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Fourier Analysis Applied to *Mimomys* (Arvicolidae, Rodentia, Mammalia) First Lower Molars – Biochronological Implications[1]

Federica Marcolini[2,3]

Fourier analysis was used in this study to help a specific determination of some Mimomys *(Arvicolidae, Rodentia, Mammalia) species. Several Pliocene and Pleistocene Central and Western European* Mimomys *species first lower molar contours have been decomposed by Complex Discrete Fourier Transform. Inter- and intra-specific comparisons have been performed on the harmonics obtained from the decomposition and some problematic specimens have been classified.*

KEY WORDS: Plio-Pleistocene, small mammal, morphometry, biochronology.

INTRODUCTION

The genus *Mimomys* (Arvicolidae, Rodentia, Mammalia; Fig. 1B) is widely used for continental biochronological reconstructions throughout the Northern Hemisphere, it being widespread during Pliocene to Early-Middle Pleistocene with well recognizable phyletic lineages. Sometimes the standard approach to recognise species by comparison of overall morphological variation in fossil samples is unfortunately not sufficient. It often happens when dealing with taxa, such as *Mimomys*, lacking extant representatives, especially when the remains are scarce. There is a general agreement on the necessity to find methods that are able to determine subtle differences in rapidly evolving genera, such as *Mimomys*, in order to improve Pliocene and Pleistocene continental biochronology. Despite the very good results obtained, "classic" morphometry based on measurements and indices on the occlusal surface of the first lower molars (m1; Brunet-Lecomte and Chaline, 1990) or on the *linea sinuosa* (the lateral enamel-dentine junction;

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[2]Dipartimento di Scienze Geologiche, Università Roma Tre, Roma, Italy; e-mail: fmarcolini@dst.unipi.it

[3]Present address: Department of Biological Sciences, Murray State University, Blackburn Science Building, Murray KY, 42 071, USA.

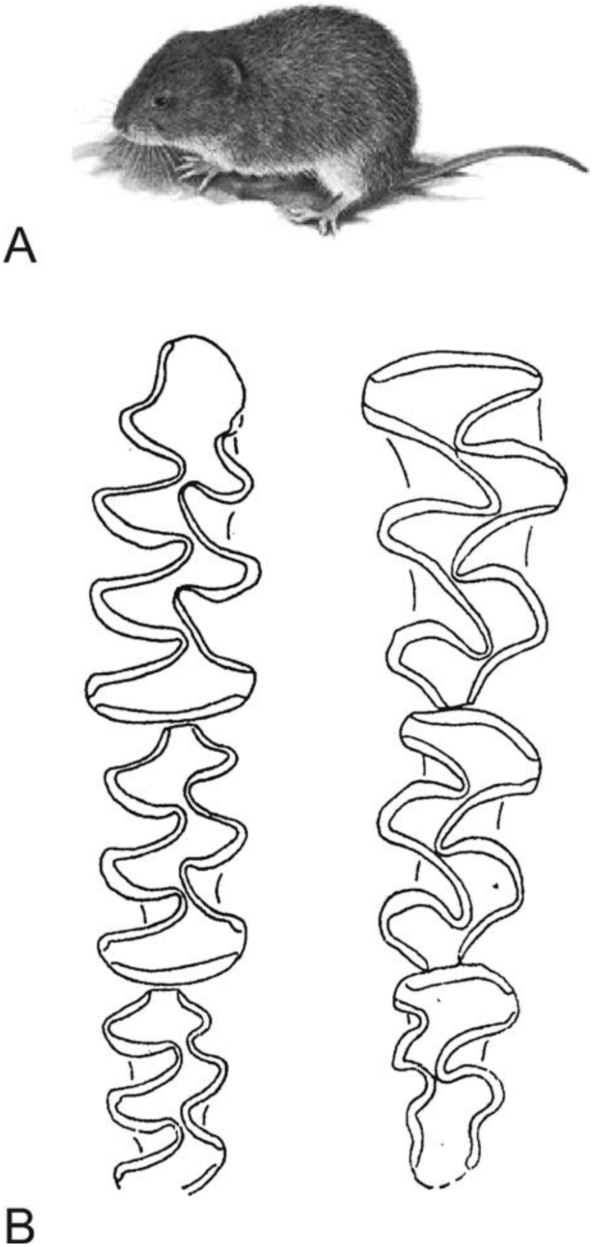

Figure 1. A: The water vole, *Arvicola terrestris*, considered very close in aspect to the extinct *Mimomys*; B: *Mimomys* right dental series, lower and upper masticatory surface of m1–m3 molars respectively.

