Erratum

Corrigendum to "The quality of the fossil record of anomodonts (Synapsida, Therapsida)" [C. R. Palevol 12 (7–8) (2013) 495–504; doi:10.1016/j.crpv.2013.07.007]

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Concerning the article by Walther and Fröbisch (2013), the authors would like to point out some mistakes and replace Figs. 2 and 3, Table 1 and the online Supplementary data of the article with the figures, table and linked online Appendix below. Part of the source data, figured diversity and completeness curves, and correlations in the original contribution did not represent what was described in the text. However, the results of the new and originally intended analyses reflect the same signal as presented in the original paper or even strengthen the signals (note the increased mean completeness at the regional scale in South Africa in Fig. 2D), and therefore, the main conclusions presented therein are correct and valid. Moreover, in contrast to the original contribution, the new analyses reveal a statistically significant strong positive correlation between some of the residual diversity estimates (based on outcrop area and number of farms) and the phylogenetic diversity estimates (see below). This indicates that the two divergent methods for correction of the biased raw diversity signal of anomodonts converge on the same potentially biological diversity signal.

In detail, the original contribution included some mistakes, which necessitate the following comments for clarification and correction:

Figure 2: the previous global taxic diversity estimate (TDE) illustrated in Fig. 2A and used for correlation in the original contribution does not represent the total taxic diversity of anomodonts, but anomodont TDE based only on the taxa included in the phylogeny in Kammerer et al.

(2011). The phylogenetic diversity estimate (PDE) in Fig. 2A is correct. The completeness curve based on a Character Completeness Metric (CCM2) displayed in Fig. 2B is correct. The previous TDE and PDE illustrated in Fig. 2C and the completeness curve in Fig. 2D that were also used for correlation tests do not represent the respective scores at the regional (local) scale of the South African Karoo Basin, but instead are based on the same global taxa used in Fig. 2A and B but using different time bins, namely the South African assemblage zones rather than the international marine stages.

Figure 3: the residual diversity estimates (RDE) illustrated in Fig. 3 and used for correlation are misleading as the source TDE to calculate the RDEs was not collected at the regional scale of the South African Karoo Basin (see above). Although it is entirely valid to calculate the RDE for a global TDE based on a regional proxy (Smith and McGowan, 2007), this was not the intention in our original publication. Hence, the corrected RDE curves are presented here and the results are consistent with the previously obtained RDE values. Therefore, the previously presented results and conclusions are also still correct and valid.

