

Ecography

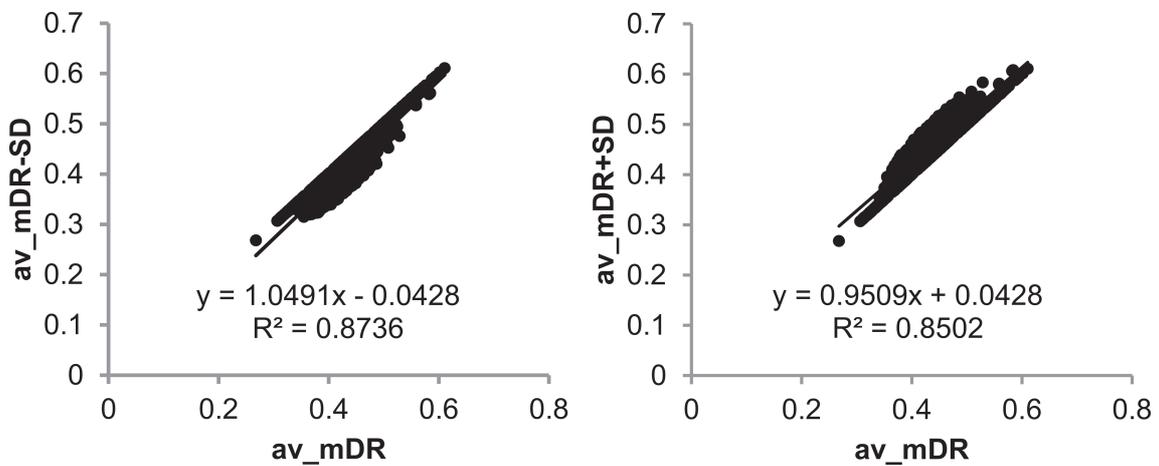
**ECOG-04102**

Maestri, R., Upham, N. S. and Patterson, B. D.  
2018. Tracing the diversification history of a Neogene  
rodent invasion into South America. – Ecography doi:  
10.1111/ecog.04102

**Supplementary material**

## Appendix 1. Analyses with mDR+SD and mDR-SD.

A randomization procedure was used to sample a maximum of 10 species for each assemblage in order to calculate the mDR metric to minimize species richness effects (see main text). The procedure was repeated 10,000 times, and the average of the randomization was used in the main text as the mDR metric. Below, the analyses in the main text were repeated after adding and subtracting the SD values obtained in the randomizations. The relationship between the average mDR (av\_mDR) of the 10,000 randomizations with the av\_mDR-SD and the av\_mDR+SD is shown in fig. S1.



**Figure A1.** Relationship between the average mDR of 10,000 randomizations (av\_mDR) with av\_mDR after subtracting standard deviation values (av\_mDR-SD) and adding standard deviation values (av\_mDR+SD). The coefficient of determination is shown for both scatterplots.

A Generalized Least Square procedure including an exponential autocorrelation structure as the covariance matrix was used to investigate the relationship between MPD and mDR. The relationship between MPD and mDR-SD was negative and significant (GLS:  $b \pm SE = -2.70 \pm 0.66$ ,  $t = -4.09$ ,  $P = 0.001$ ) and that between MPD and mDR+SD was also negative and significant (GLS:  $b \pm SE = -0.84 \pm 0.65$ ,  $t = -1.28$ ,  $P = 0.001$ ).

After conducting ANOVAs to test for differences in mDR among bioregions (see main text), significant differences in values of mDR-SD ( $R^2 = 0.39$ ;  $F = 106.1$ ;

$P < 0.001$ ) and mDR+SD ( $R^2 = 0.50$ ;  $F = 165.5$ ;  $P < 0.001$ ) were found. Lower values of mDR-SD and mDR+SD were found in the bioregions of Central America and northern South America (C, B, I and J), intermediate to low values were found in Amazonia and eastern South America (A and D, respectively), and higher values of mDR-SD and mDR+SD were found in southern and western South America (F, H, G and E).

**Appendix 2.** The average decimal latitude and longitude of the posterior distribution for all ancestors, with the 90% confidence interval (CI). Asterisks denote major tribes of the Oryzomyia, which diversified after sigmodontines colonized South America.

Tribe	Mean latitude	Lower 90% CI	Upper 90% CI	Mean longitude	Lower 90% CI	Upper 90% CI
Abrotrichini*	-35.37	-36.76	-34.01	-65.61	-67.33	-63.79
Akodontini*	-17.93	-20.66	-15.35	-60.76	-62.61	-58.71
Oryzomyini*	-14.65	-16.60	-12.69	-64.42	-66.01	62.58
Phyllotini*	-25.08	-27.29	-22.83	-62.51	-64.43	-60.57
Thomasomyini*	-10.75	-12.69	-8.72	-64.63	-65.88	-63.22
Sigmodontini	13.27	12.14	14.51	-83.53	-84.54	-82.49
Ichthyomyini	6.16	4.73	7.46	-80.45	-81.82	-79.98