Neraudeau and others, 1995) do not represent the tooth as a whole, dealing with a discrete number of measurements. Therefore the development of a method that allows the decomposition of the whole molar contour in a Fourier series, that reduces the morphological variation to a set of harmonics allowing both characterisation (at the species or genus level) and inter- and intra-specific comparisons is of considerable complimentary value. Decomposition of rodent molar contours in a Fourier series has been successfully applied by Renaud and others (1996), Cucchi and others (2002) and Renaud and Van Dam (2002) to murid molars or by Contoli, Benincasa-Stagni and Maresca (1989) and more recently by Leroy, Montuire and Marchand (2004) to insectivores. Only lately some approaches have been made on non-holomorph shapes, such as arvicolid molars contours using Elliptic Fourier methods (Hurth and others, 2004) or Complex Discrete methods (Marcolini, 2004; Marcolini and others, 2006; Navarro, Zatarain and Montuire, 2004).

The specific attribution of the small-sized species of *Mimomys* from Casa Sgherri (Lower Valdarno, Tuscany, Italy) could be quite important for the correct biochronological correlation of the assemblage. Indeed, large mammals present in the site give only a general framework for this assemblage (Marcolini and others, 2000; Marcolini, 2004), while the contemporary presence of different species of *Mimomys* might better constrain the age of the assemblage. In particular, the specific attribution of four specimens of a small-sized form of *Mimomys* which is intermediate in features between *M. pusillus* and *M. coelodus*.

The assemblage from Montagnola Senese (Fondi, 1972) comes from a karstic fissure in Central Tuscany and is composed of both large and small mammals. The arvicolids were first attributed to *Mimomys savini* (Fondi, 1972), but recently Maul and others (1998) suggested the presence of *M. pitymyoides*. However, the bigger *Mimomys* specimens of the assemblage have never been identified.

MATERIAL

The material used in this study comes from different collections of Central and Western Europe: the *Mimomys* m1 specimens from Casa Sgherri (Lower Valdarno, Central Italy; Fig. 2a–c) are stored at the University of Pisa; *M. coelodus* and *M. pusillus* from Deutsch-Altenburg 2 (Fig. 2h–j and k–m, respectively) (Rabeder, 1981) are stored at the Wien Universität (Wien, Austria); *M. pusillus* from Püspokfürdo (Fig. 2n–p), *M. coelodus* from Kislang (Holotype; Fig. 2g), *M. savini* from Villány 6 (Fig. 2y–z) (Mehely, 1914; Kretzoi, 1959) come from the Hungarian Museum of Natural History (Budapest, Hungary); *M. pitymyoides* and *Mimomys* sp. from Montagnola Senese (Fig. 2d–f and t, respectively) (Fondi, 1972) from the Institute of Geology and Paleontology of Siena (Siena, Italy);