Table 1: the correlation table in Table 1 of the original contribution is misleading at the global scale as the TDE values do not reflect the total global taxic diversity of anomodonts (see above) but instead only of those taxa included in the phylogeny. However, the results and conclusions are correct and valid. The correlation tests at the "local" scale are incorrect, as they do not reflect the regional (local) South African diversity and completeness estimates (see above). However, the correct correlation values are recorded here in the corrected Table 1 and the results and conclusions are consistent with the previous ones and are therefore, also still valid (see below).
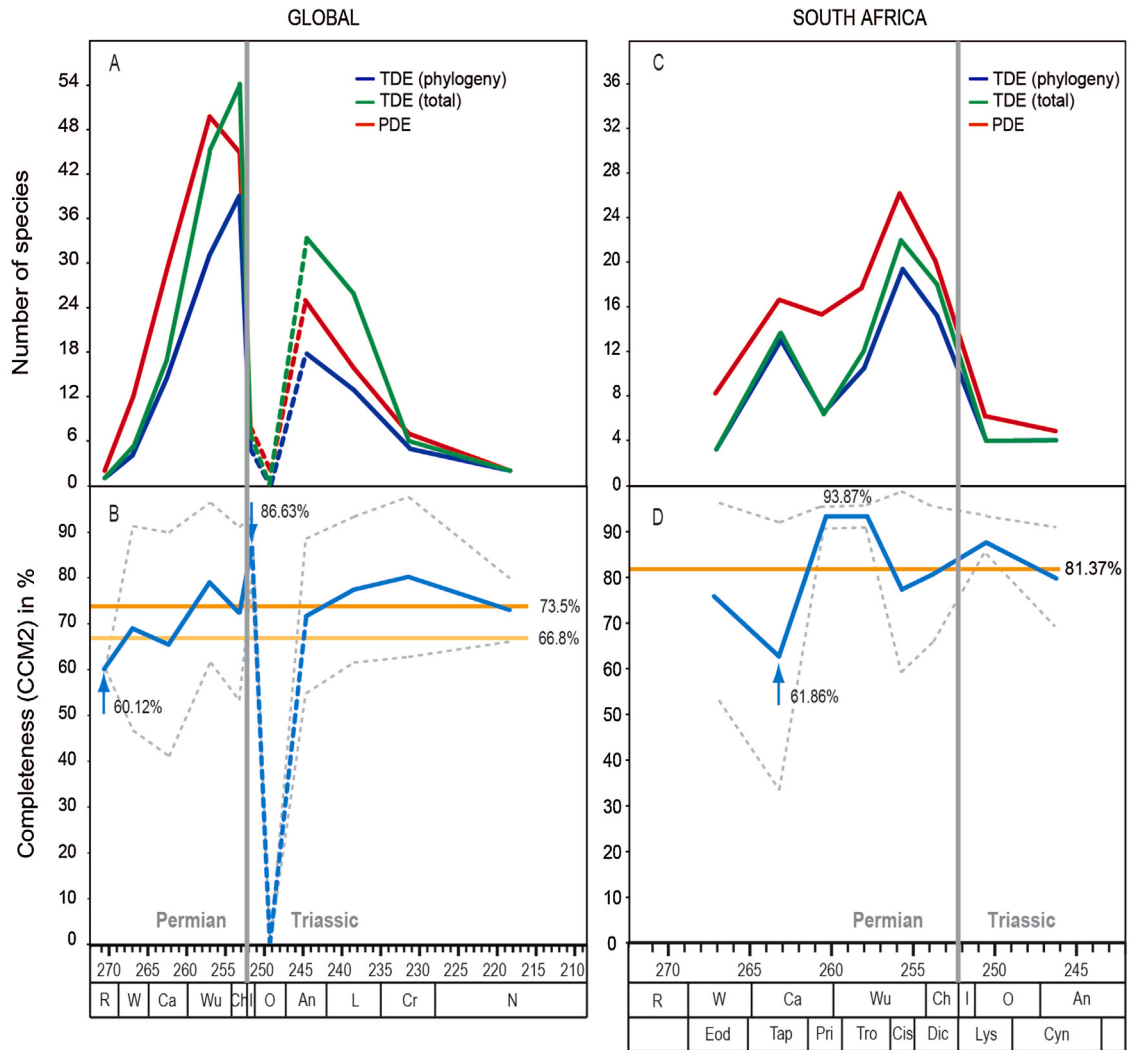
Fig. 2. A. Taxic (blue and green) and phylogenetic (red) diversity estimates and B. Character Completeness Metric (CCM2) of anomodonts at the global scale. Dark-orange line represents the mean CCM2 score, excluding the Olenekian stage, whereas the light-orange line represents the mean CCM2 score including the Olenekian stage. Dotted lines indicate the artificial decline in anomodont richness and completeness caused by a gap in their fossil record in the late Early Triassic (Olenekian). C. Taxic (blue and green) and phylogenetic (red) diversity estimates and D. Character Completeness Metric (CCM2) of anomodonts at the regional scale of the South African Karoo Basin. The dark-orange line indicates the mean CCM2 score for all assemblage zones. Abbreviations: PDE: phylogenetic diversity estimate; TDE (total): taxic diversity estimate including all valid anomodont taxa; TDE (phylogeny): taxic diversity estimate based on the taxa included in the phylogeny.

