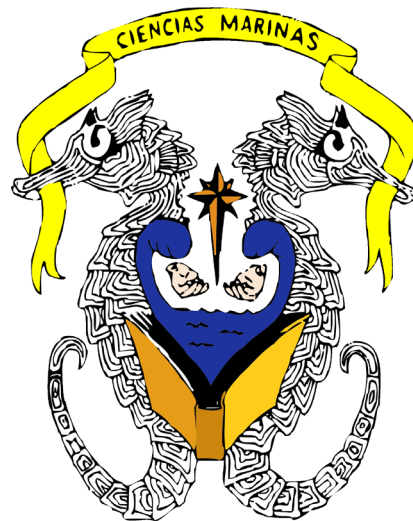




Annual Meeting

Ensenada, Baja California

Sponsored by



Universidad Autónoma de Baja California
Facultad de Ciencias Marinas

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WELCOME

Welcome to the 49th Western Society of Malacologists and 82nd American Malacological Society annual meetings. This joint conference embodies the spirit of collaboration between the two societies and represents another step forward in promoting our common goals, aspirations, and appreciation for mollusks. By meeting in Ensenada, we highlight our international vocation and celebrate our membership in Mexico and beyond.

We are very excited with the number of participants (including many students), the quality of the presentations, and the diverse scientific program, whose topics range from cutting edge research on phylogenomics, to important issues in conservation biology and mariculture, and the archaeological significance of mollusks. We are particularly grateful to the symposia organizers, Dr. Kevin Kocot (University of Alabama), Dr. Danielle Zacherl (Cal State Fullerton), Dr. Hans Bertsch (Instituto de Investigaciones Oceanológicas, UABC), Dr. Miguel Ángel del Río Portilla, and Dr. Fabiola Lafarga (CICESE), who have done an extraordinary job gathering an outstanding roster of speakers. We are also very grateful to the student assistants José Carlos Macedo, Karla Chacón, Erick González, Karina Espinoza, Isis Bastida, Nahel Rodríguez, Alvin Cruz, Lluvia Ayala, Analí Trebil, Gabriel Nava, Ilian Ortega, Marcos Muñoz, Paulina Hoyos, Selene Andrade, Andrés Razo, Itzel Pérez, Arian Castillo, Alexandra Ramírez, Enrique Nava, Jenny McCarthy, Sabrina Medrano, and Haleh Golestani. Without their help this conference would not have been possible. Last but not least, we are extremely grateful to Dr. Juan Vaca, Director of the School of Ciencias Marinas for his logistic and financial support.

The symbol chosen for the logo of this conference had a deep significance for the ancient Mexicans and represents the perfect abstraction of the fusion between nature and religious thinking in Mesoamerica. Thanks to ethnohistoric sources and the research of anthropologists, historians and archaeologists, today we know that this symbol was the representation of Ehecatl, god of the wind, one of the titles of Quetzalcoatl, perhaps the most important god in Mesoamerica. The god Quetzalcoatl often wears a pectoral plaque similar to a star, obtained from transversally sectioning a shell of *Strombus gigas*. This plaque represents the whirlwind, the *ehcacozcatl*.

We hope you enjoy the meeting and have a pleasant stay in Ensenada.

Sincerely,

Dr. Carlos Figueroa Beltrán – Universidad Autónoma de Baja California, Mexico (WSM president)
Dr. Ángel Valdés – California State Polytechnic University, Pomona, USA (AMS president)

PROGRAM

*Talk or poster eligible for the AMS Constance Boone Award for the best student presentation

June 12, 2016 – Sunday

3:00–6:30PM Registration (Hotel Coral y Marina)

4:00–6:00PM WSM Executive Board Meeting, Hotel Coral y Marina Restaurant

4:00–6:00PM AMS Council Meeting, Hotel Coral y Marina Restaurant

6:30PM Ice-breaker (Hotel Coral y Marina)

June 13, 2016 – Monday (Auditorium DIA, E-40)

9:00–9:15 Conference Inauguration

AMS Symposium Phylogenomics of Mollusks – organized by Kevin Kocot (University of Alabama)

9:15–9:30AM Symposium opening remarks

9:30–10:00AM Kocot, K.M., Poustka, A.J., Stöger, I., Halanych, K.M. and Schrödl, M. *Monoplacophoran genome sheds light on relationships among shelled molluscs*

10:00–10:30AM *Goodheart, J.A. *Phylogenomics of Cladobranchia (Gastropoda: Heterobranchia: Nudibranchia) and the evolution of nematocyst sequestration*

10:30–11:00AM *Kamel, B., Chan, P.K. and Medina, M. *Understanding molluscan biomineralization toolkits: A comparative genomic approach*

11:00–11:15AM Coffee Break

11:15–11:45AM Speiser, D.I., Oakley, T.H. and Eernisse, D.J. *Phylogenomics of Polyplacophora: When, how, and why did the shell-eyes of chitons evolve?*

11:45–12:15PM Teasdale, L., Hugall, A., Kohler, F., Herbert, D., O'Hara T. and Moussalli, A. *Phylogenomics of the pulmonate land snails*

June 13, 2016 – Monday (Auditorium DIA, E-40) – parallel session

General Session: Evolution, systematics, phylogenetics, taxonomy, chair Patrick Krug

12:15–12:30AM Cáceres Martínez, C., Barrios Ruiz, D. and Rodríguez Trejo, M. *Review of the taxonomic authorities of marine bivalves and the verification of their presence in the Mexican Pacific coast*

12:30–12:45PM Ellingson, R.A. and Krug, P.J. *Climate-driven vicariance and recurrent trans-Arctic migration in the cosmopolitan sea slug *Alderia modesta**

12:45–1:00PM *Awbrey, J.D. and Krug, P.J. *Delimiting cryptic species of sea slugs by integrating molecular data with radular characters*

1:00–2:30PM Lunch Break

June 13, 2016 – Monday (Aula Magna I, E-17) – parallel session

General Session: Ecology, biodiversity, chair Christopher Kitting

12:15–12:30AM *Arvizu Ruiz, A., Reyes Bonilla, H. and Ríos Jara, E. *Patterns of predation on gastropod mollusks in rocky shores of the Mexican Pacific*

12:30–12:45PM *Hernández Perea, F.E., Oxenford, H., Gros, O., Mateo, J., García-Moliner, G., De Jesús Navarrete, A., Paris, C. and Aldana Aranda, D. *Larval diversity of gastropods in the Greater Caribbean*

12:45–1:00PM Lemus-Santana, E., Rubio-Sandoval, K.Z. and Sanvicente-Añorve, L. *Environmental factors affecting holoplanktonic mollusk distribution in the coast of the Mexican Caribbean*

1:00–2:30PM Lunch Break

June 13, 2016 – Monday (Auditorium DIA, E-40) – parallel session

General Session: Evolution, systematics, phylogenetics, taxonomy (continued), chair Ryan Ellingson

2:30–2:45PM *Powell, J.A., Krug, P.J. and Marshall, D. *Multivariate selection and the range limit of Alderia willowi: Effects of salinity and trait covariance*

2:45–3:00PM Krug, P. J., Ellingson, R.A., Vendetti, J.E. and Valdés, A. *Challenging a paradigm of gastropod macroevolution: Species selection favors dispersive life histories in sea slugs*

3:00–3:15PM Cerda, P.A. and Duda, Jr., T.F. *Hybridization and introgression in cone snails?*

3:15–3:30PM *Golestani, H. and Valdés, A. *Asymmetric genetic introgression of a hermaphroditic invasive sea slug in a native species*

3:30–3:45PM Gurgo Sálice, P., Cáceres Martínez, C., Barrios Ruiz, D., and Rodríguez Trejo, M. *New records of marine bivalves for the coast of Baja California Sur, Mexico*

3:45–4:00PM Coffee Break

General Session: Evolution, systematics, phylogenetics, taxonomy (continued), chair Paul Valentich-Scott

4:00–4:15PM *Hoover, C.A., Padula, V., Schrödl, M., Hooker, Y. and Valdés, A. *Integrative taxonomy of the Felimare californiensis and Felimare ghiselini species complex (Mollusca, Gastropoda, Nudibranchia)*

4:15–4:30PM *McCarthy, J., Krug, P., Vendetti, J. and Valdés, A. *The slug within the bivalve: Reconciliation of shell-based taxonomy and molecular data in Juliidae (Heterobranchia: Sacoglossa)*

4:30–4:45PM *Medrano, S., Krug, P., Vendetti, J., Gosliner, T.M. and Valdés, A. *It loves me, it loves me not: Counting species of the “rose petal sea slug,” Polybranchia (Mollusca: Gastropoda) with a molecular systematics approach*

4:45–5:00PM *Moreno-Alcántara, M., Aceves-Medina, G. and García-Rodríguez, F.J. *Taxonomic revision of the species of the family Atlantidae (Gastropoda: Pterotracheoidea) in the Mexican Pacific using morphological and genetic analyses*

5:00–5:15PM Valentich-Scott, P., Coan, E.V. and Zelaya, D.G. *A seldom traveled path: New marine bivalves in the Perú-Chile Province (western South America)*

5:15–5:30PM *Wiedrick, S.G. *Phylogeny, morphology and ecology of the Eastern Pacific genus Ocinebrina Jousseaume, 1880*

