

**Seasonal Shell Growth and Longevity in the Variable Coquina Clam,
Donax variabilis, from Northeast Florida: Evidence from Oxygen Isotopes**

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The variable coquina clam, *Donax variabilis*, is a familiar inhabitant of sandy beaches from Virginia to south Florida and west to Texas. Extensive archaeological shell-midden deposits along the northeast Florida coast confirm that coquina clams were heavily exploited by pre-Columbian people since the Middle Archaic (ca. 5700 YBP). We examined the accretionary records of modern and archaeological *Donax variabilis* shells to assess seasonal shell growth and longevity in this species, and to determine if there was a seasonal component to shellfish harvest during the middle to late Holocene. Year-round collections of living clams and seawater data from Matanzas Beach, Florida, were made at monthly intervals and combined with historical temperature data to establish an environmental framework. The stable oxygen isotopic variation in two serially sampled, modern shells closely tracks the water temperature variation during spring and summer, the seasons of most rapid shell growth. In fact, the $\delta^{18}\text{O}$ profiles are completely explained by seasonal water temperature variations. Shell edge isotopic values correspond with water temperatures at the time of collection. Similar $\delta^{18}\text{O}$ profiles in four archaeological specimens from four different sites representing two distinct time periods indicate shell growth in late spring–summer, with harvest in autumn. Average longevity was 3–4 months. Paleotemperatures derived from two Preceramic Archaic specimens (ca. 5700 YBP) and two Orange Period specimens (ca. 3500 YBP) indicate temperatures warmer than modern by about 3.5 °C, perhaps reflecting the mid-late Holocene thermal maximum in this region.

Contributed Session III – Marine Mollusks

**Neogastropod Sister Group: Morphological, Chromosomal,
and Paleontological Evidences**

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Neogastropoda can be generally considered as predators. Transition from herbivory to carnivory requires complex biochemical transformations. Therefore it is logical to search the sister group of Neogastropoda among carnivorous or omnivorous Caenogastropoda. On the other hand, nearly all Neogastropoda are characterized by larger number of chromosomes when compared to lower Caenogastropoda ($2n=56-72$ and $16-36$ respectively). Among other Caenogastropoda, equivalent number of chromosomes was so far found only in three families: carnivorous Ranellidae (70), omnivorous Cypraeidae (52–72), and omnivorous Capulidae (62). Ranellidae and other Tonnoidea have long proboscis superficially similar to that of some Neogastropoda with terminal buccal mass. Nonetheless, anatomical and embryological data suggest that the neogastropod ancestor had a very short proboscis with basal buccal mass. The oldest palaeontological record of Neogastropoda is probably represented by a member of the family Ptychactidae. Recent representatives of this latter family retain the primitive foregut anatomy (short proboscis with basal buccal mass and odontophore retractors passing through the nerve ring). In addition, Tonnoidea appeared later than Neogastropoda in the paleontological record. Therefore, Tonnoidea is unlikely to be a sister group of the Neogastropoda. Capulidae is a highly specialized family with head and foregut modified for suspension feeding. This leaves the Cypraeidae, an omnivorous and carnivorous family, as a possible sister group of the Neogastropoda.

Symposium – Relationships of the Neogastropoda

Biodiversity of Russian Marine Mollusks

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Russia has a very long coastal line, and connects well-studied faunas of Europe and Japan. A catalogue of marine and non-marine mollusks of Russia and adjacent territories is being compiled. Currently, 3645 species of mollusks have been recorded from Russia. A total of 1734 species of six molluscan classes were recorded in the seas of Russia (including the low-salinity Black [235 species] and Caspian [185 species] seas). The richest areas are the Japan Sea (503 species) and southern Kurile Islands (414 species). In comparison, the fauna of Japan consists of 5106 species. The low diversity of marine mollusks results both from impoverishment of high latitude faunas as well as from insufficient study. To estimate the relationship between the number of faunal studies and the size of studies mollusks, the size structure of 1016 species of shelled gastropods and bivalves from the Russian Far-Eastern seas was compared with that of the regions with well studied faunas (Japan, Great Britain, tropical west America, Hawaii, and New Caledonia [Koumak site]). Analyses demonstrate that the percentage of small mollusks (<10 mm) studied is a function of the degree of faunal investigations rather than from latitudinal gradient. Thus in boreal well-studied British fauna the micromollusks comprise 47.25%. That is comparable to the extremely well-studied fauna of the Koumak site in New Caledonia (53.29%). In the Russian Far-Eastern seas the known percentage of micromollusks is 20.08%, leading to the conclusion that micromollusks are understudied in Russia and values from 14% to 44.5% of the total fauna are likely to be found.

