

ERRATUM

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Erratum to: Phylogeography of the sand dune ant *Mycetophylax simplex* along the Brazilian Atlantic Forest coast: remarkably low mtDNA diversity and shallow population structure

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Erratum

The original version of this article [1] unfortunately contained a mistake. The presentation of Tables two and three (Tables 1 and 2 here) were incorrect in the PDF and HTML versions of this article. The corrected Tables two and three (Tables 1 and 2 here) are given below.

The original article has been updated to reflect this change.

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Table 1 Genetic diversity and neutrality tests for each population and with all populations of *M. simplex* together

Populations	Nucleotide diversity (π) (\pm S.D.)	Haplotype diversity (h) (\pm S.D.)	Tajima's D	Fu's FS
RS1	0.00189 (0.00090)	0.667 (0.163)	-1.87333 ($P = 0.0083$)	-1.11562 ($P = 0.1609$)
RS2	0.00224 (0.00054)	0.889 (0.091)	-0.6299 ($P = 0.2859$)	-2.32907 ($P = 0.0261$)
RS3	0.00276 (0.00055)	0.933 (0.077)	-1.50661 ($P = 0.0632$)	-4.46904 ($P = 0.0025$)
SC4	0.00181 (0.00024)	0.818 (0.083)	0.43329 ($P = 0.6969$)	-1.02733 ($P = 0.1714$)
SC5	0.00268 (0.00036)	0.890 (0.060)	-1.09063 ($P = 0.1463$)	-2.8844 ($P = 0.0302$)
SC6	0.00336 (0.00039)	0.709 (0.099)	1.52257 ($P = 0.9504$)	1.62676 ($P = 0.8143$)
SC7	0.00387 (0.00064)	0.709 (0.137)	1.49895 ($P = 0.9408$)	0.7727 ($P = 0.6626$)
SC8	0.00346 (0.00042)	0.873 (0.089)	1.00501 ($P = 0.8566$)	-1.68615 ($P = 0.1229$)
SC9	0.00368 (0.00059)	0.833 (0.098)	0.92757 ($P = 0.8263$)	0.12678 ($P = 0.4978$)
NE10	0.00339 (0.00038)	0.697 (0.090)	1.68302 ($P = 0.9613$)	1.85074 ($P = 0.8387$)
All populations	0.00346 (0.00019)	0.865 (0.022)	-1.47062 ($P = 0.0422$)	-21.59803 ($P = 0.0001$)

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Cardoso et al. *BMC Evolutionary Biology* 2015 **15**:106 doi:10.1186/s12862-015-0383-4**Table 2** - Φ_{ST} values for pairwise comparisons between population of *M. simplex* (lower left) and p values (upper right)

	RS1	RS2	RS3	SC4	SC5	SC6	SC7	SC8	PR9	NE10
RS1	-	0.54618	0.01228	0.04633	0.18008	0.01792	0.01594	0.04841	0.08653	0.0492
RS2	0.01856 ^a	-	0.01683	0.00515	0.0302	0.02624	0.01465	0.04742	0.09554	0.0592
RS3	0.11411	0.13078	-	0.27888	0.02287	0.00386	0.00337	0.00485	0.01297	0.00941
SC4	0.09502	0.1619	0.01451 ^b	-	0.08455	0.00356	0.00297	0.00752	0.01733	0.01129
SC5	0.02839	0.093	0.10675^b	0.07119 ^b	-	0.00069	0.0004	0.00168	0.00713	0.00614
SC6	0.27381	0.24143	0.34481	0.34975	0.30795	-	0.78299	0.92516	0.6338	0.83912
SC7	0.29673	0.27747	0.36158	0.35894	0.32158	0.05903 ^c	-	0.59489	0.43421	0.47352
SC8	0.19818	0.17864	0.28682	0.26863	0.24282	0.06991 ^c	0.03956 ^c	-	0.93931	0.77794
PR9	0.13621	0.12338	0.23448	0.21937	0.1883	0.06591 ^c	0.0298 ^c	0.08068 ^c	-	0.94852
NE10	0.18098	0.16623	0.27856	0.27675	0.23074	0.07182 ^c	0.03535 ^c	0.06859 ^c	0.0855 ^c	-

Population names are given in the Table 1. The colors show the shallow phylogeographic structure found: southern populations (^a), central-eastern population (^b) and northern populations (^c)Bold values are significant at $P < 0.05$

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