5:30PM Group photo

6:30PM Bus departs for visit CICESE facilities

June 13, 2016 – Monday (Aula Magna I, E-17) – parallel session

General Session: Ecology, biodiversity (continued), chair Nora Foster

2:30–2:45PM Lemus-Santana, E., Rodríguez-Vázquez R.A. and Sanvicente-Añorve, L. *Chiton community structure (Mollusca: Polyplacophora) of a rocky shore in Montepío, Veracruz, Mexico*

2:45–3:00PM Sánchez-Velasco, L., Ruvalcaba-Aroche, E.D., Beier, E., Godínez, V.M., Barton, E.D., Díaz-Viloria, N. and Pacheco, R. *Paralarvae of the complex Sthenoteuthis oualaniensis-Dosidicus gigas (Cephalopoda: Ommastrephidae) in the northern limit of the shallow oxygen minimum zone of the Eastern Tropical Pacific Ocean (April, 2012)*

3:00–3:15PM Alvarez-Cerrillo, L.R., Avila-Poveda, H.O., Benítez-Villalobos, F., Escobar-Sánchez, O., Rodríguez-Domínguez, G. and García-Ibañez, S. *Epibiont biodiversity from the basibiont Chiton articulatus (Mollusca: Polyplacophora) through the Mexican Tropical Pacific*

3:15–3:30PM Bluhm, B.A., Iken, K. and Foster, N.R. *Diversity and distribution of marine mollusks along the Beaufort Sea shelf and slope: The influence of Pacific and Atlantic water masses*

3:30–3:45PM Kitting, C.L. and Bhaduri, R. *Gastropod and bivalve mollusks associated with drift plants, transported throughout the freshwater San Joaquin River Delta, California*

3:45–4:00PM Coffee Break

4:00–4:15PM Aguilar-Estrada, L.G., Ruiz-Boijseauneau, I., Sanvicente-Añorve, L., Serviere-Zaragoza,

E. and D. Rodríguez, V. *Community structure of limpets and chitons associated to macroalgal assemblages at the region of Ixtapa-Zihuatanejo, Guerrero, Mexico*

4:15–4:30PM Naranjo-García, E. and Vital, X.G. *The use of average distinctness index to analyze a freshwater mollusks community in a natural reserve in Southern Mexico*

General Session: Miscellaneous talks – parallel session, chair Jann Vendetti

4:30–4:45PM Morales-Ortega, P. and González-Barba, G. *Eocene mollusks from Baja California Sur, Mexico*

4:45–5:00PM Zúñiga-Arellano, B. *Mollusk remains in the offering 125 of the Great Temple of Tenochtitlan*

5:00–5:15PM Vendetti, J.E., Lee, C. and Willadsen, O. *Inventory of Southern Californian terrestrial gastropods: A citizen science collaboration between the public and the Natural History Museum of Los Angeles County*

5:15–5:30PM Vendetti, J.E., Hendy, A.J.W. and Estes-Smargiassi, K. *Digitization of fossil molluscs at the Natural History Museum of Los Angeles County: Introducing the EPICC TCN*

5:30PM Group photo

6:30PM Bus departs for visit CICESE facilities

June 14, 2016 – Tuesday (Auditorium DIA, E-40)

Symposium Abalone Mariculture and Restoration – organized by Miguel Ángel del Río Portilla and Fabiola Lafarga (CICESE).

9:00–9:15AM Symposium opening remarks

9:15–9:45AM Cruz-Flores, R. and Cáceres-Martínez, J. *Diseases of abalone around the World: A review*

9:45–10:15AM Cruz-Flores, R., Cáceres-Martínez, J., Muñoz-Flores, M., Vásquez-Yeomans, R., Hernández-Rodríguez, M., Del Río Portilla, M.A. and Rocha-Olivares, A. *Symbionts and parasites of abalone of commercial importance from the peninsula of Baja California, Mexico*

10:15–10:45AM Del Río-Portilla, M.A., Vargas-Peralta, C.E., Lafarga De La Cruz, F. and Farfán, F. *Mitochondrial genomes of the yellow, Haliotis corrugata, and black, Haliotis cracherodii, abalones: a protein comparison*

10:45–11:00AM Coffee Break

11:00–11:30AM Paniagua-Chávez, C.G., Del Río-Portilla, M.A. and Lafarga-De la Cruz, F. *Ex situ conservation as a strategy to enhance endangered wild population of valuable mollusks*

11:30–12:00PM Vázquez-Moreno, J.E. and Badillo-Sotelo, L.M. *Abalone seed production: Data collection and stats from a commercial scale lab perspective*

12:00–12:30PM Précoma-de la Mora, M., Boch, C., Espinoza, A., Hernández-Velasco, A., Mendoza, R., Micheli, F. and Woodson, B. *Conservation of Green and Pink Abalone: Efforts and results in Natividad Island, Baja California Sur, Mexico*

12:30–1:00PM Del Río-Portilla, M.A., Lafarga De La Cruz, F., Vargas-Peralta, C.E. and Farfán, F. *Searching for microsatellite genetic markers in abalone, Haliotis spp., a genomic approach*

1:00–2:30PM Lunch Break

June 14, 2016 – Tuesday (Auditorium DIA, E-40) – parallel session

General Session: Evolution, systematics, phylogenetics, taxonomy (continued), chairs Thomas Duda Jr. and Alan Kohn

2:30–2:45PM *Wilk, J.A. *Using ontogenetic vectors to inform systematic decisions in Isognomoninae Woodring, 1925 [1828]*

2:45–3:00PM Granados-Cifuentes, C., Rawlings, T.A., Bieler, R., Golding, R.E., Sharp, P. and Collins, T.M. *Gene rearrangement and molecular evolution within vermetid gastropod mitochondrial genomes*

3:00–3:15PM Eernisse, D.J. *Well-traveled chitons on tsunami debris or imported oysters have helped unravel the Acanthochitona achates (Gould, 1859) species complex*

3:15–3:30PM Ghanimi, H. *Phylogenetic reconstruction of the genus Berthella using molecular and morphological traits*

3:30–3:45PM Eernisse, D.J., Wiedrick, S.G. and Pilgrim, E.M. *Southern California marine shelled gastropod barcode project*

3:45–4:00PM Coffee Break

4:00–4:15PM *King, C. and Valdés, A. *Southern invasion: Population genetics of Phidiana hiltoni*

4:15–4:30PM *Linnenbrink, J.L., Walter, R.P., Zacherl D.C. and Eernisse, D.J. *Genetic population structure of the Olympia oyster, Ostrea lurida, in southern California*

General Session: Miscellaneous talks, chair Douglas Eernisse

4:30–4:45PM *Pavón Paneque, A.C. and García Gómez, J.C. *Managing conservation of the endangered Patella ferruginea (Gastropoda: Patellidae) in a marina about to be enlarged. A potential artificial marine micro-reserve network*

4:45–5:00PM Kohn, A.J. *Human injuries and fatalities due to venomous marine snails of the family Conidae*

5:00–5:15 *Macedo-Carranco, J.C., Ramirez-Rosas, B.A. and Figuroa-Beltrán, C. *Local public opinion of Baja California's mollusk production*

5:30–6:30PM Poster Session (Auditorium DIA, E-40)

7:00PM Evening AMS/WSM auction (Hotel Coral y Marina)

June 14, 2016 – Tuesday (Aula Magna I, E-17) – parallel session

General Session: Fisheries, mariculture, chairs Carlos Cáceres and Esteban Felix Pico

2:30–2:45PM Cáceres Martínez, J., Cruz-Flores, R. and Vásquez-Yeomans, R. *Symbionts, parasites and diseases of the Generous Clam (Panopea generosa) from the Pacific coast of Baja California, Mexico*

2:45–3:00PM Camacho-Mondragón, M.A., Ceballos-Vázquez, B.P., Arellano-Martínez, M., Ramírez-Luna, S., Medina-López, M.A. and Rivera-Camacho, A.R. *Tunicate invasion threatens recovery of a population of the penshell Atrina maura (Bivalvia: Pinnidae) in the Gulf of California*

3:00–3:15PM Vargas-Peralta, C.E., Lafarga De La Cruz, F., Farfán, C. and del Río-Portilla, M.A. *Genetic and genomic resources for the California Butterclam Saxidomus nuttalli (Conrad, 1837)*

3:15–3:30PM Félix-Pico, E.F. and Ramírez-Rodríguez, M. *Growth of black ark from tagging/recapture experiments in La Paz Bay, BCS, Mexico*

3:30–3:45PM *Romero-Romero, C.C. and Sánchez-Saavedra, M.P. *Effect of light qualities on the growth and proximal composition of Amphora sp.*

3:45–4:00PM Coffee Break

4:00–4:15PM Romo-Piñera, A., Arellano-Martínez, M. and García-Domínguez, F. *Size at first maturity of Squalid Callista Megapitaria squalida*

4:15–4:30PM Sánchez-Saavedra, M.P. *Benthic diatom culture for abalone nourishment*

4:30–4:45PM *Yee-Duarte, J.A., Ceballos-Vázquez, B.P., Shumilin, E., Arellano-Martínez, M., Rivera-Camacho, A. and Kidd, K. *Infection intensity by trematodes in Megapitaria squalida (Bivalvia: Veneridae) and its impact on the reproduction*

4:45–5:00PM *Cicala F., Del Río-Portilla M.A. and Rocha-Olivares A. *Molecular description of the intestinal bacterial flora in wild Mexican population of Haliotis corrugata and Haliotis fulgens*

5:00–5:15PM Castañeda-Fernández de Lara, V. and Gómez-Rojo, C. *The Octopus commercial fishery in Baja California Sur, Mexico is composed of several species*

