
A fully marine stem amphibian from the Late Triassic of China

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Supplementary Information to accompany

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Lipin Diao¹, Ryosuke Motani^{2,*}, Da-yong Jiang^{3,4,*}, Jiaxu Hao¹, Shengyu Wang¹.

¹ Geological Museum of Guizhou, Guiyang 550008, China.

² Department of Earth and Planetary Sciences, University of California, Davis, California, USA.

³ Laboratory of Orogenic Belt and Crustal Evolution, Ministry of Education.

⁴ Department of Geology and Geological Museum, Peking University, Yiheyuan Street 5#, Beijing 100871, China

*Corresponding authors. Email: rmotani@ucdavis.edu; djiang@pku.edu.cn

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Supplementary Table 1. Strontium isotope ratios measured from the samples collected from the holotype, paratype, and associated matrix rock.

sample No.	points	sample collected from	84Sr/88Sr	84Sr/86Sr	87Sr/86Sr	sample average
	MC	Ref. coral standard			0.7091894	0.709180
	MAD	Apatite standard			0.7117844	0.71180
1	1	holotype	0.006756544	0.05715335	0.7078457	0.707886725
	2	holotype	0.006770604	0.05727228	0.7078752	
	3	holotype	0.006732823	0.05695269	0.707936	
	4	holotype	0.006811784	0.05762062	0.70789	
2	1	holotype	0.006799784	0.05751911	0.7077537	0.707818525
	2	holotype	0.006761144	0.05719226	0.707809	
	3	holotype	0.006784133	0.05738672	0.7078782	
	4	holotype	0.0067709	0.05727478	0.7078332	
3	1	paratype	0.006807431	0.05758379	0.7077014	0.707786975
	2	paratype	0.006768866	0.05725757	0.707864	
	3	paratype	0.006834591	0.05781354	0.7077621	
	4	paratype	0.006774196	0.05730266	0.7078204	
4	1	matrix rock associated holotype	0.006830173	0.05777617	0.7080226	
	2	matrix rock associated holotype	0.006802366	0.05754096	0.7080371	
	3	matrix rock associated holotype	0.006742153	0.05703161	0.7086758	
	4	matrix rock associated holotype	0.006775972	0.05731769	0.708562	
	5	matrix rock associated holotype	0.006736421	0.05698313	0.7086467	0.708371913
	6	matrix rock associated holotype	0.006760833	0.05718963	0.708335	
	7	matrix rock associated holotype	0.00677978	0.0573499	0.7085939	
	8	matrix rock associated holotype	0.006788545	0.05742404	0.7081022	
5	1	matrix rock associated paratype	0.007074827	0.05984569	0.7082691	0.708642113
	2	matrix rock associated paratype	0.007032713	0.05948945	0.7080829	
	3	matrix rock associated paratype	0.007031093	0.05947574	0.7086449	
	4	matrix rock associated paratype	0.007029976	0.0594663	0.7088997	

	5	matrix rock associated paratype	0.006997067	0.05918792	0.7087904
	6	matrix rock associated paratype	0.006981755	0.05905839	0.7092431
	7	matrix rock associated paratype	0.00706964	0.05980181	0.7086315
	8	matrix rock associated paratype	0.006988533	0.05911573	0.7085753

R Script containing data to produce Fig. 4a and Table 1

```
###
### Data
###

Sratos <-
data.frame(Points=c("1","2","3","4","1","2","3","4","1","2","3","4","1","2","3","4","5","6","7","8","1",
",","2","3","4","5","6","7","8"),
SrRatio=c(0.7078457,0.7078752,0.707936,0.70789,0.7077537,0.707809,0.7078782,0.7078332
,0.7077014,0.707864,0.7077621,0.7078204,0.7080226,0.7080371,0.7086758,0.708562,0.7086
467,0.708335,0.7085939,0.7081022,0.7082691,0.7080829,0.7086449,0.7088997,0.7087904,0.
7092431,0.7086315,0.7085753),
Type=c("HB","HB","HB","HB","HB","HB","HB","HB","PB","PB","PB","PB","HM","HM","HM","HM",
"HM","HM","HM","HM","PM","PM","PM","PM","PM","PM","PM","PM"))

###
### Fig. 4a
###

xrange <- c(0.707,0.7105)

#pdf(file="Fig4_a.pdf",w=8,h=8)
boxplot(SrRatio~Type, data=Sratos,ylim=xrange,horizontal=T, range=0)
#dev.off()

###
### Table 1
###

basic <- cbind(aggregate(SrRatio~Type,Sratos, FUN=mean),
               aggregate(SrRatio~Type,Sratos, FUN=sd)[,2],
               aggregate(SrRatio~Type,Sratos, FUN=length)[,2],
               aggregate(SrRatio~Type,Sratos, FUN=quantile)[,-1])
colnames(basic) <- c("Type","Sr Ratio","sd","n","min","25%","median","75%","max")
write.csv(basic,"Table_1.csv")
```

