		53	24	11	9.8	13.4	13.1	10.5	6.9	5.1	6.0	4.6	5.8	1.7
MNHNP 2798		56	27	10	8.7	12.8	12.5	11.0	7.5	4.3	5.6	4.3	5.0	1.9
MNHNP 11790	50	23	8	10.1	11.7	12.1	10.1	6.8	3.8	4.9	4.1	4.5	1.6	
MNHNP 11793	45	20	7	8.3	11.2	11.1	9.1	6.0	4.1	5.1	3.9	4.4	1.4	

Table S2

Raw meristic data used for statistical analyses. See Materials and Methods section for explanation of the characters. Missing data indicated with “?”.

	Voucher	DT	TVS	LVS	4TL	3FL	IL	SL	Sex
<i>Homonota horrida</i>	LJAMM-CNP 6520	30	43	19	19	16	7	9	F
	LJAMM-CNP 6530	28	45	15	20	14	7	9	F
	LJAMM-CNP 6532	33	48	16	18	13	6	7	M
	LJAMM-CNP 6533	31	36	15	19	14	7	8	F
	LJAMM-CNP 6535	34	44	18	21	17	7	8	M
	LJAMM-CNP 6967	34	42	17	16	15	7	9	M
	LJAMM-CNP 6968	30	42	18	17	15	8	8	M
	LJAMM-CNP 7670	35	47	14	20	14	6	8	F
	LJAMM-CNP 7674	35	40	13	20	14	6	8	F
	LJAMM-CNP 7804	34	43	17	20	16	7	8	F
	LJAMM-CNP 8713	32	48	17	20	16	6	8	M
	LJAMM-CNP 10493	32	39	14	17	14	6	8	M
	LJAMM-CNP 10496	33	39	16	18	15	6	8	F
	LJAMM-CNP 10523	32	41	15	19	14	6	8	F
	LJAMM-CNP 10526	34	39	13	21	16	6	8	F
	LJAMM-CNP 10576	33	46	20	22	17	7	8	M
	LJAMM-CNP 10577	34	42	16	20	16	7	7	F
	LJAMM-CNP 10578	36	42	19	21	15	7	9	F
LJAMM-CNP 10579	37	42	15	?	16	7	8	F	
LJAMM-CNP 10584	33	43	16	20	15	6	9	M	
LJAMM-CNP 13948	29	42	14	18	14	6	8	M	
LJAMM-CNP 14551	36	45	16	21	14	8	9	M	
<i>Homonota septentrionalis</i>	MNHNP 12238	32	42	19	17	13	6	9	F
	MNHNP 11860	31	37	19	18	12	7	7	F
	MNHNP 11850	31	39	18	18	12	7	6	M
	MNHNP 11855	28	43	17	16	12	6	8	F
	MNHNP 2821	29	42	17	20	14	6	8	F
	MNHNP 11872	32	?	?	19	13	6	8	M
	MNHNP 9038	31	40	12	17	12	7	8	M
	MNHNP 11423	32	41	19	19	14	6	8	M
	MNHNP 9037	34	42	16	19	15	6	8	F
	MNHNP 11421	28	41	15	17	13	6	7	M
	MNHNP 9131	29	40	17	17	13	6	8	M
	MNHNP 11410	28	?	?	?	13	6	7	M
<i>Homonota</i> sp. nov.	SMF 101441	32	34	16	19	15	7	9	F
	MNHNP 7832	33	37	16	22	13	6	8	M
	MNHNP 2810	27	35	14	18	14	6	9	M
	MNHNP 9726	28	41	18	17	14	6	8	F
	SMF 101438	28	36	17	17	13	7	7	M
	MNHNP 10534	28	40	17	20	14	5	7	F
	MNHNP 2795	35	40	16	19	16	6	7	F
	MNHNP 11791	31	43	18	18	13	5	8	M
	SMF 101442	30	37	14	18	16	6	3	F
	MNHNP 10744	32	40	14	18	14	6	7	M
	MNHNP 2798	29	43	16	17	11	5	7	F
	MNHNP 11790	30	43	15	17	15	6	6	M
MNHNP 11793	32	36	15	18	15	6	8	M	