5:15–5:30PM López-Galindo, L.L., Galindo-Sánchez, C.E., Rosas C., Díaz F. and Cante-Cua, Z.P. *Temperature effect in males of Octopus maya and their sperm quality*

5:30–6:30PM Poster Session (Auditorium DIA, E-40)

7:00PM Evening AMS/WSM Auction (Hotel Coral y Marina)

June 15, 2016 – Wednesday (Auditorium DIA, E-40) – parallel session

Symposium Mollusk Conservation – organized by Danielle Zacherl (California State University Fullerton)

8:30–8:45AM Symposium opening remarks

8:45–9:15AM *Bird, A.C., Neuman, M., and Zacherl, D.C. *Determining population structure, reproductive potential, and habitat associations of pinto abalone (Haliotis kamtschatkana) in southern California*

9:15–9:45AM Searcy-Bernal, R. *Review and perspectives of abalone (Haliotis spp.) restocking in México*

9:45–10:15AM Wang, S., Neuman, M.N., Ben-Horin, T., Friedman, C.S., Gruenthal, K., Lonhart, S., Moore, J., Raimondi, P., Richards, D., Shanks, A., Steinbeck, J., Taniguchi, I., Ugoretz, J., Van-Blaricom, G. and Whitaker, S. *It's black or white: A different roadmap to restoring the endangered black abalone, Haliotis cracherodii*

10:15–10:45AM Neuman, M.J., Wang, S.M., Stierhoff, K.L., Witting, D.A., Hyde, J.R., Rogers-Bennett, L., Moore, J.D., Taniguchi, I.K., Catton, C.A., Aquilino, K.M. and Cherr, G.N. *Rock hard abs in five (not so) simple steps: Restoration efforts for the first federally endangered marine invertebrate in the United States, White Abalone (Haliotis sorenseni)*

10:45–11:00AM Coffee Break

11:00–11:30PM Aquilino, K.M., Ashlock, L.W., Kawana, S.K., Walker, B., Marshman, B.C., Vines, C.A., Moore, J.D., Rogers-Bennett, L., Catton, C., Vater, A., Simon, S., Wilson, T., Trautwein, S., Plante, C., Darrow, K., Velarde, M., Hyde, J., Bush, D., Wang, S.S., Neuman, M.J. and Cherr, G.N. *Mood lighting and spa treatments: Captive propagation of the endangered white abalone (Haliotis sorenseni)*

11:30–12:00PM Ford, T., Witting, D., Reynolds, A., Burdick, H., Wang, S. and Neuman, M. *Restoration techniques for green abalone (Haliotis fulgens) in Southern California*

12:00–12:30PM Kawana, S., Juhasz, C., Taniguchi, I., Stein, D., Hofmeister, J.K.K., Walker, B., Maguire, A., Catton, C.A. and Rogers-Bennett, L. *Experimental stocking of Red Abalone (Haliotis rufescens) in Southern California artificial reefs*

General Session: Fisheries, mariculture (continued), chair Ricardo Searcy Bernal

12:30–12:45PM Hofmeister, J.K.K., Kawana, S., Walker, B., Catton, C.A., Taniguchi, I., Stein, D., Maguire, A. and Rogers-Bennett, L. *Predation and predator response to experimental stocking of red abalone (Haliotis rufescens) in Southern California*

12:45–1:00PM Neuman, M.J., Witting, D.A., Stierhoff, K.L., Bird, A.C. and Hagey, W. *To move or not to move, is that the question?: Preliminary results from acoustic tracking of Pinto Abalone (Haliotis kamtschatkana)*

1:00–2:30PM Lunch Break

June 15, 2016 – Wednesday (Aula Magna I, E-17) – parallel session

Symposium Mollusks and Human Cultures – organized by Hans Bertsch (Instituto de Investigaciones Oceanológicas, UABC)

9:00–9:15AM Symposium opening remarks

9:15–9:45AM Etnier, M.A., Partlow, M. and Foster, N.R. *Alutiiq subsistence economy at Igvak, a Russian-American Artel in the Kodiak Archipelago*

9:45–10:15AM Boyd, G.E. and Roman, D.V. *Mytilus californianus shell fragments at inland archaeological sites: An archeo-malacological mystery*

10:15–10:45AM *Fonseca Ibarra, E., Téllez Duarte, M. and Guía Ramírez, A. *Patterns of shellfish*

consumption during the Middle to Late Holocene in the Bajamar-Jatay region of Baja California

10:45–11:00AM Coffee Break

11:00–11:30AM Figueroa-Beltrán, C., Fonseca-Ibarra, E. and Ramírez-Valdez, A. *Archaeology and Malacology in Baja California: Building bridges between anthropology and conservation*

11:30–12:00PM Vanderplank, S., Ezcurra, E., Mata, S. and Figueroa-Beltrán, C. *Aragonite shell middens increase biodiversity in Baja California*

12:00–12:30PM Berry, S.S., Hubbs, C.L., Bertsch, H. and Eernisse, D.J. *The distribution, past and present, of Cryptochiton*

12:30–1:00PM Fujita, H. and Cáceres-Martínez, C. *Early and Middle Holocene pearl ornaments at Covacha babisuri on Espiritu Santo Island, Baja California Sur, Mexico*

1:00–2:30PM Lunch Break

June 15, 2016 – Wednesday (Auditorium DIA, E-40) – parallel session

General Session: Fisheries, mariculture (continued), chair Michel Hendrickx

2:30–2:45PM *Braciszewski, A.R. and German, D.P. *Relatedness and differential disease resistance in eastern Pacific haliotids*

2:45–3:00PM *Macedo-Carranco, J.C., Searcy-Bernal, R., and Montaña-Moctezuma, C.G. *Comparison between two Red Abalone (*Haliotis rufescens*) tagging methods*

3:00–3:15PM *Pérez-Bustamante, I.S. and García-Ezquivel, Z. *Effect of five chemicals on the metamorphosis of Cortez geoduck clam larvae, Panopea globosa*

3:15–3:30PM *Muñoz-Hernández, M., Rodríguez-Hernández, D., Valenzuela-Espinoza, E., González-Gómez, M.A., García-Pámares, J. and Olivares-Bañuelos, T.N. *Larval and post-larval growth, and spat production of the clam *Chione cortezi* (Carpenter, 1864)*

3:30–3:45PM *Nava-Gómez, G.E., García-Ezquivel, Z., Carpizo-Ituarte, E.J. and Olivares-Bañuelos, T.N. *Survival and growth of geoduck clam larvae (*Panopea generosa*), reared at different densities in a flow-through seawater system*

3:45–4:00PM Coffee Break

4:00–4:15PM Pérez-Carrasco, L., Galindo-Sánchez, C., Carpizo-Ituarte, E., Díaz-Herrera, F., Lafarga-De la Cruz, F., López-Landaveri, E., García-Ezquivel S. and Hernandez-Ayón, J.M. *Effect of stress by decreasing the pH in the expression of genes in geoduck larvae *Panopea globosa**

4:30–5:30PM WSM Business Meeting

5:30–6:30PM AMS Business Meeting

7:00PM Banquet (Hotel Coral y Marina)

June 15, 2016 – Wednesday (Aula Magna I, E-17) – parallel session

Symposium Mollusks and Human Cultures – organized by Hans Bertsch (Instituto de Investigaciones Oceanológicas, UABC)

2:30–3:00PM *Rodríguez-Obregón, D. and Carpenter Slavens, J. *The genus *Corbicula* as a dating group for Prehispanic archaeological sites*

3:00–3:30PM *Gutiérrez Ramírez, J. *Shell objects found in the archaeological site of El Ocote, Aguascalientes*

3:30–4:00PM Velázquez-Castro, A., Valentín-Maldonado, N., Martínez Mora, E. and Fiehring, B.W. *The use of fresh water mussels in Tamtoc, San Luis Potosí, Mexico*

4:00–4:30PM Valentín-Maldonado, N., Aparicio-Hernández M., Velázquez-Castro, A. and Juárez Cossío, D. *Taxonomical identification of nacreous species in Jaina, Campeche, Mexico*

4:30–5:30PM WSM Business Meeting (Aula Magna I, E-17)

5:30–6:30PM AMS Business Meeting (Aula Magna I, E-17)

7:00PM Banquet (Hotel Coral y Marina)

June 16, 2016 Thursday

Field trips: San Quintin, Valle de Guadalupe

June 16, 2016 Thursday

8:00AM–4:00PM First Binational Abalone Workshop – Salón de Usos Múltiples (SUM), Centro de Investigación Científica y de Educación Superior de Ensenada (CICESE)

POSTER TITLES

- Aldana Aranda, D. and Enriquez Díaz, M. *Will it be possible to rear the larval stages of queen conch Strombus gigas from the Caribbean sea (Mollusca Gastropoda) under near-future predictions of ocean temperature?*
- *Aristeo-Hernández J., Mayén-Estrada R. and Naranjo-García E. *Pomacea flagellata Say, 1827 as basibiont of Acineta tuberosa Ehrenberg, 1838 (Ciliophora: Suctorina)*
- Burciaga-Cifuentes, L.M., Urbano, B. and Rivas, G. *The Solenogastres, Caudofoveata and Monoplacophora classes in México: The current state of knowledge*
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ABSTRACTS