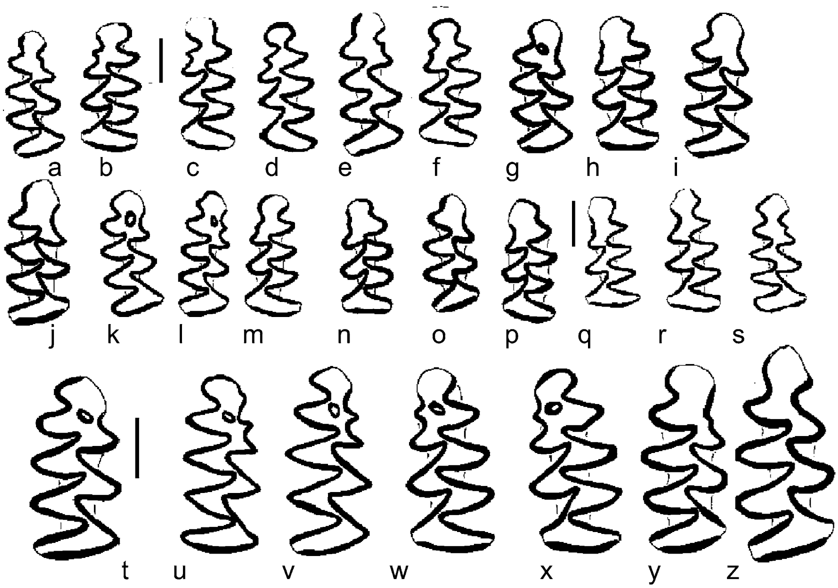

Figure 2. *Mimomys* specimens used in this study: a-c *Mimomys* Casa Sgherri; d–f *Mimomys pitymyoides* Montagnola Senese; g *M. coelodus*, Kislang holotype; h–j *M. coleodus* Deutsch-Altenburg; k–m *M. pusillus* Deutsch-Altenburg; n–p *M. pusillus* Püspokfürdo; q–s *M. pitymyoides* Montoussè 5; t Montagnola Senese IGPS 64; u–v *M. medasensis* Islas Medas; w–x *M. ostramosensis* Montoussé 5; y–z *M. savini* Villány 6. Scale bar represent 1 mm.

M. ostramosensis and *M. pitymyoides* from Montoussé 5 (Fig. 2w–x and q–s, respectively) (Clot and others, 1976) from the Université de Dijon (Dijon, France); *M. medasensis* from Islas Medas (Fig. 2u–v) (Michaux, 1971) come from the Université de Sciences et Technique de Languedoc (Montpellier, France).

METHODS

The occlusal pattern of the m1 has been drawn using a *camera lucida* and scanned with a resolution of 300 dpi. An analysis of the uncompressed tiff black and white image of the contour has been carried out. The standard approach, successful with murine rodents (Renaud and others, 1996; Renaud and van Dam, 2002), could not be used with arvicoline molars due to their peculiar, non-holomorph shape. A Fourier decomposition by means of a matrix of complex numbers (cfr. Gonzalez and Woods, 1992) has been used here. This method considers simultaneously the coordinates x and y of each point and 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 (see also Leroy, Montuire and Marchand, 2004). The outline is described by n equally spaced points, whose coordinates x (or $x(n)$) and y (or $y(n)$) were extracted.

We can define a periodic complex series $s(n)$ using the complex pairs of N points equally spaced on the outline: $s(n) = x(n) + iy(n)$ with n going from 0 to $N-1$.

Since outlines are described from a finite number of their sampled points and not by a continuous function, a Discrete Fourier Transform (DFT) has been applied to decompose the complex discrete series. Each harmonic is defined from the N complex pairs and $S(k)$, the coefficient of the k-th harmonic of this Fourier decomposition is:

$$S(k) = \frac{1}{N} \sum_{n=0}^{N} s(n)\, e^{(-i2\pi kn)/N}$$

This method allows the description of any outline with a finite number of harmonics. Generally, a simple shape is adequately described by few harmonics (Crampton, 1995; Dommergues and others, 2003), but in the case of a complex outline, an accurate description is ensured by the first harmonics and by their conjugates where the harmonic $N - k$ is, for $k \geq 1$, the conjugate of the harmonic k.

In order to consider shape alone, independent of form size contribution, all harmonic amplitudes were standardized in size, by dividing them by the square root of the area. For *Mimomys* species harmonics 1–10 and their conjugates (harmonics 30–39) together accounted for more than 98% of the total power. Because the set of intermediate harmonics had a relatively low contribution to the amount of shape information, amplitudes of these harmonics (harmonics 11–29) were excluded from the statistical analyses. Coordinate extractions and calculations were performed using the program CDFT developed by C.H. Dommergues at the Université de Belfort-Montbeliard (Dommergues, 2000). CDFT also allows a reconstruction of the original outline corresponding to any pairs of harmonics using the discrete inverse Fourier transform. Multivariate statistics have been carried out using the software package SPSS 11® (SPSS, 2001).