Highlighting of divergent results and conclusions: For the exact course of the corrected and here presented diversity and completeness curves, the reader is referred to the replacement Figs. 2 and 3. For the here presented diversity curves and correlations, we introduced the distinction between TDE (total), including all valid taxa at the global and regional scales respectively, and a TDE (phylogeny), including all taxa that were included in the phylogeny by Kammerer et al. (2011) at the global and regional scales, respectively. The newly calculated Character Completeness Metric (CCM2) of anomodonts at the regional scale of the South African Karoo Basin in the here presented Fig. 2D indicates an even higher mean completeness of 81.37%. The new correlation tests (Table 1) indicate an even stronger

and statistically significant positive correlation of the different sampling proxies with TDE (total) and TDE (phylogeny) at the regional scale of South Africa. Therefore, we added an RDE curve for South African anomodonts based on the number of specimens in Fig. 3. We further added correlation tests of all three RDEs (outcrop area, number of farms, number of specimens) with the regional and global PDEs, once including and once excluding the *Lystrosaurus* Assemblage Zone. Overall, all main conclusions of the original contribution are correct and valid. However, in contrast to the original contribution, the updated correlation tests reveal a statistically significant strong positive correlation between the RDEs (based on outcrop area and number of farms) and the global PDE when including the *Lystrosaurus* Assemblage
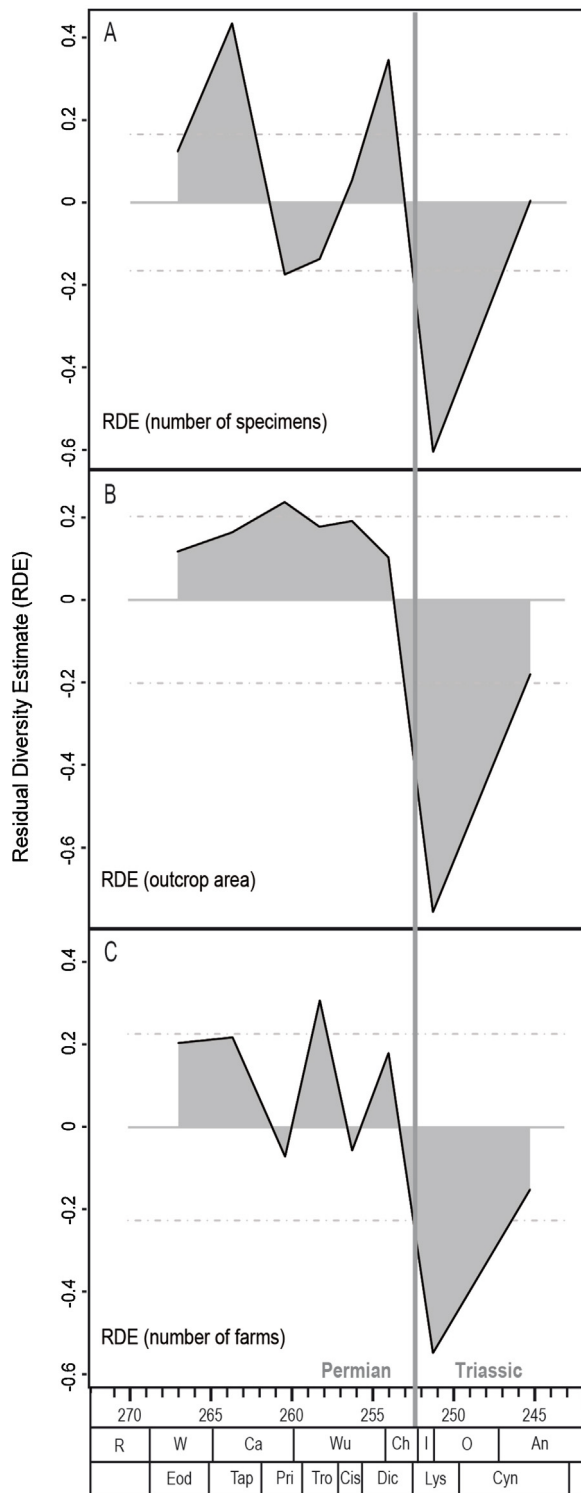
Fig. 3. Residual diversity estimates (RDEs) for South African anomodonts based on (A) number of specimens, (B) outcrop area, and (C) number of farms (localities), with dashed-dotted line indicating 1.96 standard deviations (95% confidence intervals) of the model.