1. SYMPOSIUM PHYLOGENOMICS OF MOLLUSKS

Monoplacophoran genome sheds light on relationships among shelled molluscs

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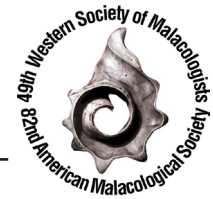
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Despite their diversity and importance, evolutionary relationships among the major lineages of Mollusca have long been debated. Recent studies provided the first largely well-resolved phylogeny for Mollusca, showing that there are two major clades: Aculifera (chitons and aplacophorans) and Conchifera (all other shelled molluscs). However, relationships among conchiferan taxa have been inconsistent among studies. Monoplacophora is traditionally viewed as the sister taxon of the rest of Conchifera. Nevertheless, analyses of datasets dominated by nuclear ribosomal genes recover Monoplacophora sister to Polyplacophora and the one phylogenomic study sampling this clade recovered it sister to Cephalopoda. We conducted phylogenomic analyses using deeply sequenced transcriptomes or genomes from all major lineages of Mollusca, including newly sequenced genomic data from *Laevipilina antarctica*. Whereas a partitioned maximum likelihood (ML) analysis recovered Monoplacophora sister to Cephalopoda with moderate support, Bayesian inference (BI) analysis using the site heterogeneous CAT-GTR model recovered Monoplacophora sister to all other conchiferans with strong support. A supertree approach also recovered Monoplacophora sister to the remainder of Conchifera although support for the node grouping other conchiferans to the exclusion of Monoplacophora was weak. ML and BI analyses recovered Gastropoda and Scaphopoda as sister taxa although Gastropoda + Bivalvia was weakly supported in the supertree analysis. A molecular clock analysis based on our Bayesian topology dates the origin of Mollusca to 564±3.51 MYA and the origin of Conchifera to 556±2.88 MYA. Results from this comprehensive phylogenomic dataset largely support a basal conchiferan placement of Monoplacophora and a sister-taxon relationship of Gastropoda and Scaphopoda. Implications of support for a basal conchiferan position of Monoplacophora for understanding ancestral character states of Mollusca and Conchifera will be discussed. Future studies incorporating additional genomes from other molluscan taxa will hopefully continue to solidify our understanding of early molluscan evolution, impacting all disciplines investigating molluscs.



Phylogenomics of the pulmonate land snails

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Molecular techniques are increasingly being used to help resolve phylogenetic relationships within many molluscan taxa. Up until recently this approach has been restricted by the limited number of molecular markers available for use in many molluscan groups. In particular, the markers used (including the mitochondrial genome) often do not provide enough information to clearly resolve deeper relationships. 'Next generation' sequencing (NGS) is revolutionising the field of evolutionary biology by vastly increasing the amount of genetic data available for studying relationships between taxa. Our research involves the application of NGS in both RNA and DNA sequencing to obtain sequences for hundreds of genes to address the evolutionary relationships within the land snails (Eupulmonata). The broad objectives of our study are first to sequence and assemble transcriptome datasets (i.e. the majority of the protein coding genes present in the genome) to address the deeper evolutionary relationships within Eupulmonata. Secondly, to design an exon-capture protocol targeting 500 orthologous genes from genomic material, with a particular emphasis on utilising historic specimens held in natural history collections. In this talk we will present an overview of this research project to date including transcriptome phylogenies for Panpulmonata and exon-capture results for the Australasian radiation of the family Camaenidae and Rhytididae.

Phylogenomics of Cladobranchia (Gastropoda: Heterobranchia: Nudibranchia) and the evolution of nematocyst sequestration.

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Cladobranchia (Gastropoda: Nudibranchia) is a diverse clade (~1000 species) composed of exclusively marine gastropods within the order Nudibranchia. A number of interesting characters have evolved within this clade, including the ability to sequester stinging organelles from cnidarian prey (nematocyst sequestration). In order to fully understand ecological and morphological character evolution of nudibranchs within Cladobranchia (like nematocyst sequestration), a strong hypothesis of the relationships within and evolutionary history of this group is necessary. Recent attempts using molecular data have addressed some relationships within this group, but a robust phylogenetic hypothesis for the entire clade



has yet to be achieved. A major concern is that recent phylogenetic studies are contradictory and generally lack support for competing groupings of taxa within Cladobranchia. Even at a fundamental level, it is unclear whether the three traditional groups within Cladobranchia (Arminida, Dendronotida and Aeolidida) are monophyletic. In our research, we have successfully addressed some of these long-standing issues by utilizing RNA-Seq data (transcriptomes). These data provide a well-supported and almost fully resolved phylogenetic hypothesis of the sampled taxonomic groups in Cladobranchia. We then use this phylogenetic hypothesis to map the evolution of traits associated with nematocyst sequestration in Cladobranchia, though more work remains to be done in regards to the determination of the evolutionary steps involved in the origin of this ability.

Phylogenomics of Polyplacophora: When, how, and why did the shell-eyes of chitons evolve?

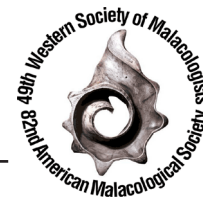
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Learning how and why complex traits like eyes originate is a fundamental goal of evolutionary biology. New molecular resources are revealing that light-detecting structures are distributed more broadly across metazoan taxa and tissue types than suspected previously. Here, I will discuss how we are using the diverse array of light-detecting structures found in mollusks — particularly those associated with the aesthetes of chitons (Class Polyplacophora) — to ask how eyes evolve through stepwise processes and why eyes may be present in certain lineages but not others. The eyes of chitons are of particular interest because individuals can have vast numbers of them (up to hundreds or thousands) embedded in their shell plates, they may have evolved recently relative to other types of eyes, and they are the first eyes known to form images using lenses made of the mineral aragonite (CaCO₃). To study how the shell-eyes of chitons have evolved, we are first identifying the molecular components of vision in these animals using transcriptome sequencing and a high-throughput, tree-based approach for sequence annotation. Second, we are studying the patterns of expression of these eye-related genes across taxa. So far, our results indicate that the shell-eyes of chitons may be homologous to the light-sensitive aesthetes embedded in the shell plates of their eyeless relatives. Third, by building a new molecular phylogeny of chitons and inferring ancestral character states related to eyes and vision, we are constructing a stepwise account of the evolution of light-detecting structures in chitons. To address why eyes may have evolved in certain lineages of chitons (and not others), we are studying the functional benefits, costs, and constraints associated with transitions from non-visual light-sensitive organs to those that provide spatial information about light. Spatial vision may benefit chitons by helping them distinguish approaching predators from uniform decreases in illumination, thereby reducing costly defensive responses to non-existent threats. However, by incorporating more elaborate sensory structures into their shell plates, chitons may weaken the ability of their armor system to protect them from predators or adverse environmental conditions.



Understanding molluscan biomineralization toolkits: A comparative genomic approach

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Biomineralization, a process that is found across the Tree of Life, is the formation of minerals by living organisms. Animal calcification in particular is the controlled deposition of calcium carbonate to produce supportive structures in both vertebrates and invertebrate taxa. The ability to calcify was an evolutionary innovation that is thought to be greatly responsible for what has been coined as the “Cambrian Explosion,” a major adaptive radiation event that took place at the late Neoproterozoic-Cambrian boundary. Multiple extant animal (metazoan) phyla have the ability to calcify, however, little is known about the genetics of the ancestral metazoan biomineralization toolkit. Therefore, at present it is not possible to establish with clarity whether there was an ancestral metazoan biomineralization core toolkit shared by all the extant calcifying animal lineages. Genomic and post-genomic approaches are opening a new window of opportunity to engage in questions regarding homology and evolution of this important biological innovation. In order to test different hypotheses related to the evolution of the biomineralization toolkit we developed a bioinformatics pipeline (Biomine) that we used to identify shared protein families involved in biomineralization related processes across cnidarians, mollusks, echinoderms, and vertebrates (available at <http://biomine.net/>). In order to increase the phylogenetic representation of the lophotrochozoan biomineralization genetic information we undertook the sequencing of transcriptomes from the biomineralizing tissue (mantle) of several molluscan species with publicly available whole genome data: *Lottia gigantea*, *Crassostrea gigas*, *Aplysia californica* and *Biomphalaria glabrata*. The transcriptomes were compared against each other after filtering through the Biomine pipeline to determine which biomineralization protein families are shared between these taxa. Taxonomically restricted families were also detected. This study sheds light on the shared molluscan biomineralization protein families.



2. SYMPOSIUM MOLLUSKS AND HUMAN CULTURES

Alutiiq subsistence economy at Igvak, a Russian-American *Artel* in the Kodiak Archipelago

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Igvak was a Russian-American fur hunting outpost (artel) on the south end of Afognak Island, Alaska, that was occupied from the 1790's to about 1830. Midden samples were recovered from deposits adjacent to the Alutiiq workers' barracks as part of the Dig Afognak program. Although the remains of small amounts of European domesticated animals were present, the bulk of the workers' diet, as indicated by midden material, consisted of traditional local foods. The dominant species included cod, harbor seals, and puffins, with a mix of intertidal invertebrates including Katy chitons, (*Katharina tunicata*) mussels (*Mytilus* sp.), butter clams, *Saxidomus gigantea* and periwinkles (*Littorina sitkana*). A single whale barnacle species was also identified.

Mytilus californianus shell fragments at inland archaeological sites: An archeo-malacological mystery

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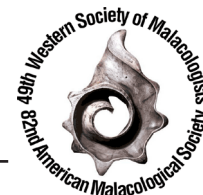
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Chumash people thrived on the northern Santa Barbara Channel Islands and portions of the Alta California mainland for thousands of years prior to European contact. The archaeological sites of their known villages and camps are often found to contain large quantities of *Mytilus californianus* shell fragments. These have long been considered evidence of food preparation for feasting events or even reliance on mussels as part of subsistence diets (Gamble, 2008: 26, 154). However, some of the village sites with shell fragment deposits are so far inland as to raise the question of whether whole mussels could have been transported to those locations in time for safe and edible consumption.