Phylogeny of *Elimia caelatura* Complex of Upper Coosa Basin, Alabama

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Numerous freshwater mollusks are threatened from habitat destruction or elimination. One such imperiled group is represented by the freshwater gastropods in the family Pleuroceridae. Pleuroceridae is the most diverse family of freshwater gastropods and have their greatest diversity in the southeastern United States. Many of the pleurocerids are currently considered extinct, endangered, or threatened. One aspect hindering the conservational efforts is that their evolutionary relationship is unclear because it is solely based on shell morphology. The taxonomy of this group is based on late 19th- and early 20th-century studies. Many previous and ongoing studies have shown that they do not correspond to the real evolutionary species. In this study, we conducted a phylogenetic analysis of the *Elimia caelatura* complex and related species including *Pleurocera* using morphological and mitochondrial cytochrome c oxidase subunit I (COI) gene sequences. Preliminary molecular analysis suggests that they do not correspond to the species and subspecies and also do not seem to match with the geographical distribution in the Upper Coosa Basin, Alabama.

Poster Session

**No Pre-Mating Reproductive Isolation
Between *Physa acuta* and *P. pomilia***

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Within a physid species, there is no pre- or post-mating reproductive isolation as reported in previous behavioral trials. However, a breakdown does occur in the ability to outcross between physid species. We performed a series of mating trials between one population of *P. pomilia* and one of three different populations of *P. acuta*. We looked for evidence of size-assortative mating and species-assortative mating, and attempted to correlate behaviors that affected mate decision choices. We found that in pairings between species, *P. acuta* served as male significantly more often than *P. pomilia*. In addition, *P. pomilia* exhibited significantly more instances of rejective behavior when paired with *P. acuta* than with other *P. pomilia*.

Poster Session

Generic Hyperdiversity in Time and Space

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Several mainly tropical marine prosobranch gastropod genera are hyperdiverse, containing more than 200 extant species. With well more than 500 species, *Comus* is pre-eminent among these, and it is the most diverse genus of marine animals. We address (but do not answer all of) the following questions: (1) This richness of very similar species and the geologic youth of the genus (~55my) indicate very rapid rates of speciation. When, where, and how did all these speciation events take place? (2) What molecular, anatomical, ecological, developmental, and environmental attributes might foster rapid diversification? (3) In addition to high general species richness (γ diversity), many species co-occur at finer spatial scales (α diversity: up to 36 species on a single coral reef). Do these species avoid competition by partitioning resources, and if so, how? (4) Recently, molecular techniques have enabled the recognition of widespread sympatric sibling species in the Indo-West Pacific and explosive radiation of a species flock resulting in many narrowly distributed similar species in the Eastern Atlantic. How do these discoveries affect estimates of diversity and hypotheses of speciation? (5) How are species-level phylogenetic hypotheses, also available only recently from gene sequence data, affecting our understanding of evolutionary history and past and present geographic distribution patterns?

Special Session – Biodiversity of Marine Mollusks

**Neogastropoda: Questions of Tempo and Mode in
Macroevolution and Macroecology**

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Traditionally considered an order (following Thiele), Neogastropoda contains some 5000 species usually grouped in 15–20 families in 4–5 suborders or superfamilies. Despite its species richness and taxonomic diversity, the Neogastropoda is a rather conservative group in its homogeneity of anatomy, habits, and habitats. The most conspicuous gastropods in many marine habitats, neogastropods are almost exclusively marine, benthic, and carnivorous. A very few species have invaded fresh water and are herbivorous; some are scavengers and some parasites. I will briefly explore some broad themes of macroevolution and macroecology in the Neogastropoda, because these are still poorly known and disputed but are active and promising fields of research. Macroevolution concerns spatial and temporal patterns of speciation and extinction, how structures and functions evolve in lineages, and the shapes of clades or how lineages diversify. Salient macroevolutionary themes in neogastropods that need to be better understood include questions of ancestry and monophyly of the group, the relationship of phylogenetic patterns to the evolutionary history and diversification, and why some families and genera are much more diverse than others. Macroecology concerns broad spatial and temporal patterns of resource use among species and species diversity and abundance. Macroecological themes to be addressed include ecological diversification and disparity, with emphasis on exploitation of habitats and food types that may have been inaccessible to their ancestors.