RESULTS

Canonical Discriminant Analysis (CDA) has been applied to the 10 harmonic pairs obtained by decomposing the m1 contour of three different species of small size *Mimomys*: *M. pitymyoides* from Montoussé 5, *M. pusillus* from the type

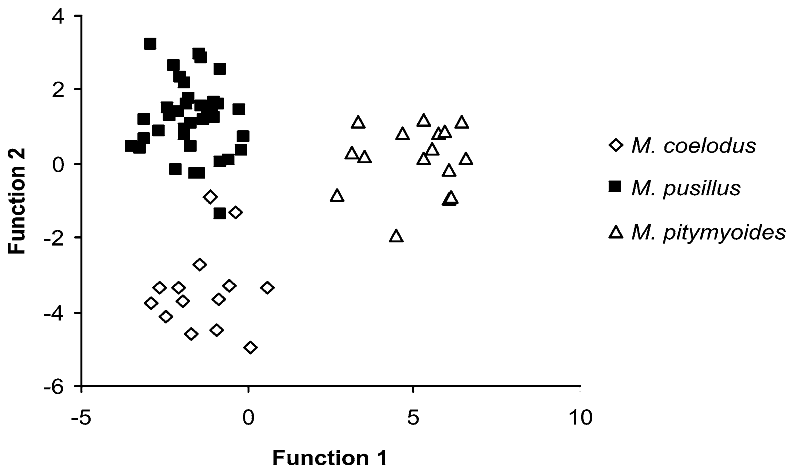

Figure 3. Canonical discriminant analysis: *M. coelodus*, *M. pitymyoides*, *M. pusillus*.

population of Püspokfürdo and from Deutsch-Altenburg 2, the holotype of *M. coelodus* and *M. coelodus* from Deutsch-Altenburg 2 (Fig. 3). 97.6% of the original specimens have been correctly classified by the analysis (Table 1). Four unknown small-sized *Mimomys* specimens from Casa Sgherri and a fifth specimen originally classified as *M. pitymyoides* have been added to these populations as unknown specimens, and a second CDA was performed (Fig. 4). The specimen originally classified as *M. pitymyoides* has been attributed to the *M. pitymyoides* group (Table 2), while the other four were assigned to *M. coelodus*.

The same kind of analysis has been performed on the four small-sized *Mimomys* from Montagnola Senese (Fig. 5) attributed by Fondi (1972) to *M. savini*, and referred lately to *M. pitymyoides* (Maul and others, 1998*)*. Table 3 shows all four specimens have been classified by CDA as *M. pitymyoides*.

Table 1. Canonical Discriminant Analysis *M. coelodus*, *M. pitymyoides*, *M. pusillus*

		Predicted group membership			
	SITE	*M. coelodus*	*M. pusillus*	*M. pitymyoides*	Total
Original Count	*M. coelodus*	13	1	0	14
	M. pusillus	1	53	0	54
	M. pitymyoides	0	0	16	16
%	*M. coelodus*	92.9	7.1	.0	100.0
	M. pusillus	1.9	98.1	.0	100.0
	M. pitymyoides	.0	.0	100.0	100.0

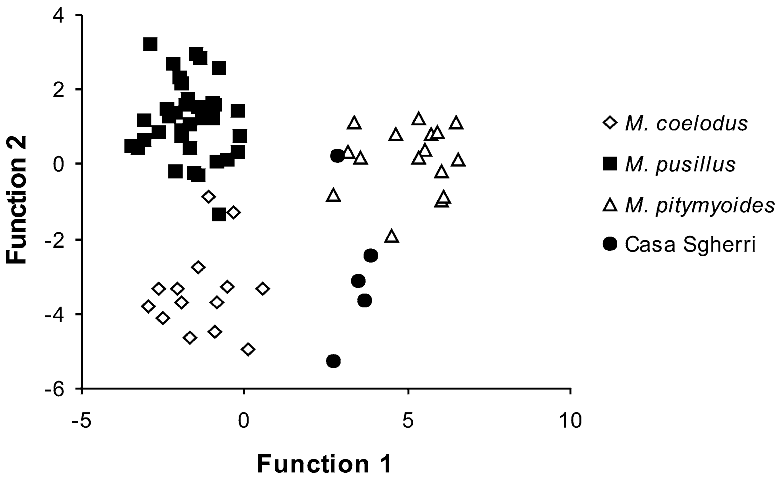

Figure 4. Canonical discriminant analysis: *M. coelodus*, *M. pitymyoides*, *M. pusillus* and Casa Sgherri.