The present study investigated this question through a geographic information system estimate of the inter-village trail network in a portion of southern Ventura and Los Angeles Counties, calculation of walking travel times across the network considering the terrain, and review of food safety literature. The results suggested that mussels would not likely remain edible over the time intervals required for transport to the more distant inland villages.

Reference

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Patterns of shellfish consumption during the Middle to Late Holocene in the Bajamar-Jatay region of Baja California

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Shellfish harvesting seems to have been essential in the diet of the prehistoric human groups that inhabited the northwest coast of the peninsula of Baja California. For this reason, the qualitative and quantitative analysis of the shellfish remains located in the coastal camps (middens) is ideal for understanding these populations. In this study, eight middens were analyzed in the area of Bajamar-Jatay, Baja California in order to explain the pattern of settlement, harvest strategies and timing of the use of coastal resources from ecological and environmental perspectives. A preference in the harvest of black abalone (*Haliotis cracherodii*), California mussel (*Mytilus californianus*) and owl limpet (*Lottia gigantea*) from Middle to Late Holocene was determined. However, in the settlements of the late Middle Holocene there is a higher use of black abalone and owl limpet, combined with the exploitation of green abalone (*Haliotis fulgens*), which disappears or diminishes considerably in the Late Holocene sites. By contrast, in the late camps an increase of mussel consumption is observed and clam (*Tivela stultorum*) is incorporated into the diet. So apparently, species composition of each strata can allow chronological inferences about the occupation of the settlements. Also, some cultural factors that could influence food preferences and environmental factors (climatic anomalies) that probably caused changes in the availability of resources are discussed. Finally we analyze the methodological problems associated with taphonomic bias resulting from the use of the variables Weight, Minimum Number of Individuals (MNI) and Meat Weight Contribution of the consumed species.

Aragonite shell middens increase biodiversity in Baja California

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Indigenous peoples of Baja California spent winters on the coast avoiding the cold of the mountains, and taking advantage of the protein-rich resources of the ocean and adjacent areas. Their activities resulted in the deposition of large quantities of mollusk shells in their frequented fishing grounds. In Baja California these 'middens' are visible along the coast. Midden composition varies with their position e.g., those adjacent to rocky shores are composed primarily of muscle and abalone shells, whereas those adjacent to sandy shores are composed predominantly of clam shells. These shell-rich soils have often show variation in plant species composition, and can harbor unique plant assemblages in NW Baja California. Over



thousands of years, the predictable winter rains of have weathered calcium from shells which has changed soil properties, remediated sodic and saline soils, and resulted in a unique microhabitat. The impact of the shells on these plant communities varies considerably with shell composition and soil properties. Clam shells on clay or silt soils have the most significant impact on plant communities, presumably as a result of the additional calcium to the soil, which adjusts nutrient availability. These archeological sites (mostly ~5,000 years old) have become part of the landscape, and form islands of unique habitat within the heterogeneous matrix of the region. Native plant biodiversity and landscape heterogeneity are significantly increased on the anthropogenic soils of these shell middens. Conservation efforts in this region may be furthered by identifying the overlapping biological and archeological priorities to enable a multi-disciplinary approach to habitat preservation in these cultural landscapes.

The distribution, past and present, of *Cryptochiton*

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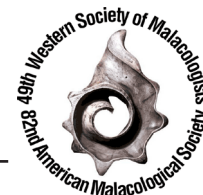
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In the late 1940s and early 1950s, Carl L. Hubbs, S. Stillman Berry and William K. Emerson discovered *Cryptochiton stelleri* valves in midden mounds in northwestern Baja California, far south of this species' present distribution. Using unpublished documents and manuscripts (Berry and Hubbs, ms., ca. 1954) and published articles (e.g., Emerson, 1956; Hubbs, 1959), we describe the radiocarbon dating and oxygen isotopic evidence from dated midden mounds (ca. 950-1850 CE) for past climate changes and water temperatures along the Pacific Coast of northwest Baja California, and their effects on the distributions of the gumboot chiton. For the first time, we illustrate the material collected by Hubbs and Berry (now in the collections of the Santa Barbara Museum of Natural History), and present in situ images of *C. stelleri* valves in middens between La Bocana Santo Tomás and Punta China, Baja California. We contrast these data and those from other Californian midden sites (e.g., Braje and Erlandson, 2008) with the modern distribution of *C. stelleri*.

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Early and Middle Holocene pearl ornaments at Covacha babisuri on Espiritu Santo Island, Baja California Sur, Mexico

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On Espiritu Santo Island, situated in the La Paz Bay in the southern Gulf of California, there is a rock shelter named “Covacha Babisuri”, which is the oldest excavated site in the Baja California peninsula, dated to 10,970±60 RCYBP or 12,367–11,871 cal BP (Beta-236259), with evidences of the Ancient Californios, such as numerous shellfish, other faunal and flora remains, as well as various artifacts made of stone, shell, coral and bone. In addition, a flexed human adult male burial associated with numerous metal objects, including an iron lance point, a shaft called “regatón” and nails, and a bronze ring were found. The presence of pearls was recorded in the lower and middle stratum, corresponding to the Early and Middle Holocene, approximately between 11,000 and 5,000 years ago.

We analyzed 14 pearls (with an average large axis of 8.26±1.94 mm), 13 belong to the species *Pinctada mazatlanica* as function of its nacre characteristics and the other is from *Megapitaria squalida* with porcelain surface instead nacre (large axis of 9.2 mm, a minor axis of 8.2 mm and, a channel width of 0.9±0.06 mm). All pearls were gently smoked and show one or two carving channels or incisions.

There are two different groups with respect to the width of channels in pearls; the average width of the first group is 0.511±0.004 mm and that of the second group is 1.09±0.022 mm, in both cases with lower Pearson Variation Coefficient, 23% for the first group, and 19% for the second. For the first group, one model of width distribution was proposed offering an average of channel width of 0.5 mm ($y=0.571x^2+5.71x-10.94$; $r^2=0.95$), suggesting the use of a calibrated tool, as were reported for analysis of pearls found in “Ensenada de Muertos” excavations (Caceres and Rosales, 2011).

Shark teeth (n=30) were measured in their edge saw thickness (with an average of 0.59±0.003 mm) and the results were compared to pearl channel width dimensions. Our results may support the hypothesis of the use of shark teeth as a tool for grooving. However, it is also possible that a thin stone flake also might have been used for grooving. The use of pearls and the significance of the tradition of carving technique by Ancient Californios from the southern part of the peninsula of Baja California are discussed.

Shell objects found in the archaeological site of El Ocote, Aguascalientes

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One of the most appreciated of raw materials for the production of objects in Mesoamerica was the shell. These mollusc shells often came from distant places and had to be obtained through exchange or trade, or by going to where they occurred. With these raw elements, ornamental or votive items were made that principally individuals of high hierarchical standing were privileged to own (Velázquez Castro, 2007; Moholy Nagy, 1995: 7–8).

The archaeological site El Ocote, dated from the late/epi-classic period between 650–900 A.D. (Pelz Marín, 2000), is located in the current state of Aguascalientes on the northern border that divides Mesoamerica and Aridoamerica. It is striking that despite being an inland site, it is the only place in the state in which molluscan shell objects have been found. This research aims to identify taxonomically the raw materials and the possible areas from where they were obtained. I will also describe the archaeological context in which these worked elements were found.

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The use of fresh water mussels in Tamtoc, San Luis Potosi, Mexico

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Tamtoc was a Huastec city that flourished between 400 B.C. and the sixteenth century Spanish conquest (Córdova-Tello *et al.*, 2012). Their inhabitants used different species of mollusk shells to manufacture objects, mostly ornaments. Noteworthy among them is the presence of species of the Unionidae family (*Lampsilis tampicoensis*, *Nephronaias aztecorum* and *Megaloniais nickliniana digitata*), that live in the nearby rivers. In this paper the archaeological evidence of the use of these species as food, as the material to manufacture tools and ornaments, and their ritual use as offerings will be presented.

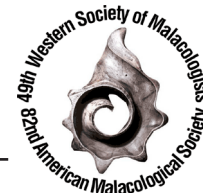
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The genus *Corbicula* as a dating group for Prehispanic archaeological sites

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The clam *Corbicula fluminea* is originally from southeastern Asia and was introduced to the American continent between 1920 and 1930, possibly via Chinese immigrants (Darrigran, 1992; Keen, 1971; Valentich-Scott, 2012). Today, this mollusk lives in rivers in northwestern Mexico; the principal characteristics identifying this species are the lateral serrated teeth, absent in the native species.

Recent investigations in archaeological projects revealed the presence of *Corbicula fluminea* in archaeological sites dated between 1050-1600 CE (Carpenter *et al.*, 2010; Watson and García, in press). This discovery has led us to further investigate the arrival of this bivalve to the Yaqui and Fuerte rivers, both of these drainages representing critical resources for providing food, raw material and fresh water for the ancient communities who lived in these regions.

