

Fourier analysis applied to *Mimomys* (Arvicolidae, Rodentia, Mammalia) first lower molars



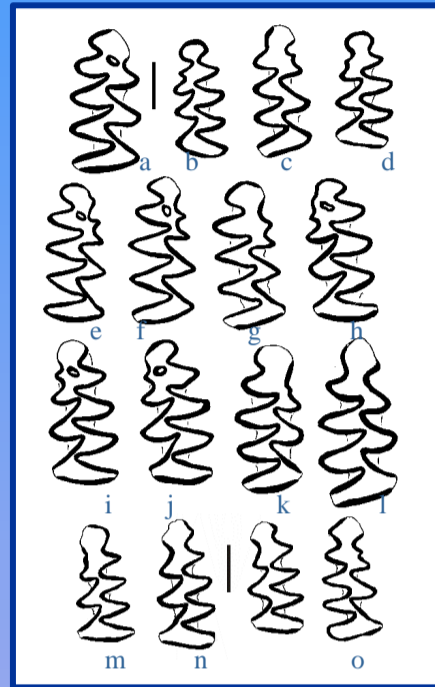
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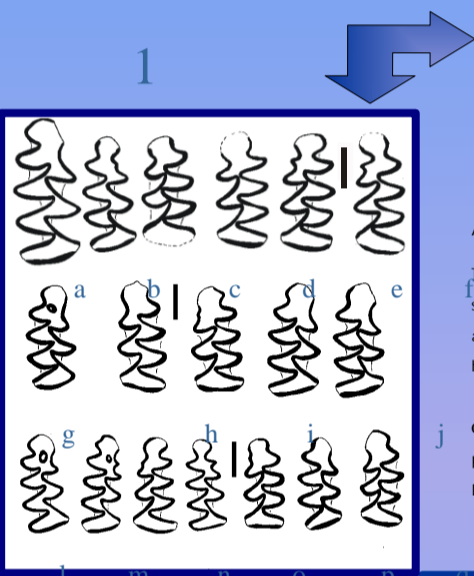
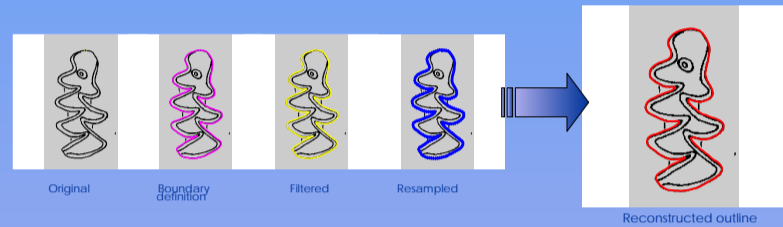
Material

The material used in this study comes from different collections of Central and Western Europe: the various *Mimomys* from Casa Sgheri (Fig. 1 a-f) are stored at the University of Pisa; Hungarian Museum of Natural History: *M. pusillus* from Püspökfürdő (Fig. 1p-r), *M. coelodus* from Kislang (Holotype; Fig. 1g), *M. savini* from Villány 6 (Fig. 2k-l) (Mehely 1914, Kretzoi, 1956; 1959); Université de Dijon (France): *M. ostramosensis* and *M. pitymyoides* from Montoussé 5 (Fig. 2 h-j and m-p respectively) (Clot et al., 1976a; 1976b); Université de Sciences et Technique de Languedoc (France): *M. medasensis* from Islas Medas (Fig. 2 e-g) (Michaux, 1970); Wien Universität (Austria): *M. coelodus* and *M. pusillus* from Deutsch-Altenburg 2 (Fig. 1h-k and Fig. 1l-o, respectively) (Rabeder 1981); Institute of Geology and Paleontology of Siena (Italy): *M. savini* from Montagnola Senese (Fig. 2 a-d) (Fondi, 1972).



