

COMPOSITIONAL FIDELITY OF MOLLUSCAN ASSEMBLAGES OF TOURO PASSO FORMATION (PLEISTOCENE-HOLOCENE) REVEALS DRAMATIC CHANGES IN THE FRESHWATER MOLLUSCAN FAUNA OF THE TOURO PASSO RIVER, SOUTHERN BRAZIL

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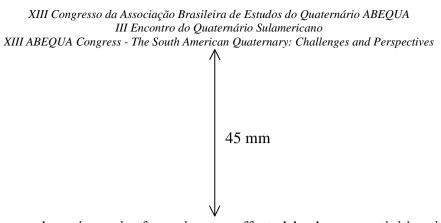
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1. INTRODUCTION

Freshwater habitats are among the environments most impacted by human activities, since the anthropogenic threats-have been affecting these ecosystems for long periods of time (~5000 ka), although the records may vary according to region. In some cases, aquatic benthic communities may have been modified to such a degree that their original structure is permanently lost (National Research Council, 2005). Freshwater mollusks are among the most threatened groups in the world. Fortunately, the Quaternary fossil record can provide useful information for assessing certain changes induced by anthropogenic effects and data on the original structure of modern mollusk assemblages (see Erthal *et al., in press*). Quantitative fidelity, which is the "quantitative faithfulness of the record of morphs, age classes, species richness, species abundances, trophic structure, etc. to the original biological signal" (Behrensmeyer *et al.*, 2000, p. 120) is one of the main approach used to do so. Most of quantitative fidelity studies deal with comparisons between living (LA) and death assemblages (DA), in order to quantitatively assess the preservation potential of the former.

2. AIMS AND SCOPE OF THIS CONTRIBUTION

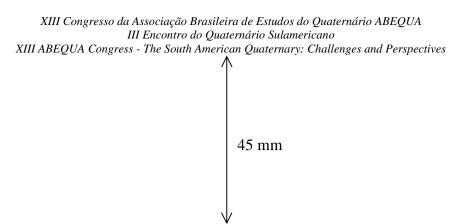
This study is the first assessment of freshwater mollusk fossil assemblages (FAs) relative to the compositional fidelity of modern mollusk living (LAs) and death assemblages (DAs). Indeed, fidelity studies comparing modern LAs or DAs with Late Pleistocene–early Holocene fossil assemblages (FA, i.e., from outcrops) are relatively few (Valentine *et al.*, 2006). Difficulties in identifying Pleistocene mollusks at the species level and the uneven availability of sedimentary bodies with fossil species that locally match modern assemblages hamper comparisons at large (regional) spatial scales. Additionally, taphonomic studies have shown that post-burial taphonomic processes can destroy shells, leaving no freshwater mollusk record in some areas (Behrensmeyer *et al.*, 1995). The Touro Passo River (TPR, southernmost Brazil) is particularly well suited to fidelity studies of FAs for freshwater mollusks. Similarly



to many other modern rivers, its fauna is now affected by human activities, including the introduction of exotic invasive Asiatic bivalves (Martello *et al.*, 2006). However, freshwater mollusk LAs and DAs are common and easily found and sampled. Outcrops of the Touro Passo Formation (TPF) contain Late Pleistocene (18.57–20.69 ka) shell beds (Kotzian *et al.*, 2005), with mollusk species clearly corresponding to the modern species of the region (Martello *et al.*, 2006), allowing us to compare the Late Pleistocene assemblages with modern ones. Additionally, the taphonomic signatures of the mollusk assemblages of the TPR were previously analyzed, allowing us to understand the taphonomic processes that may affect dead shells (Kotzian & Simões, 2006).