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Taxonomical identification of nacreous species in Jaina, Campeche, Mexico

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Jaina is an important Maya settlement on the west coast of the Yucatan peninsula that flourished during the Classic period (300–900 A.D.) (Benavides-Castillo, 2007). This place is famous because of the finding of many human burials with clay figurines that accompanied the dead in their journey to the underworld. Approximately 7,000 shell objects were also buried as offerings (Velázquez-Castro, 1988). Among these pieces are a set of nacreous shell inlays of different shapes (rectangular, quadrangular and eccentric). The purpose of this paper is to show the specific biological characteristics that allowed the identification of the different shell species used to manufacture these pieces.



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Archaeology and Malacology in Baja California: Building bridges between anthropology and conservation

Figuroa-Beltrán, C., Fonseca-Ibarra, E. and Ramírez-Valdez, A.

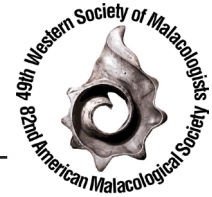
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The study of the past presupposes, among other things, the use of techniques and methods to understand long-term changes in the composition and structure of the intertidal communities, as well as patterns of resource exploitation by prehistorical hunter-gatherer fishermen.

Recent interdisciplinary approaches in the study of the past, have allowed the interlace of archaeology, ecology and malacology to generate key knowledge to understand the environmental history underlying the intertidal zones of Baja California. However, this knowledge should also enhance the conservation of coastal ecosystems and species that have been exploited for thousands of years.

The interruption of the way of life of Indians in prehistoric times by the arrival of Europeans, had direct implications for the ecology of species that were fundamental in the diet of the hunter-gatherer-fishermen. From this event, overexploitation of coastal resources led to the decline and (in some cases) the disappearance in their natural environment of mollusks that were abundant in the pre-European epoch, as it has been showed by the archaeological record.

Archaeological research has proven to be very useful in territorial planning and public policy, especially for the establishment of Natural Protected Areas, as in the cases of the Channel Islands in Southern California and other regions in the world; those examples should inspire archaeologists studying the prehistory of Baja California to perceive and apply their contributions with a more active role in the solution of current environmental research, management and policy.



3. SYMPOSIUM ABALONE MARICULTURE AND RESTORATION

Diseases of abalone around the World: A review

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Abalones are a group of marine gastropods that are considered a luxury seafood with associated high economic value. These sea snails due to their economic importance once supported some of the most important fisheries worldwide. However, in recent years a steady decline in natural populations and their fisheries has become a trend. The observed declines have been associated with a variety of infectious agents such as viruses, bacteria, fungi, protozoans and burrowing worms among others. Of the diseases that affect abalone none have a more devastating effect than those of viral origin, which typically cause up to 100% mortality just 2–3 days after the onset of external signs of disease; these diseases include Abalone Ganglioneuritis caused by Abalone Herpes Virus and abalone Shriveling Syndrome caused by a bacteriophage-related chimeric marine virus. Bacterial diseases include Withering Syndrome caused by the intracellular rickettsiales-like prokaryote *Candidatus Xenohalictis californiensis*, which is endemic and has caused considerable damage in North American abalone populations. Other bacterial diseases such as Vibriosis caused by *Vibrio harveyi* and *Vibrio parahaemolyticus* also had a devastating effect on wild and farmed populations of *Haliotis tuberculata* in Europe and *Haliotis diversicolor supertexta* in Asia. Recently, we have documented in Mexico a *Vibrio* outbreak in post-larvae and brood stock causing up to 80% mortality. Mycotic diseases in abalone are rare, most notable is Abalone Tubercle Mycosis caused by *Halioticida noduliformans* that has caused mortality outbreaks in *Haliotis midae* in culture facilities in South Africa. Protozoan related diseases include Perkinsus Disease caused by *Perkinsus olseni* that affects Australian and Tasmanian abalone population and Abalone Coccidiosis caused by *Margolisiella haliotis*, which is commonly found in North American abalone species and has been reported to cause mortality outbreaks in Chilean cultured populations. Shell diseases caused by burrowing worms such as *Terebrasabella heterouncianata* and *Boccardia proboscidae* affect South African and Mexican abalone respectively and have shown to cause a reduction in the growth and marketability of cultured abalone. Burrowing clams such as *Penitella conradii* and *Litophaga palmulla* and other parasites such as an amoeba-like protozoan, a gregarine-like protozoan, pyramidellid snails and pycnogonids have been recorded in North America, however their role as disease agents is unknown. The study and understanding of these diseases and parasites is essential to develop control measures around the world.

Symbionts and parasites of abalone of commercial importance from the peninsula of Baja California, Mexico

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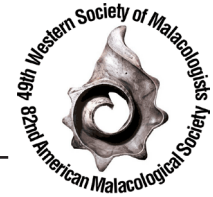
Abalone fisheries and culture are activities of great importance and tradition for numerous communities of the peninsula of Baja California, Mexico. In recent years, abalone production, both wild and farmed, have declined drastically and these declines have been associated with parasites among other factors. In this work, a compilation of histological records of the symbionts and parasites associated with wild Blue Abalone *Haliotis fulgens*, wild Yellow Abalone *Haliotis corrugata* and cultured Red Abalone *Haliotis rufescens* is presented. A total of 182 Blue Abalone and 170 Yellow Abalone obtained during the 2012–2013 capture season were sampled; while a total of 125 cultured Red Abalone were obtained thought 2014–2016. In the branchial cavity, ciliated protozoa were commonly found in Blue Abalone, Yellow Abalone and Red Abalone with a prevalence of 31.7%, 30.4% and 88.0% respectively. Also in the branchial cavity, *Ancistrocoma*-like ciliates were observed exclusively in Blue Abalone with a prevalence of 4.2%. Copepods were observed between the branchial filaments of Blue Abalone with a prevalence of 6.5%, while in Yellow Abalone these copepods showed a prevalence of 58.3%. In the esophageal pouch, multinucleated protozoa were detected in Blue Abalone, Yellow Abalone and Red Abalone with a prevalence of 4.5%, 1.0% and 78% respectively. An amoeba-like protozoan was observed in the stomach of Blue Abalone with a prevalence of 10.3%, this parasite was associated with the erosion of the stomach epithelium. The renal coccidian parasite *Margolisiella haliotis* was detected in a low to moderate prevalence in Blue and Yellow Abalone, while in Red Abalone a high prevalence up to 72.3% was observed. The prevalence of the rickettsiales-like prokaryote *Candidatus Xenohaliotis californiensis* was 80% in Blue Abalone, 62% in Yellow Abalone and 97% in Red Abalone. These records of symbionts and parasites constitute baseline information for future more detailed studies of symbionts, parasites and associated diseases of abalone species of the peninsula of Baja California, Mexico.

Mitochondrial genomes of the yellow, *Haliotis corrugata*, and black, *Haliotis cracherodii*, abalones: a protein comparison

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The yellow *Haliotis corrugata*, and black, *Haliotis cracherodii* abalones inhabit the coasts of Baja California, Mexico, and California, USA. The yellow abalone, *H. corrugata*, represents 10% of the fishery, behind the blue abalone, *H. fulgens*. In Mexico, an evaluation the black abalone, *H. cracherodii*, populations is lacking. At present (April 2016), there are 55 and 46 mitochondrial sequences in GenBank for *H. corrugata* and *H. cracherodii*, with a maximum length of 816 pb. Next generation sequencing has been developed in the past decade allowing to obtain a large number of reads or small sequences in non model organisms, such as abalones. The main objective of this work was to obtain the mitogenome of



the yellow and black abalone by next generation sequencing. Total DNA from gill tissue was extracted and sequenced using MiSeq by Illumina. Reads were cleaned, trimmed and *de novo* assembled with the CLC Genomics Workbench 6.5 software and annotation was carried out with DOGMA (Wyman *et al.*, 2004), and MITOS (Bernt *et al.*, 2013) programs. Protein translation was checked with ExPASy program (<http://www.expasy.org>) and alignment and phylogenetic analysis was carried out with MEGA software (Tamura *et al.*, 2013), which currently contains options for building sequence alignments, inferring phylogenetic histories, and conducting molecular evolutionary analysis. In version 6.0, MEGA now enables the inference of timetrees, as it implements the RelTime method for estimating divergence times for all branching points in a phylogeny. A new Timetree Wizard in MEGA6 facilitates this timetree inference by providing a graphical user interface (GUI). The total reads obtained were 2,670,827 bp and 2,037,325 bp for *H. corrugata* and *H. cracherodii* respectively. The mitochondrial genomes (mitogenomes) were not found in a single contig, however, protein sequences could be obtained from some contigs. When the 13 protein genes were translated, a higher similarity was found between *H. cracherodii* and *H. rufescens* than between *H. cracherodii* and *H. corrugata*. Distances among *Haliotis* species were between 0.006 and 0.083, while the minimum distance with other species was 0.0286. Further comparison among abalone mitogenomes will be presented.

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***Ex situ* conservation as a strategy to enhance endangered wild population of valuable mollusks**

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Conservation of wild aquatic populations can be pursued by designating protected areas and managing them effectively, as well as by monitoring how exploited populations are coping with changing conditions. If necessary, conservationists can resort to moving important aquatic genetic resources to other *in situ* sites or into *ex situ* collections and gene banks. Also, there is an urgent need to expand *in situ* and complementary *ex situ* conservation of aquatic genetic resources, with particular attention to resources that have potential loss due to different factors such as overharvesting and climate change. In this context, the National Subsystem for Aquatic Genetic Resources (SUBNARGENA) of Mexico contains state-of-the-art facilities and specialized human resources to help in the strategies for conservations of genetic resources. The SUBNARGENA is specialized in *ex situ* conservation of aquatic species, evaluation of germplasm quality, genetic characterization as well as monitoring the possible pathogen transfer in collected and stored samples. *Ex situ* conservation of aquatic genetic resources can assist on the development of important actions related to endangered organisms such as black and white abalone. There-



fore, strategies offered by SUBNARGENA will strongly help to enhance endangered wild population of valuable mollusks by 1) designing specific protocols for ex situ conservation of important organisms, 2) promoting sustainable use of aquatic genetic resources, 3) characterizing genetically the germplasm collected among others.