Keynote Speaker – Symposium – Relationships of the Neogastropoda

Revisionary Systematics of *Conus*

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We report initial progress on three fronts of a project designed to improve and modernize the classification and systematics of *Conus*, the most diverse marine molluscan genus, to enhance understanding of its evolutionary history, and to facilitate broad access to the results. (1) We have established The *Conus* Biodiversity Website¹. Its first completed component is a catalogue of all available species-group names in *Conus* published from 1758 that have come to our attention. It incorporates previously published and computerized catalogues as well as subsequently published names, and earlier names omitted by previous catalogues. At present the catalogue contains 3157 species-group names, and it is periodically updated. Currently we are adding a gallery of photographs of type specimens to the site. (2) We have been adding to the molecular and morphological taxonomic bases. The next component to be incorporated in the Website will be an entry for each valid species, including descriptions and illustrations in a format similar to the Indo-Pacific *Manual of Living Conidae* by Röckel et al. but focusing on the Western Atlantic and Caribbean *Conus* fauna. (3) We are developing species-level molecular-based phylogenetic and phylogeographic hypotheses. Phylogenetic reconstructions presently based on sequences of one mitochondrial and one nuclear gene from 138 species indicate that extant species of *Conus* descend from two major clades that diverged between the origin of the genus 55 mya and 33 mya, and that these clades differ strikingly in diversity and in the proportions of their species from different geographic regions.

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**The Biodiversity of Shallow-Water Marine Mollusks
of Southwest Florida Revisited**

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The southwest coast of Florida, including Sanibel and Captiva islands, possibly represents one of the best-sampled areas in the world for shallow-water (intertidal to shallow subtidal depths) mollusks. Hobbyists and amateur malacologists have been consistently collecting there for many decades. Perry and Schwengel (1955, *Marine Shells of the Western Coast of Florida*), published an earlier inventory for the area but since then no other work has updated their findings. The Bailey-Matthews Shell Museum houses about 3500 dry and preserved lots of pertinent material, most of which were obtained through bequeathed collections. Curatorial work led museum staff to recognize the relevance of this material as the foundation for a much-needed, updated inventory of local shallow-water mollusks. The ongoing project started as a Web identification guide and aims to generate biodiversity and taxonomic data at the regional level. Literature data and records from other institutions are being used to substantiate and supplement collection information. Material is being critically reviewed to prevent inclusion of specimens of questionable origin. The presence of multiple lots of less-common species confirms their occurrence in the area and warrants their inclusion. Taxa that have not been recently collected in the area are included. In addition, the museum is engaged in sampling Sanibel and Captiva for micromollusks with help from local collectors and museum docents. At present, selected specimens of 220 species of Gastropoda, Bivalvia, Polyplacophora, and Cephalopoda have been illustrated in iconographic format¹. Collection data for about 3000 regional records already catalogued are also available online².

¹http://www.shellmuseum.org/sanibel_shells.html

²<http://www.shellmuseum.org/collection.html>

Ribbed Mussels of the Caribbean: The Curse of the Sibling Species Complex

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The intertidal scorched mussel *Brachidontes exustus* (Linnaeus, 1758) is nominally distributed continuously along the coast from North Carolina to Venezuela and is also present on nearby continental (Greater and Lesser Antilles, Bahamas) and oceanic islands (Bermuda). This regional evolutionary landscape has experienced a dynamic recent geological history that has reconfigured continental and oceanic interfaces. We were interested in establishing what imprint these events may have had on the cladogenesis of the Caribbean Basin scorched mussel. We present mitochondrial and nuclear gene trees based on hundreds of individuals sampled throughout the Caribbean and incorporating potential geminate species from the eastern tropical Pacific. Gene tree topologies consistently recovered three stem Caribbean lineages and six well-differentiated terminal clades, which represent six regional sibling species. The cladogenic origins of the stem lineages pre-date the closure of the Isthmus of Panama, whereas those of at least four of the six sibling species occurred after the closure. Caribbean sibling species have an intriguing pattern of within-basin distribution characterized by distinct geographic areas of ecological dominance adjoining those of sister taxa. However, species are not restricted to their core distributional areas and may be found (often co-occurring in low frequency with the local dominant) in other parts of the Caribbean Basin. These observations, coupled with the maintenance of genetic cohesion among geographically disjunct populations, imply that the distributional limits of sibling species are maintained by ecological factors rather than by barriers to larval-mediated gene flow. Our data are consistent with a history of geographically partitioned within-Basin cladogenesis that has been largely maintained by environmental exclusion.

