Appendix S4: Results of the biogeographic cluster analyses conducted on middle and late Miocene Asian carnivoran faunas

In this appendix, we report the extended results of the biogeographic cluster analyses conducted on middle and late Miocene Asian Carnivora faunas. In the literature, clusters of fossil localities are based on two main families of methods, by ordination or by agglomeration (Dommergues et al., 2009). In this study, we use these two approaches, a non-metric multidimensional scaling ordination (NMDS) and a hierarchical agglomerative cluster algorithm (UPGMA), as well as an intermediate approach, for which the results are presented in the main paper section, hierarchical clustering on principle components (HCPC).

We present the results of ordinations (NMDS) and agglomerations (UPGMA) directly calculated on the Simpson (**Figures S1 to S16**) and Raup&Crick (**Figures S17 to S32**) dissimilarity matrices, as well as ANOSIM results to test if clusters illustrated in the main section of this manuscript by HCPC methods are composed of significantly different faunas (**Table S1**). Finally, we show the HCPC tree, excluded from the main manuscript, computed on late Miocene genera (**Figures S33 and S34**).

Analysis for genera of the middle Miocene (Simpson dissimilarity)



Figure S1. Eigenvalues computed with PCoA to choose the number of principal axes for NMDS, for genera of the middle Miocene – Simpson dissimilarity. The first four axes are selected.



Figure S2. Stressplot of NMDS on 4 PC axes for genera of the middle Miocene – Simpson dissimilarity.



Figure S3. NMDS plot on 4 PC axes for genera of the middle Miocene – Simpson dissimilarity.

UPGMA on dissim. matrix with Simpson index



Figure S4. UPGMA for genera of the middle Miocene – Simpson dissimilarity. The framed localities are not in the same clusters between the ordination by NMDS and the UPGMA agglomeration.

Analysis for genera of the late Miocene (Simpson dissimilarity)



Figure S5. Eigenvalues computed with PCoA to choose the number of principal axes for NMDS, for genera of the late Miocene – Simpson dissimilarity. The first four axes are selected.



Figure S6. Stressplot of NMDS on 4 PC axes for genera of the late Miocene – Simpson dissimilarity.





Figure S7. NMDS plot on 4 PC axes for genera of the late Miocene – Simpson dissimilarity.

UPGMA on Simpson dissim. matrix



Figure S8. UPGMA for genera of the late Miocene – Simpson dissimilarity.

Analysis for species of the middle Miocene (Simpson dissimilarity)



Figure S9. Eigenvalues computed with PCoA to choose the number of principal axes for NMDS, for species of the middle Miocene - Simpson dissimilarity. The first four axes are selected.

Eigenvalues



Figure S10. Stressplot of NMDS on 4 PC axes for species of the middle Miocene – Simpson dissimilarity.



Figure S11. Stressplot of NMDS on 4 PC axes, for species of the middle Miocene – Simpson dissimilarity.

UPGMA on dissim. matrix Simpson



Figure S12. UPGMA for species of the middle Miocene – Simpson dissimilarity.



Analysis for species of the late Miocene (Simpson dissimilarity)

Figure S13. Eigenvalues computed with PCoA to choose the number of principal axes for NMDS, for species of the late Miocene – Simpson dissimilarity. The first three axes are selected.

Index



Figure S14. Stressplot of NMDS on 3 PC axes for species of the late Miocene – Simpson dissimilarity.



Figure S15. NMDS on 3 PC axes for species of the late Miocene – Simpson dissimilarity.



UPGMA on dissim. matrix Simpson

Figure S16. UPGMA for species of the late Miocene – Simpson dissimilarity.

Analysis for genera of the middle Miocene (Raup&Crick dissimilarity)



Figure S17. Eigenvalues computed with PCoA to choose the number of principal axes for NMDS, for species of the middle Miocene - Raup&Crick dissimilarity. The first four axes are selected.



Figure S18. Stressplot of NMDS on 4 PC axes for genera of the middle Miocene – Raup&Crick dissimilarity.



Figure S19. NMDS on 4 PC axes for genera of the middle Miocene – Raup&Crick dissimilarity.



UPGMA on dissim. matrix. Raup&Crick Figure S20. UPGMA for genera of the middle Milocene – Raup&Crick dissimilarity.

Analysis for genera of the late Miocene (Raup&Crick dissimilarity)



Figure S21. Eigenvalues computed with PCoA to choose the number of principal axes for NMDS, for genera of the late Miocene – Raup&Crick dissimilarity. The first three axes are selected.



Figure S22. Stressplot of NMDS on 3 PC axes for genera of the late Miocene – Raup&Crick dissimilarity.



Figure S23. NMDS on 3 PC axes for genera of the late Miocene - Raup&Crick dissimilarity.

UPGMA on dissim. matrix. Raup&Crick



Figure S24. UPGMA for genera of the late Miocene – Raup&Crick dissimilarity.

Analysis for species of the middle Miocene (Raup&Crick dissimilarity)



Figure S25. Eigenvalues computed with PCoA to choose the number of principal axes for NMDS, for species of the middle Miocene – Raup&Crick dissimilarity. The first two axes are selected.



Figure S26. Stressplot of NMDS on 2 PC axes for species of the middle Miocene – Raup&Crick dissimilarity.



Figure S27. NMDS on 2 PC axes for species of the middle Miocene – Raup&Crick dissimilarity.

UPGMA on dissim. matrix Raup&Crick



Figure S28. UPGMA for species of the middle Miocene – Raup&Crick dissimilarity.

Analysis for species of the late Miocene (Raup&Crick dissimilarity)



Figure S29. Eigenvalues computed with PCoA to choose the number of principal axes for NMDS, for species of the late Miocene – Raup&Crick dissimilarity. The first three axes are selected.



Figure S30. Stressplot of NMDS on 3 PC axes for species of the late Miocene – Raup&Crick dissimilarity.



Figure S31. NMDS on 3 PC axes for species of the late Miocene – Raup&Crick dissimilarity.

UPGMA on dissim. matrix. Raup&Crick



Figure S32. UPGMA for species of the late Miocene – Raup&Crick dissimilarity.

Analysis of Similarity (ANOSIM) of clusters computed by HCPC results and illustrated in the main manuscript (except for late Miocene genera, illustrated in the next pages)

	Simpson		Raup&Crick	
	P-value	R	P-value	R
Middle Miocene GENERA	0.0001	0.64	9.10-5	0.64
Middle Miocene SPECIES	0.003	0.72	0.003	0.71
Late Miocene GENERA	9.10-5	0.37	9.10-5	0.46
Late Miocene SPECIES	9.10-5	0.57	9.10-5	0.65

Table S1. P-value and R value of ANOSIM analysis computed on the clusters calculated by HCPC.

Hierarchical clustering on principal components for late Miocene genera (HCPC), Simpson dissimilarity



Figure S33. Hierarchical clustering computed on NMDS on Simpson dissimilarity matrix from late Miocene genera.





Figure S34. Hierarchical clustering computed on NMDS on Raup&Crick dissimilarity matrix from late Miocene genera.

References

Dommergues, J.L., E. Fara, and C. Meister. 2009. Ammonite diversity and its palaeobiogeographical structure of the early Pliensbachian (Jurassic) in the western Tethys and adjacent areas. Palaeogeography, Palaeoclimatology, Palaeoecology 280 (1-2): 64–77.