3. MATERIAL AND METHODS

The Touro Passo River, a small tributary of the Uruguay River (Paraná River basin), is located in western Rio Grande do Sul state, southern Brazil. It flows for about 55 km, draining a basin of 800 km2 with an altitude range of 100 m. The river is up to 6 m deep, with straight and meandering channels and a mostly sandy bed; the banks are covered by short riparian vegetation. The composition of the living mollusk assemblages of the TPR is well known. Frequent sampling of living mollusks along the entire length of the TPR since 1992 allows us to assign seven native species to the river (Table 1) as well as the invasive Asiatic bivalves, Corbicula largillierti and C. fluminea. Several recent species were also found in the riverbed as empty shells (i.e., dead individuals) by Martello et al. (2006). The Pleistocene-Holocene Touro Passo Formation (TPF) is a sedimentary unit coeval to the Uruguayan Sopas Formation and the Argentinean Luján Formation (Bombin, 1976). This unit was deposited by the ancient floodplains of the TPR. Its depositional setting shows no significant climate shift. Two members constitute the formation. The lower member (50 cm thick) is mostly an orthoconglomerate rock formed by channel deposition (frontal accretion), and lies in discordance on Mesozoic basalt rocks from the Serra Geral Formation (Jurassic-Cretaceous). The upper member, thicker (4.5 m) than the lower one, is a pale-brown to yellowish-brown muddy rock (mostly floodplain deposits), essentially formed by clayey siltstone and silty to silty-clayey sandstone (Bombin, 1976). It also holds the majority of fossil occurrences from the TPF, as well as archeological material (12.0-3.5 ka; Bombin, 1976). Sedimentary structures (physical and biogenic) as well as bedding planes and sharp lithological contacts are not evident and carbonate concretions are very common (Bombin, 1976). All fossil shells analyzed in this study were collected in the upper member. Finally, the analyses of the FA were conducted using only shells and shell fragments identifiable at species level and the species were analyzed with respect to their proportional abundance (%). A correction factor of 0.5 for mismatching valves was applied in order to avoid overestimation of bivalve abundance, because a single valve has twice the probability of being collected as the single shell of gastropods. For the fidelity study of the FA, we used the small-scale approach, when the FA was compared with the LAs and DAs of the meandering segment (2000 m; pooled data of the five sites, comprising 25 m^2) of the TPR. We chose this segment for comparison because it is possible that the fossil bed analyzed here originated in a similar setting. For the



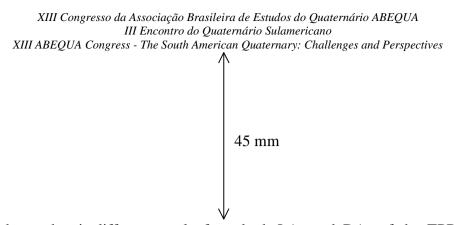
large scale approach (river scale), the FA was compared with the LAs and DAs of the TPR as a whole (pooled data for the five sites of the meandering segment + pooled data for the five sites of the straight segment, 5000 m), comprising 50 m^2 of sampling area. Finally, the fidelity analyses focused on the three indices proposed by Kidwell and Bosence (1991), which include: F1, the percentage of shelly species found alive that were also found dead [(NS 3 100)/(NS + NL)]; F2, the percentage of species found dead that were also found alive [(NS 3 100)/(NS + ND)]; and F3, the percentage of dead individuals that can be assigned to species found alive [(dead individuals of NS 3 100)/(dead individuals from (NS + ND))], where NS = number of species shared by the two assemblages; ND = number of species found only in DA; and NL = number of species found only in LA. Additionally, these indices were adapted to compare the fidelity of the FA in relation to the LA and DA, as follows: (1) F1, the percentage of species found alive that were also found in the FA, and the percentage of species found dead that were also found in the FA; (2) F2, the percentage of species found in the FA that were also found live, and the percentage of species found in the FA that were also found in the DA; and (3) F3, the percentage of fossil individuals which are from species found live, and the percentage of fossil individuals which are from species found dead.

4. RESULTS

Tables 1 (below) summarizes our compositional fidelity results where fossil mollusk assemblage (FA) from the TPF was compared to living (LA) and death assemblages (DA) of the TPR. The data revealed little resemblance between FA and LA species composition. Although the FA and DA agree closely in richness, species composition, and species relative abundances (both proportional and rank), the fossil assemblage (FA) differs significantly from modern assemblage in most of these measures. The FA is dominated by the native endemic corbiculid bivalve *Cyanocyclas limosa* and the gastropod *Heleobia* aff. *bertoniana*. These are absent in the LA, and both living (LA) and death assemblages (DA) are dominated by the alien Asiatic corbiculid *C. fluminea*, which is absent in the Pleistocene fossil assemblage. This also contains, overall, a higher proportional abundance of relatively thick shelled species, suggesting a genuine bias against the thinner- and smaller shelled species (Table 1).