Methods

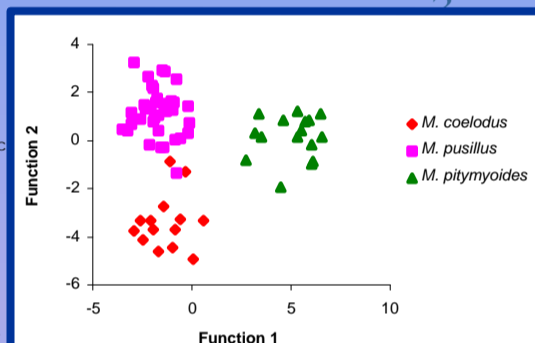
A decomposition of the first lower molar external contour in a Fourier series has been carried out. Such an attempt has proven to be successful with murine rodents (Renaud et al., 1996; 2002). A Fourier decomposition by means of a matrix of complex numbers (cfr. Gonzalez & Woods, 1992) has been used with arvicoline molars due to their peculiar, non-holomorph shape. Such a method, composes the polar coordinates of the points of the tooth outline in a Fourier series, where the higher the rank of the harmonics of the Fourier series, the more detailed is the description of the contour. A reconstruction of the original outline corresponding to any set of Fourier harmonic can be obtained using the inverse Fourier transform (red outline in Fig. 3). The used program, CDFT developed by C.H. Dommergues at the Université de Belfort-Montbelliard (Dommergues, 2000), feedbacks also a fit index to the original outline. Using 20 harmonics with *Mimomys* the fit index is never less than 98.5%.



Analyses

The Fast Fourier Transform has been tested on several populations of *Mimomys* coming from different sites of Central and Western Europe (Marcolini, 2001) and it has proven here to resolve the problematic attribution of the small sized *Mimomys* from Casa Sgheri (Lower Valdarno, Central Italy). Moreover it has been applied to the *Mimomys* from Montagnola Senese.

Canonical Discriminant Analysis has been applied to three different species of small size *Mimomys*, *M. coelodus*, *M. pusillus* and *M. pitymyoides* from Montoussé 5, *M. pusillus* from the type population of Püspökfürdő and from Deutsch-Altenburg 2, the holotype of *M. coelodus* and *M. coelodus* from Deutsch-Altenburg 2 (Fig. 4).

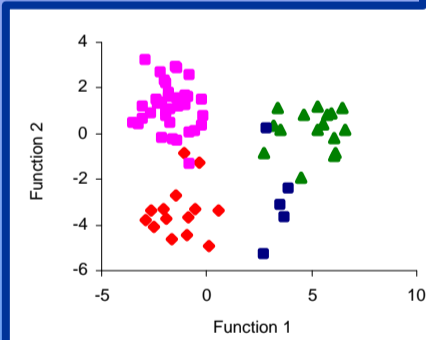


Classification Results^a

Original	Count	Predicted Group Membership			Total
		<i>M. coelodus</i>	<i>M. pusillus</i>	<i>M. pitymyoides</i>	
<i>M. coelodus</i>	13	13	1	0	14
<i>M. pusillus</i>	1	0	53	0	54
<i>M. pitymyoides</i>	0	0	0	16	16
%		92,9	7,1	,0	100,0
		2,6	97,4	,0	100,0
		,0	,0	100,0	100,0
Casa Sgheri	4	4	0	0	100,0

^a. 97,6% of original grouped cases correctly classified.

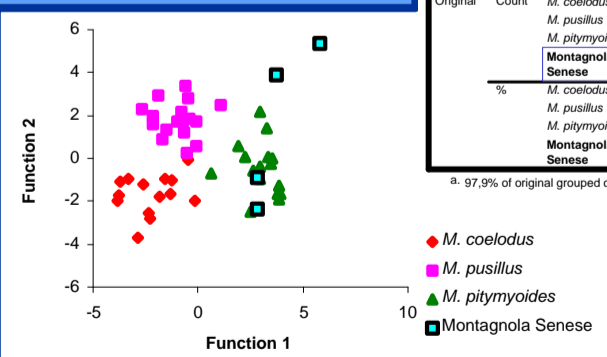
To these two groups the *Mimomys* specimens from Casa Sgheri have been added as unknown specimens and a second DA has been performed (Fig. 5)