In the Montagnola Senese assemblage a large-sized form is present, IGPS64, and it was initially referred to as *M. savini* too (Fondi, 1972), while Maul and others (1998) left it unclassified as *Mimomys* sp. A CDA has been performed on larger sized *Mimomys* from different species: *M. savini* from Villány 6, *M. ostramosensis* from Montoussé 5 and *M. medasensis* from Islas Medas (Fig. 6). Though classification of these large-sized species is more affected by error, 89.7% have been considered correctly classified and specimen IGPS64 has been classified by the analysis as *M. medasensis* (Table 4).

Table 2. Canonical Discriminant Analysis *M. coelodus*, *M. pitymyoides*, *M. pusillus* and Casa Sgherri

		Predicted group membership			
	SITE	*M. coelodus*	*M. pusillus*	*M. pitymyoides*	Total
Original Count	*M.coelodus*	13	1	0	14
	M. pusillus	1	37	0	38
	M. pitymyoides	0	0	16	16
	Casa Sgherri	4	0	1	5
%	*M. coelodus*	92.9	7.1	.0	100.0
	M. pusillus	2.6	97.4	.0	100.0
	M. pitymoides	.0	.0	100.0	100.0
	Casa Sgherri	80.0	.0	20.0	100.0

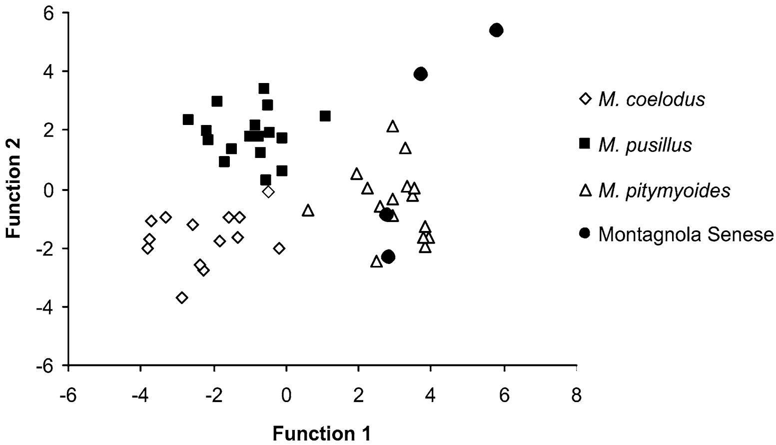

Figure 5. Canonical discriminant analysis: *M. coelodus*, *M. pitymyoides*, *M. pusillus* and Montagnola Senese small size *Mimomys*.

DISCUSSION AND CONCLUSIONS

M. pusillus and *M. coelodus* are morphologically close species, whose size ranges overlap and they are usually distinguished on the basis of the *linea sinuosa* morphology (Rabeder, 1981). They have a partially-overlapping biochronological distribution, at least in Eastern Europe, and *M. coelodus* has not yet been recovered in Italy. Casa Sgherri specimens had an intermediate *linea sinuosa* between the two species and their size falls in the overlapping range between the two. A specific attribution was therefore quite difficult. On the contrary, specimen CS3 was already tentatively attributed to *M. pitymyoides* on the basis of its overall morphology (Marcolini, 2004; Marcolini and Montuire, 2004). The discriminant

Table 3. Canonical Discriminant Analysis *M. coelodus*, *M. pitymyoides*, *M. pusillus* and Montagnola Senese small size *Mimomys*

		Predicted group membership			
	SITE	*M. coelodus*	*M. pusillus*	*M. pitymyoides*	Total
Original Count	*M. coelodus*	13	1	0	14
	M. pusillus	0	17	0	17
	M. pitymyoides	0	0	16	16
	M. Senese	0	0	4	4
%	*M. coelodus*	92.9	7.1	.0	100.0
	M. pusillus	.0	100.0	.0	100.0
	M. pitymyoides	.0	.0	100.0	100.0
	M. Senese	.0	.0	100.0	100.0