Abalone seed production: data collection and stats from a commercial scale lab perspective

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We present the data collected during the abalone seed production at the commercial scale laboratory located in Eréndira, Baja California, Mexico during the seasons 2012 to 2015. The abalone seed survival varied from 11% in 2012 to 14% in 2015. We used two different abalone larvae densities 30,000 and 55,000 per tank. We present the survival rate, the average abalone per tank, the seawater temperature and dissolved oxygen in the reported period. We include the data generated during an experiment made for testing two different post larval abalone food. The survival and growth of the juveniles are presented, finally we made an economic assessment of the results for determining the best food source.

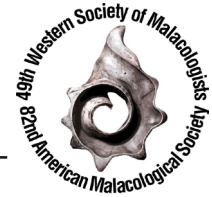
Restoration techniques for green abalone (*Haliotis fulgens*) in Southern California

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Green Abalone (*Haliotis fulgens*) were once abundant in Southern California, but populations have severely declined largely due to overharvesting and disease. The California green abalone fishery was closed in 1997 and the green abalone was listed as a Federal Species of Concern in 2004. Researchers are developing techniques for restoring populations of green abalone off of the Palos Verdes Peninsula in Southern California. First, a genomic technique called restriction site associated DNA sequencing (RADSeq) was used to assess the genetic structure of the remaining wild population in southern California (Gruenthal *et al.*, 2013). Results of the study suggested that the species may be panmictic throughout the sampled range, therefore allowing for translocation of broodstock and offspring to different local populations in southern California. New spawning techniques are currently in development to produce larvae and juvenile abalone for outplanting experiments on rocky reef areas near Palos Verdes Peninsula. A method called “deck spawning” is being tested, where adult abalone are taken from the wild, spawned on the deck of a research vessel, and returned to the wild within 24 hours. This method could reduce the need for keeping broodstock in captivity. Outplanting techniques and equipment are also in development.



To date, 863 juvenile green abalone have been outplanted into an experimental plot off of Palos Verdes and are being monitored for movement and survival. Researchers have also developed a prototype larval outplanting pump that can seal water-tight to accurately measure deployment numbers and make larval outplanting more efficient. These methods and techniques will be directly applicable to restoration of the endangered white and black abalone (*Haliotis sorenseni*) and (*Haliotis cracherodii*).

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Searching for microsatellite genetic markers in abalone, *Haliotis* spp., a genomic approach

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In the Peninsula of Baja California, abalone is a very important fishery and aquaculture resource with a significant impact in the regional socio-economic activities. In 2013, abalone production was 479 MT (14.2% from aquaculture and 85.5% from fisheries), positioning the resource in place 49th by volume and 29th by value. However, the mean rate of growth of the abalone industry, in the last ten years, is negative with a calculated value of -2.96%, meaning that the fisheries of target species are declining and aquaculture production is stagnant (CONAPESCA, 2013). Taking this into account, by 2015, the Baja California government proposes to develop a plan to improve abalone aquaculture and conservation. Therefore, the genetic evaluation of wild populations stocks will be the first genetic information needed to accomplish the plan goals. Microsatellites are short nucleotide sequences repeated in tandem (one after another); this sequence is called repetition motive and can be of two, three, four, five and six nucleotide in length (called di-, tri-, tetra-, penta- and hexa-nucleotide, respectively). Although there are several microsatellite markers for the peninsula of Baja California abalones, their number is still small and some of them do not cross-amplified among species. Next generation sequencing has been used to increase the number of known microsatellite loci in non-model species (Guichoux *et al.*, 2011; Fernandez-Silva *et al.*, 2013). The objective of this work was to identify potential microsatellite loci, which could amplify in all abalone species from the peninsula of Baja California. Total DNA from gill tissue from yellow (*Haliotis corrugata*), black, (*Haliotis cracherodii*), blue (*Haliotis fulgens*) and red (*Haliotis rufescens*) abalones was extracted and individually sequenced using MiSeq by Illumina. Reads were cleaned, trimmed and *de novo* assembled with the CLC Genomics Workbench 6.5 software and the contigs were submitted into the msatcommander (Faircloth, 2008) program to obtain the microsatellite loci and possible primers. Microsatellites were found in all four species with an average of 1,643.5 ($\pm 1,101.5$) microsatellites per species. All microsatellite types (di-, tri-, tetra-, penta- and hexanucleotides) were found in the four-abalone species evaluated. The less common type was the hexanucleotide in all species (0.61–0.93%). While the most common microsatellite type, in yellow and red abalones was the tetranucleotide (45 and 44 % respectively); and in the black (42%) and blue (41%) abalones the dinucleotide microsatellite type was the most common. The composition of microsatellite length and motifs found in abalones will be discussed

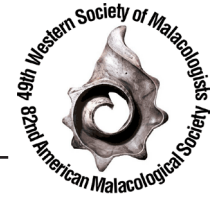


Abstracts - 49th Western Society of Malacologists and 82nd American Malacological Society Annual Meetings
June 12-16, 2016 Ensenada, Baja California, Mexico

compared with other mollusks and vertebrates species. These genetic resources can be use for population genetics studies and pedigree analysis of pure and hybrid progenies.

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4. SYMPOSIUM MOLLUSCAN CONSERVATION

Conservation of Green and Pink Abalone: Efforts and results in Natividad Island, Baja California Sur, Mexico

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Natividad Island is located in central Baja California, Mexico approximately at 9.6 km west of Punta Eugenia. The social and economic development of the cooperative in the Island “Sociedad Cooperativa de Producción Pesquera (SCPP) Buzos y Pescadores de la Baja California (SCL)” is based on the catch and extraction of marine concession species e.g., abalone, spiny lobster, sea cucumber and sea snail. Despite the productive and diverse marine communities in the region, some key resources like green (*Haliotis fulgens*) and pink (*Haliotis corrugata*) abalone suffered drastic decreases in their population density since 1996. For this reason, since 2006 two marine reserves were established in the island (La Plana/Las Cuevas and Punta Prieta) covering more than 8% of the fishing territory. Evaluations of these marine reserves have been done over ten years in collaboration with 27 local certified divers, academics (Reef Check California and Hopkins Marine Station) and COBI (Comunidad y Biodiversidad, A.C.) through biological and oceanographic monitoring. Our biological data indicate larger abalone sizes for both species inside the marine reserves, suggesting a larger reproductive potential in these areas. Oceanographic data show hypoxic events in summer 2010-2011 and 2013-2015 and high temperatures (particularly in late summer-early fall 2012, 2014 and 2015) around the island, which could be associated with abalone mortality in 2009–2010. Our results indicate that the marine reserves have supported the resilience of Natividad abalone populations to climate events and have motivated the local cooperative to strengthen experimental economic alternatives like aquaculture, restocking, pearl culture and sustainable finfish fisheries.

Determining population structure, reproductive potential, and habitat associations of pinto abalone (*Haliotis kamtschatkana*) in southern California

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Seven species of abalone (genus *Haliotis*) are native to the west coast of California. The pinto abalone (*Haliotis kamtschatkana*) once supported a modest fishery in southern California. However, stock collapse of this and other abalone species led to the closure of fisheries in central and southern California in 1997. In 2013 NMFS was petitioned to list the pinto abalone as threatened or endangered under the U.S. ESA. Although a 2014 status review by NMFS concluded that listing was not warranted at this time, they noted that a significant lack of baseline data increased the uncertainty of their assessment and pointed to a need for improved monitoring of the species throughout its range. Pinto abalone are included in the 2005 CDFW Abalone Recovery and Management Plan, in which two criteria are used to define abalone recovery: evidence of a broad size distribution and minimum spawning density (MSD) of 0.2 animals/m². Because basic demographic data from targeted surveys are lacking, I completed surveys via SCUBA in San Diego, California, where pinto abalone are present. My data indicate that there is evidence of recent pinto abalone recruitment and a broad size range (13–151mm maximum shell length). However, pinto abalone in San Diego are at very low densities (0.004/ m²). The majority of individuals (76%) are solitary (no neighbor within a 2 m radius). Of those that had a neighbor less than 2m away, average aggregation size is 1.3±0.09 abalone. The proportion of pinto abalone with neighbors less than 2m away is 30% and 45% have a neighbor within 4m. Ongoing surveys will continue to examine population structure, reproductive potential, and habitat associations for pinto abalone in San Diego. These data and procedures will inform recovery efforts for pinto and other abalone species.

Review and perspectives of abalone (*Haliotis* spp.) restocking in México

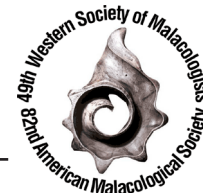
Searcy-Bernal, R.

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Abalone restocking in the peninsula of Baja California, México, has been practiced for more than two decades by fishermen cooperatives. From 2005 to 2011, 2.2 million seeds (>15 mm) and 692 million competent larvae were produced by six cooperative hatcheries and released in their fishing grounds. Of these, 90.1% of the seeds and 80.7% of the larvae corresponded to *Haliotis fulgens*, whereas the figures for *H. corrugata* were 9.9% and 19.3%, respectively (Searcy-Bernal *et al.*, 2013).