R Script containing data to produce Fig. 4b

```
###
### Scales
###

scl <- NULL
for(i in -5:10) scl <- c(scl,seq(10^i,9*10^i,10^i))
log10scl <- log10(scl)

###
### Helper Function
###

add.ch.one <- function(x,y,series=2,xlim=range(x),ylim=range(y),main="",
                        xlab="x",ylab="y",colorfill=TRUE,fcolor=fillcolor,pcolor=pointcolor,
                        lwdv=lwd,trans=0.5){
  ch.list <- chull(x,y)
  ch.points <- cbind(x[ch.list],y[ch.list])
  if(colorfill)
  {polygon(ch.points,border=pcolor[series],col=scales::alpha(fcolor[series],trans),lwd=lwdv)
   }else{polygon(ch.points,border=pcolor[series],lwd=lwdv)}
  invisible(ch.points)
}

###
### Data
###

tomita <- data.frame(TL=c(1210, 950, NA, 680, 600, 1000, 510, 740, 750, 4740, 3900, 800, NA,
740, 400, 1190, 2250, 4810, 1060, 510, 530, 5440),
                     ML=c( 118.3, NA, NA, 57.6, 45.5, 107.8, NA, NA, 86.6, 470, NA, NA, NA, 88.2,
NA, 72.3, NA, NA, NA, 33.4, 40.3, NA),
                     MW=c(153.3, NA, NA, 82.1, 70.3, 155.2, NA, NA, 111.1, 604.8, NA, NA, NA,
151.3, NA, 130.5, NA, NA, NA, 59.6, 68.2, NA),
                     MD=c(NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA, NA,
NA, NA, NA, NA, NA, NA),
                     CL=c(75, 54, 68, 42, 35, 71, 29, 53, 49, 435, 261, 42, 48, 62, 24, 48, 94, 290,
64, 19, 22, 620),
                     a=c(17.2, 12.3, 6.1, 8.2, 7.1, 8.7, 2.8, 6.7, 4.1, 97, 45.4, 10.9, 11.2, 15.1, 6.8, 16.3,
26.2, 92.3, 16.9, 6.3, 5, 112.5),
                     b=c(8.9, 6, 4.4, 5.5, 4.1, 7.7, 2.1, 3.9, 3.8, 14.2, 23.2, 4.1, 8.5, 9.2, 5.8, 13.4, 24.7,
49.6, 11.5, 6.3, 3.4, 65.1),
                     ant=c(17.6, NA, NA, 8.4, 7.1, 20, NA, NA, NA, NA, NA, NA, NA, 20.4, NA, 16.1,
```

```

NA, NA, NA, 3.3, 4, NA),
  CrossI=c(2.224399, 0.545054, 0.047804, 0.14555, 0.069798, 0.249514,
0.002262, 0.05762, 0.013203, 635.84787, 106.51364, 0.260503, 0.585017, 1.549855, 0.089476,
2.858672, 21.659876, 1913.5352, 2.725744, 0.07778, 0.020719, 4547.6625),
  Residual=c(1.24457, 1.443427, 213.621422, 0.09742, 0.264691, 207.187742,
211.121339, 208.164557, 212.878942, 207.048135, 205.263154, 2.68286, 3.951477, 3.325251,
8.64994, 10.533895, 6.984598, 5.309011, 5.201755, 12.842878, 3.823534, 205.1542),

Feeding=c("Ram","Ram","Ram","Ram","Ram","Ram","Ram","Ram","Ram","Ram","Ram","Ram","Oppor
tunist","Opportunist",
"Suction","Suction","Suction","Suction","Suction","Suction","Suction","Suction","Ram")
)
rownames(tomita) <- c("Lamna ditropis","Isurus oxyrinchus","Mitsukurina
owstoni","Carcharhinus macroti","Prionace glauca","Cephaloscyllium
umbratile","Chlamydoselachus anguineus","Notorynchus cepedianus","Hexanchus
griseus","Cetorhinus maximus","Galeocerdo cuvier","Squalus acanthias","Triakis
semifasciata","Squatina japonica","Isistius brasiliensis","Ginglymostoma cirratum","Nebrius
ferrugineus","Rhincodon typus","Orectolobus japonicus","Chiloscyllium
plagiosum","Scyliorhinus retifer","Megachasma pelagios")
tsuction <- tomita[tomita$Feeding=="Suction",]
tram <- tomita[tomita$Feeding=="Ram",]

###
### Fig. 4b
###

pointcolor=c(2,4)
fillcolor=pointcolor

#pdf(file="Fig4b.pdf",h=4.5,w=4)
plot(log10(b)~log10(CL),tomita,type="n",axes="F")
  add.ch.one(log10(tsuction$CL),log10(tsuction$b),lwd=1,series=1)
  add.ch.one(log10(tram$CL),log10(tram$b),lwd=1,series=2)
  points(log10(b)~log10(CL),tsuction,col=2,pch=18)
  points(log10(b)~log10(CL),tram,col=4,pch=18)
  points(log10(14.563/14.019*50),log10(3.78/14.019*50),col=1,cex=2,pch=16)
  points(log10(25.3),log10(7.2),col=1,cex=2,pch=17)
  points(log10(41.1),log10(13.1),col=1,cex=2,pch=17)
  axis(1,at=log10scl,label=scl,las=3)
  axis(2,at=log10scl,label=scl,las=1)
  box()
#dev.off()

```