Table 1

Pearson's product moment correlation coefficients and probability values (*P*) of the statistical comparisons of time series, comparing completeness (CCM2), biodiversity estimates, and sampling proxies after generalized differencing.

A) Global		*P*
Including Olenekian time bin		
TDE (total) vs mean CCM2	0.690	**0.027**
TDE (total) vs PDE	0.968	**4.52E-006**
TDE (total) vs TDE (phylogeny)	0.994	**4.74E-009**
PDE vs mean CCM2	0.598	0.068
TDE (phylogeny) vs mean CCM2	0.698	**0.025**
Without Olenekian time bin		
TDE (total) vs mean CCM2	0.346	0.362
TDE (total) vs PDE	0.972	**1.19E-05**
TDE (total) vs TDE (phylogeny)	0.992	**1.48E-07**
PDE vs mean CCM2	0.461	0.212
TDE (phylogeny) vs mean CCM2	0.362	0.338

A) Regional		*P*
TDE (total) vs mean CCM2	−0.243	0.599
Outcrop area (km²) vs mean CCM2	−0.295	0.521
Number of specimens (n) vs mean CCM2		
Number of farms (n) (localities) vs mean CCM2	−0.064	0.892
Outcrop area (km²) vs TDE (total)	0.889	**0.007**
Number of specimens (n) vs TDE (total)	0.472	0.285
Number of farms (n) (localities) vs TDE (total)	0.843	**0.017**
Outcrop area (km²) vs number of specimens (n)	0.538	0.213
TDE (phylogeny) vs mean CCM2	−0.271	0.556
Outcrop area (km²) vs TDE (phylogeny)	0.860	**0.013**
Number of specimens (n) vs TDE (phylogeny)	0.447	0.315
Number of farms (n) (localities) vs TDE (phylogeny)	0.859	**0.013**
RDE (outcrop area) vs mean CCM2	0.173	0.710
RDE (specimens) vs mean CCM2	0.292	0.525
RDE (number of farms) vs mean CCM2	−0.694	0.084
RDE (outcrop area) vs PDE (global)	0.943	**0.001**
RDE (specimens) vs PDE (global)	0.653	0.112
RDE (number of farms) vs PDE (global)	0.831	**0.021**
RDE (outcrop area) vs PDE (regional)	0.619	0.138
RDE (specimens) vs PDE (regional)	0.359	0.429
RDE (number of farms) vs PDE (regional)	0.349	0.443
Without Lystrosaurus Assemblage Zone		
Outcrop area (km²) vs TDE (total)	0.967	**0.002**
Number of specimens (n) vs TDE (total)	0.891	**0.017**
Number of farms (n) (localities) vs TDE (total)	0.862	**0.027**
Outcrop area (km²) vs TDE (phylogeny)	0.958	**0.003**
Number of specimens (n) vs TDE (phylogeny)	0.867	**0.026**
Number of farms (n) (localities) vs TDE (phylogeny)	0.888	**0.018**
RDE (outcrop area) vs mean CCM2	0.759	0.080
RDE (specimens) vs mean CCM2	−0.097	0.855
RDE (number of farms) vs mean CCM2	−0.928	**0.008**
RDE (outcrop area) vs PDE (global)	0.341	0.508
RDE (specimens) vs PDE (global)	0.254	0.628
RDE (number of farms) vs PDE (global)	0.785	0.065
RDE (outcrop area) vs PDE (regional)	0.578	0.229
RDE (specimens) vs PDE (regional)	0.139	0.793
RDE (number of farms) vs PDE (regional)	0.698	0.123

Bold font indicates statistically significant correlations; PDE: phylogenetic diversity estimate; RDE: residual diversity estimate; TDE: taxic diversity estimate.

Zone, indicating that the two divergent methods for correction (residual diversity estimates and phylogenetic diversity estimates) of the biased raw diversity converge on the same potentially biological diversity signal for anomodonts.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at http://dx.doi.org/10.1016/j.crpv.2013.10.006.

References

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