Special Session – Biodiversity of Marine Mollusks

**Analyzing Shell Deposits to Aid in Site Selection for Bay Scallop Restoration
in Pine Island Sound, Florida**

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A recreational bay scallop (*Argopecten irradians*) fishery existed throughout Pine Island Sound, southwest Florida, until the late 1980s. Since then scallops have disappeared from the area, except for a small relict population in the northern part of the Sound. The loss of this important resource and the potential for its reintroduction through restoration play a role in critical water management decisions related to the estuary. Thirty-six sites in lower Pine Island Sound and San Carlos Bay were sampled for shell deposits. In addition, scallop shells were placed in the field to determine shell dissolution rates. Maps of shell deposits revealed a high density of shells centered inside York Island (immediately west of St. James City) and spreading into the shallow grass flats to the north and east. Two other foci of lower density, but equally broad scallop shell distributions, were identified: one near the mouth of the Caloosahatchee River and the other at the opening to Tarpon Bay. Average scallop shell dissolution rates ranged from 1.01 to 1.32 percent annually, suggesting that the shells had been buried in the sediments for roughly 100 years. If water quality becomes suitable to support bay scallops again, these areas may offer the most optimal locations for future restoration efforts.

Special Session – Coastal Molluscan Assemblages as Environmental Indicators and Monitors of Restoration Efficiency

Are Taxonomists Needed in a Molecular World?

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In the wake of the current biodiversity crisis and advances in molecular systematics, some researchers have suggested that DNA taxonomy can supplant traditional taxonomy. Proponents of this “DNA barcoding” envision that a short fragment of mtDNA can be used to diagnose taxa, increasing the speed, objectivity, and efficiency for circumscribing species. This suggestion has been met with strong opposition from both the systematic and taxonomic communities. However, most debate has remained philosophical and little empirical evidence has been put forth to test the barcoding approach because of a lack of sufficiently sampled, comprehensive phylogenetic datasets. Herein, I present evidence from three independent datasets (Cypraeidae, the *Astralium rhodostomum* complex, and the *Patelloida profunda* complex) to place error rates on barcoding. While the four commonly recognized sources of error are each relatively low (~2%), they are compounded, resulting in an overall error rate of approximately 10%. Most significantly, however, I identify a fifth source of error using a novel phylogenetic approach: the preponderance of false negatives if a threshold difference (e.g. 3% divergence value) is employed. These results demonstrate that at least 20% of recently derived taxa would be artificially lumped with closely related species, and indicate that up to 40% of global diversity falls within this recent window. Only through careful traditional taxonomy or extensive intraspecific molecular sampling can these units be differentiated.

Special Session – Biodiversity of Marine Mollusks

**Marine Bivalves of the Florida Keys: A Qualitative Faunal Analysis
Based on Original Collections, Museum Holdings, and Literature Data**

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Marine bivalve diversity in the Florida Keys was studied from original collections plus critically reviewed museum specimens and literature data. The 12000-record dataset representing 389 species resulted in a 139% increase compared to the 1995 Florida Keys National Marine Sanctuary checklist. Using multivariate non-metric statistics and *a priori* geographic groups along and across the island chain, the data showed distinct differences in benthic community structure across several spatial gradients. No northeast-to-southwest gradient was found along the oceanside fauna of the island chain, but this was pronounced within Florida Bay. The shallow-water communities of bayside and oceanside were significantly different, but resulted from different percentages of the same species. In contrast, the deeper oceanside community differed substantially from both shallow-water groups in supporting a different set of species. A comparison of this bivalve fauna with other well-documented faunas of the western Atlantic grouped the Florida Keys closer to the Gulf of Mexico and Cuba than to eastern peninsular Florida, Yucatan, and the Bahamas. Aspects of the heterogeneous (live/dead/literature) nature of the dataset are discussed and compared to analyses based on live-only data (the latter resulting in less resolution but the same general patterns). Rapid assessment methods contrasted against the long-term results show effectiveness when based on a range of sample types and habitats. The importance of data-rich gray literature sources is emphasized, and the discrepancy between the “all-species-ever-recorded” list and the results of original project collections is explored.

Special Session – Biodiversity of Marine Mollusks

**Spawn of *Zafrona pulchella* (Blainville, 1829) and *Anachis helenae* (Costa, 1983)
(Caenogastropoda: Columbellidae) from the Colombian Caribbean**

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We describe the egg capsules and embryos of *Zafrona pulchella* and *Anachis helenae* collected at the Colombian Caribbean between 20-160 m depth. *Zafrona pulchella* had one layer of 24 egg capsules attached to the shell. *Anachis helenae* was completely covered by several layers of egg capsules; only the external layer of capsules, however, contained embryos; the rest had their escape apertures open. Egg capsules of both species were translucent, dome-shaped, with an oval escape aperture at the center of the dome top; the surface was smooth with no ridges nor sutures; egg capsules were attached to the shell by an oval basal membrane which was surrounded by a thin, irregular flange. Egg capsules of *Z. pulchella* measured 2 mm in diameter and contained six embryos/capsule; egg capsules of *A. helenae* measured 1 mm in diameter and contained 25 embryos/capsule. Embryos of *Z. pulchella* were all at the gastrula stage and measured 750–900 µm in length. Uncleaved eggs of *A. helenae* measured 150 µm in diameter; the veliger had an operculum, a transparent shell measuring 188–219 µm in length, and a small velum. No nurse eggs were observed in the two species, but late cannibalism among sibling embryos may occur in *A. helenae*.