Original	Count	Predicted Group Membership			Total
		<i>M. coelodus</i>	<i>M. pusillus</i>	<i>M. pitymyoides</i>	
<i>M. coelodus</i>	13	13	1	0	14
<i>M. pusillus</i>	1	0	37	0	38
<i>M. pitymyoides</i>	0	0	0	16	16
Casa Sgheri	4	4	0	0	4
%		92,9	7,1	,0	100,0
		2,6	97,4	,0	100,0
		,0	,0	100,0	100,0
Casa Sgheri	80,0	0	20,0	0	100,0

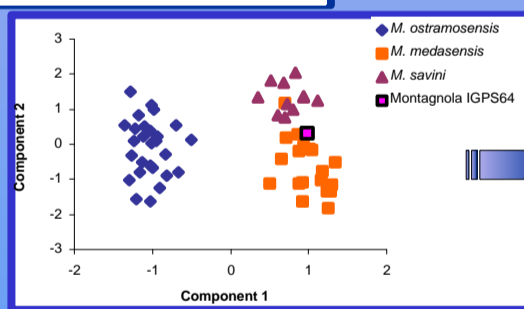
^a. 97,1% of original grouped cases correctly classified.

The same kind of analysis has been performed on the small *Mimomys* from Montagnola Senese (Fig. 6) attributed by Fondi (1972) to *M. savini*, and referred lately to *M. pitymyoides* (Kotsakis et al., 2003).

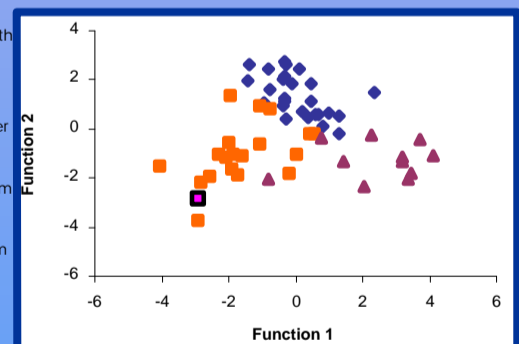


Original	Count	Predicted Group Membership			Total
		<i>M. coelodus</i>	<i>M. pusillus</i>	<i>M. pitymyoides</i>	
<i>M. coelodus</i>	13	13	0	0	13
<i>M. pusillus</i>	0	0	17	0	17
<i>M. pitymyoides</i>	0	0	0	16	16
Montagnola Senese	0	0	0	4	4
%		92,9	7,1	,0	100,0
		,0	100,0	,0	100,0
		,0	,0	100,0	100,0
Montagnola Senese	,0	,0	100,0	0	100,0

^a. 97,9% of original grouped cases correctly classified.



Another attempt has been made with the big sized *Mimomys* from Montagnola Senese, IGPS64. A PCA has been used to reduce the number of variables to 10 (Fig. 7), then a DA has been performed on *M. savini* from Villány 6, *M. ostramosensis* from Montoussé 5 and *M. medasensis* from Islas Medas (Fig. 8).



Classification Results^a

Original	Count	Predicted Group Membership			Total
		<i>M. ostramosensis</i>	<i>M. medasensis</i>	<i>M. savini</i>	
<i>M. ostramosensis</i>	26	26	0	1	27
<i>M. medasensis</i>	4	0	15	0	19
<i>M. savini</i>	1	0	0	10	11
IGPS64	0	0	1	0	1
%		96,3	,0	3,7	100,0
		21,1	78,9	,0	100,0
		9,1	,0	90,9	100,0
IGPS64	,0	100,0	0	0	100,0

^a. 89,5% of original grouped cases correctly classified.

Discussion

The decomposition of the *Mimomys* M1 outline by a Fast Fourier Transform represents a quantitative description of a complex morphology, that allows a statistical treatment of the data. Multivariate analyses has confirmed that small Casa Sgheri specimens may be attributed to *M. coelodus* as suggested by other morphometric analyses, (Marcolini & Montuire 2004), while those from Montagnola Senese belong to *M. pitymyoides*. The bigger IGPS64, on the contrary, is morphologically closer to the *M. medasensis* group. These attributions allow a better understanding of the biochronological position of these two sites, that may be definitely correlated with the Costa San Giacomo F.U. (Late Villanyian).

Acknowledgements

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