5. DISCUSSION AND CONCLUSIONS

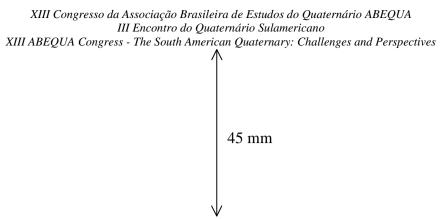
The Touro Passo Formation (TPF) was generated by the floodplain of the ancient Touro Passo River (TPR) during the Pleistocene. Since that time, the length and channel morphology of the TPR may have remained fairly stable; however, some climate changes have led to wetter and rainier conditions in the last 4 kyr (Behling *et al.*, 2009). Considering that the (1) fossil shells studied are Late Pleistocene; (2) freshwater species taxocoenosis of this time interval corresponds to the modern ones at the species level, and (3) freshwater mollusks, including those of the TPR, are not restricted to particular environments, we should expect that the FA would have a species composition similar to that exhibited by LA and DA, but not necessarily richer, and possibly biased toward thick-shelled and abundant species due to preferential preservation. However, our study on the fidelity of fossil assemblages of the Touro Passo



Formation shows that it differs strongly from both LAs and DAs of the TPR in species composition (identities), rank abundance, and proportional abundance of species. These differences are caused by bias driven by (a) taphonomic processes, which favor the long-term preservation of thick shelled species; (b) human-induced changes in freshwater environments, such as the introduction of invasive alien species; and, (c) to a lesser extent, the differences in the magnitude of time averaging. Briefly, our results suggest that contemporary environmental changes, such as the introduction of some alien freshwater mollusk species, together with post-burial taphonomic processes, are the main factors leading to the poor fidelity of the studied FA. Hence, the taxonomic composition of the Late Pleistocene mollusks from the Touro Passo Formation probably would show greater similarity to present-day assemblages wherever the mollusk biodiversity is not disturbed by human activities.

Table 1 - Rank order of species proportional abundance (%) of the FA assemblages from the TPF and LA and DA assemblages from the TPR. Codes are A- alien species, B- bivalve, E-epifauna, F- suspension feeder, G- gastropod, I- infauna, R- grazer. Data for LA and DA assemblages were compiled from Martello *et al.* (2006) and Erthal *et al.* (*in press*).

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	Ecology	Thickness	FA	DA	LA	DA	LA
				Meander Scale		River Scale	
Cyanocyclas limosa	B; I; F	Thick	43.16			1.28	
Heleobia aff. Bertoniana	G; E; R	Thick	19.42	2.38		1.60	
Delodontus rhuacoicus	B; I; F	Thick	5.99				
Heleobia aff. Piscium	G; E; R	Thick	5.03				
Potamolithus aff. Lapidum	G; E; R	Thick	4.55				
Potamolithus aff. Orbignyi	G; E; R	Thick	4.31	27.14	41.68	27.65	50.16
Potamolithus aff. Callosus	G; E; R	Thick	3.83				
Anodontites sp.	B; I; F	Thick	3.59		0.09		0.08
Delodontus delodontus	B; I; F	Thick	3.35	1.19	0.38	1.12	0.32
Heleobia aff. Parchappei	G; E; R	Thick	2.87				
Diplodon parallelopipedon	B; I; F	Thick	2.15			1.28	
Monocondylaea minuana	B; I; F	Thick	1.43				
Eupera klappenbachi	B; I; F	Thin	0.23	0.47	0.09	0.32	0.16
Pomacea canaliculata	G; E; R	Thin	0.23	0.47		3.53	0.40
Potamolithus sp.	G; E; R	Thick		42.38	45.17	28.6	38.09
Corbicula largillierti	B; A; I; F	Thick		13.09	9.96	19.77	8.40
<i>Biomphalaria</i> sp.	G; E; R	Thin		8.09	0.09	9.64	0.24
Corbicula flumínea	B; A; I; F	Thick		2.38	1.16	3.53	0.97
Pisidium sterkianun	B; I; F	Thin		1.42	0.87	0.96	0.73
M. siliquosa	B; I; F	Thin		0.95		0.64	
Diplodon sp.	B; I; F	Thick			0.38		0.32
P. punctiferum	B; I; F	Thick			0.09		0.08
Gastropod individuals			167	169	899	221	1090
Gastropod species			7	5	3	5	4
Bivalve individuals			250	41	127	90	136
Bivalve species			7	6	8	8	8
Total of individuals (N)			417	210	1026	311	1226
Total of species (S)			14	11	11	13	12



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