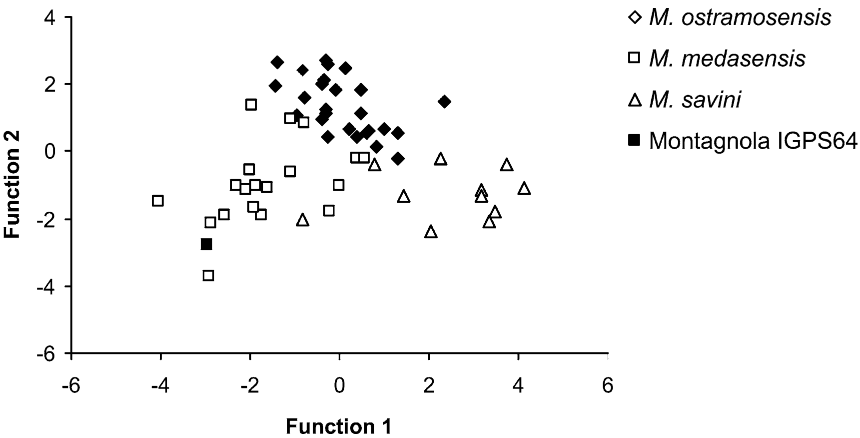

Figure 6. Canonical discriminant analysis: *M. medasensis*, *M. ostramosensis*, *M. savini* and Montagnola Senese specimen IGPS64.

analysis (Fig. 4, Table 2) not only has confirmed such an attribution, but it has also classified the other four unknown specimens as *M. coelodus*. *M. coelodus* is reported from some Late Villanyian and Earliest Biharian sites of central and Eastern Europe (Akkulaevo, Pevzner, Vangengeim and Tesakov, 2001; Deutsch-Altenburg 2c and 4b, Rabeder, 1981; Drăgăneşti-Olt and Izvoru, Radulescu and Samson, 1983, 2001).

Casa Sgherri Local Fauna, on the basis of the contemporary presence of *Mimomys ostramosensis*, *M. pitymyoides* and *M. coelodus* associated f.i. with *Acinonyx pardinensis* can be correlated with Costa San Giacomo or Olivola Faunal Unit (Late Villanyian, Late Pliocene).

Table 4. Canonical Discriminant Analysis *M. ostramosensis*, *M. medasensis*, *M. savini* and Montagnola Senese specimen IGPS64

		Predicted Group Membership			
	SITE	*M. ostramosensis*	*M. medasensis*	*M. savini*	Total
Original Count	*M. ostramosensis*	26	0	1	27
	M. medasensis	4	15	0	19
	M. savini	1	0	10	11
	IGPS64	0	1	0	1
%	*M. ostramosensis*	96.3	.0	3.7	100.0
	M. medasensis	21.1	78.9	.0	100.0
	M. savini	9.1	.0	90.9	100.0
	IGPS64	.0	100.0	.0	100.0

Montagnola Senese has always been attributed to the Early Pleistocene because of the presence of *Mimomys savini*. Indeed, Maul and others (1998) and Kotsakis and others (2003) suggested a correlation with Late Villanyian or earliest Early Biharian due to the presence of *M. pitymyoides*. Such a presence has been confirmed here by morphometric analyses (Fig. 5, Table 3). Moreover it has been possible to ascribe sample IGPS64 (which certainly did not belong to *M. pitymyoides*, nor to *M. savini*), to *M. medasensis* (Fig. 6, Table 4), a species only found to date in Italy in Torre di Picchio, Late Villanyian (Late Pliocene) and it has been widespread since the Late Pliocene in the Iberoccitane province (Casablanca I and Islas Medas, Spain and Trassanel, Languedoc, France; Michaux, 1971; Agustí, 1990; Bachelet, 1990).

In conclusion, the use of a Discrete Fourier Transform represents a quantitative description of a complex morphology, such as that of *Mimomys* m1 occlusal outline, and allows a statistical treatment of the data, more accurate interspecific correlations and, therefore, biochronologic correlations, representing an interesting instrument for further micromammalian studies.

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