Poster Session

**The Subfamily Lamelliariinae (Gastropoda: Velutinidae)
in the Magellanic and Antarctic Area**

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Most of the Lamelliariinae species from the Magellan and Antarctic regions were described as results of classic expeditions from the last century. Since then, there has not been a comprehensive revision of Lamelliariinae gastropods. Around 30 species names were proposed for this area under the genera *Lamellaria* Montagu, 1815, and *Marseniopsis* Bergh, 1886. These species were described mostly based on external morphology. Several works also included the descriptions of internal shell, radulae, and basic anatomical information. Both genera are largely distributed around the Magellanic and Antarctic regions, probably because of their long planktonic larval life. This work is a first approach to the study of the anatomy of these prosobranchs, including data on living specimens (color patterns and ecological aspects). Specimens used in this study are deposited in the collections of the Museo Argentino de Ciencias Naturales “Bernardino Rivadavia” and Museo de La Plata. Type material of most of the species from European museums was revised. The anatomy, radulae, and jaws (including SEM micrographs of the latter two) of several species of *Lamellaria* and *Marseniopsis* are described. In addition, a preliminary list with the taxonomic status of the species described under these genera is included.

Poster Session

Protein Content of Embryos and Intracapsular Liquid of *Melongena melongena* (Linnaeus, 1758) (Caenogastropoda: Melongenidae) During Intracapsular Development

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Eggs of *M. melongena* develop inside round, flat egg capsules that contain a gelatinous intracapsular fluid. To determine whether this gel represents a nutritional source for the developing embryos, we measured the amount of proteins of the embryos throughout development from egg to the hatching stage, as well as the protein content of the intracapsular liquid at the same stages of development. Egg capsules of *M. melongena* were collected at Golfete de Cuare, Venezuela, between 1–2 m depth. Uncleaved eggs measured 352–480 μm and each contained 8–15 μg of protein. This amount of protein was not significantly different at the trochophore, veliger, and pediveliger stages; however, it decreased significantly at the hatching stage to 6 μg /hatchling (hatchlings are pediveliger larvae measuring around 720 μm in shell length). The protein concentration of the intracapsular liquid was 0.18 $\mu\text{g}/\mu\text{l}$ at the egg stage and it reached 0.13 $\mu\text{g}/\mu\text{l}$ at the prehatching stage, however, the total amount of protein in the intracapsular fluid was not significantly different throughout development from one stage to the other. Results indicate that embryos of *M. melongena* do not use the intracapsular liquid as an extraembryonic food source; furthermore, about 2–5% of the eggs do not develop and remain intact without being ingested as nurse eggs by the developing embryos.

Poster Session

**The Channeled Apple Snail (*Pomacea canaliculata*)
in Florida and Elsewhere**

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The channeled apple snail is an emerging concern in Florida. This paper will present information on this snail, including: basic biology, known distribution, impacts, and implications of the species as a vector for the rat-lung trematode *Angiostrongylus cantonensis*. An overview of its status in the world and in the United States will be discussed.

Special Session – Snails and Slugs as Agricultural and Horticultural Pests

Natural History of *Oxyloma retusa* at the Shore of a Maryland Lake

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The land snail *Oxyloma retusa* (Lea) lives on cattails (*Typha* sp.) and on wet soil along the shores of Lake Churchill, a small artificial lake in Germantown, Maryland. Microscopic examinations of the feces of snails collected in April and June indicated that the snails feed almost exclusively on dead plant matter. The generation cycles of the snails in the field were monitored for two years. The snails spend the winter as juveniles and then start growing rapidly and mating in the early spring. The cohort that survives the winter reaches its maximum shell size in June, and then dies off. The first generation offspring grows through the summer and is replaced by the second generation offspring by September. This last cohort survives the winter. The two years (2002–2003) during which the populations were monitored differed in monthly temperature and precipitation means, but similar generation cycles were observed in both years.

Contributed Session II – Terrestrial Gastropods