In 2009, atypical mortalities of abalones in Central Baja severely impacted the fishery (Michelli *et al.*, 2012). As a result, the need to improve the efficiency of restocking received special consideration (Searcy-Bernal *et al.*, 2010) but, on the other hand, fishermen began to explore the possibility of growing seeds to commercial size in controlled systems rather than using these for restocking. In 2013, at least 17% of the seeds produced by cooperative hatcheries were allocated to grow-out operations, and this percentage shows an increasing trend (Searcy-Bernal *et al.*, 2015).

This presentation provides a review of the abalone restocking efforts in México, addresses the need to improve the evaluation of these using modern approaches, such as PIT tags and molecular markers (Searcy-Bernal *et al.*, in press), and examines new potential restocking strategies.



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It's black or white: A different roadmap to restoring the endangered black abalone, *Haliotis cracherodii*

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Since the mid-1980s, black abalone (*Haliotis cracherodii*) populations in southern California have experienced dramatic (more than 80 percent) declines in abundance due to a disease called withering syndrome. Today, most populations in southern California remain at low abundance/density and the disease



continues to progress northward along the coast during warm-water events, threatening healthy populations to the north that have not yet been affected. These factors led to the listing of black abalone as an endangered species under the federal Endangered Species Act (ESA) in 2009. The National Marine Fisheries Service (NMFS) is charged with protecting and recovering the species and is currently developing a plan to guide the species' recovery. We provide an overview of the species' status and threats, the preliminary recovery strategy, and the next steps for developing specific, measurable recovery targets that will be used to evaluate the species' progress toward the overall goal of establishing healthy, naturally self-sustaining populations of black abalone throughout their range. We highlight differences between the recovery needs for black abalone and white abalone (*Haliotis sorenseni*; also an endangered species). Although low density is the main threat for both species, they differ in several ways, including: current status; the factors causing low densities; and the information available on status, trends, and past and ongoing threats. These differences have resulted in different recovery needs, targets, and strategies for the two species. We focus on information from long-term black abalone monitoring programs throughout the California coast to support our recovery approach and emphasize the importance of choosing the correct metrics — in this case aggregation as opposed to density metrics — to gauge the viability of black abalone populations in the wild. Our goals are: to demonstrate how recovery strategies must be tailored to the specific needs of each species and the important role of long-term population monitoring data; to generate discussion and receive input on the preliminary recovery strategy for black abalone; and to facilitate coordination among researchers and resource managers throughout California and Baja California to work together to help recover black abalone throughout the species' range.

Mood lighting and spa treatments: Captive propagation of the endangered white abalone (*Haliotis sorenseni*)

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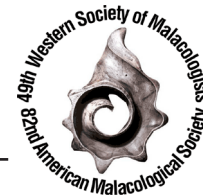
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Without significant intervention by captive breeding and outplanting efforts, endangered white abalone (*Haliotis sorenseni*) are likely to go extinct within decades. Captive breeding success has increased substantially since 2012 through advancements in animal husbandry achieved via strong partnerships among research universities, federal and state agencies, aquaria, and aquaculture farms. Efforts to control disease, increase post-settlement survival rates, and improve the reproductive condition of broodstock have resulted in a thriving captive population, with more animals in captivity than likely exist in the wild. However, captive production remains limited compared to the production of commercial abalone growers and relative to what is necessary to recover the species. Continued focus, particularly on reproductive conditioning, optimal conditions for grow-out, genetic integrity of broodstock, and preparation of captive-bred animals for wild stocking, are necessary to for successful recovery.

Experimental stocking of Red Abalone (*Haliotis rufescens*) in Southern California artificial reefs

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Commercial and recreational abalone fisheries in southern California, south of San Francisco, closed by 1997 due to overfishing and disease impacts. Many abalone populations remain at low densities today and are at risk of recruitment failure (Rogers-Bennett *et al.*, 2004; CDFW, 2005). Particularly concerning is the status of the endangered white abalone (*H. sorenseni*) which may go extinct within the next 10-15 years without active restoration (Catton *et al.*, in press). Since 2004, California Department of Fish and Wildlife (CDFW) has established artificial reefs (BARTs) in white abalone habitat (20-23m) to assess natural recovery potential and to prepare for future stocking. No endangered white abalone juveniles



have been observed in the BARTs at any of the locations, although a few adult white abalone have been observed in nearby reefs. Four other species of abalone juveniles have been observed in the BARTs – the red abalone (*H. rufescens*) were the least prevalent. A pilot stocking experiment was conducted for red abalone at one of the BARTs locations in January 2016, to enhance red abalone populations and optimize methods for future white abalone stocking. A total of 12 BARTs are distributed amongst three sites, two of which received stocked abalone. We stocked a total of 3,200 tagged red abalone of two size classes (small – 30 mm; large – 60 mm), and monitored initial survival and dispersal. After one week post-stocking, 8.2% and 11.9% of the tagged abalone were found within 10 meters of the BARTs, using non-invasive survey techniques. Dispersal within the first week differed dramatically between the two stocking sites. Ninety-seven percent of abalone encountered during the survey remained inside the BARTs at one site (small – 100%; large – 91%), while 66% were dispersed outside of the BARTs (small – 52%; large – 79%) at the other site. Differences in habitat characteristics at the two sites may influence the initial dispersal behavior of stocked farm-raised abalone. Additional monitoring, including invasive survey techniques, is planned throughout 2016 and 2017. The results of this study will inform methods, numbers of juveniles and site selection for future abalone restoration efforts in southern California.

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Rock hard abs in five (not so) simple steps: Restoration efforts for the first federally endangered marine invertebrate in the United States, White Abalone (*Haliotis sorenseni*)

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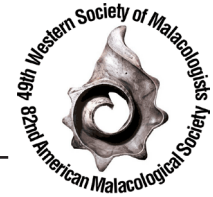
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The National Marine Fisheries Service's (NMFS) White Abalone Recovery Plan identifies five key challenges that must be addressed and overcome in order to recover this federally endangered abalone. The first is to develop methods for reliable and increased production of healthy captive raised white abalone



that will be used to increase the abundance and reproductive success of the wild population. The second is to develop effective outplanting methods. The third is to identify which habitat characteristics maximize the survival of white abalone so that appropriate outplanting sites can be selected for captive raised animals. The fourth is to develop methods and tools that will effectively monitor the demographics of enhanced white abalone populations over time and gauge the overall success of the program. The fifth is to strengthen existing partnerships and forge new ones through the development of an outreach plan that communicates the key messages of the recovery program and highlights the important roles partners will play in recovering white abalone throughout its range. NMFS co-manages a captive breeding program with the University of California at Davis' Bodega Marine Laboratory and the California Department of Fish and Wildlife (CDFW) and in partnership with five other facilities. The production of captive raised white abalone has increased steadily since 2012, resulting in thousands of animals currently being held in land-based facilities. NMFS works collaboratively, in a variety of capacities, with several partners including the Bay Foundation, Get Inspired, the Puget Sound Restoration Fund, CDFW, and several academic partners/institutions to test methods for outplanting larval and juvenile stages of surrogate abalone species. These same partners, along with the National Marine Sanctuary Program, the National Park Service, the U.S. Navy, and citizen scientists are using photography, video, multi-beam sonar, water quality sensors, and detailed visual surveys to identify features of abalone habitat that promote white abalone survival. Our initiative to identify and track the fate of outplanted and wild white abalone receives significant support from genetic, remote sensing, and underwater researchers at NMFS, CDFW, academic, aquaria, non-profit and citizen science organizations and is crucial for ascertaining which monitoring methods are most effective for gauging the success of the program. Finally, communicating the efforts presented above in a clear, consistent, and concise manner will help define the roles of existing partners, identify gaps in our capabilities, and recognize new collaborators who can help fill those gaps. For example, it is critical that new partnerships be forged within Baja California, Mexico in order to recover white abalone throughout its range and remove the species from the U.S. endangered species list.

Predation and predator response to experimental stocking of red abalone (*Haliotis rufescens*) in Southern California

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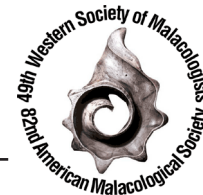
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Abalone (*Haliotis* spp.) populations in southern California have declined since the 1960s, primarily due to overfishing and disease. Despite the fishery closure and conservation efforts, many abalone populations remain at low densities, and are at risk for recruitment failure (Rogers-Bennett, 2004; ARMP, 2005). A critical component of the abalone recovery is the stocking of captive-bred juveniles into the wild for red and white abalone (Rogers-Bennett et al., in press). One of the largest barriers to the success of stocking efforts is predation mortality (Catton et al., in press). During a recent pilot experiment (S. Kawana, this conference), we measured the response of predators to the addition of juvenile red abalone (*H. rufescens*) into the environment. We established permanent 10m radius survey arrays (N=3) and documented and removed as many benthic predators as possible, primarily octopuses (*Octopus bimaculatus* and *O. bimaculoides*) and Kellet's whelks (*Kelletia kelletii*). At each site, we outplanted tagged juvenile (30–60mm) red abalone (N=1,600) and monitored survival and dispersal with monthly surveys (S. Kawana, this conference). Intense predation was a primary factor contributing to abalone mortality after stocking. Octopus densities increased within the survey areas following the first week of stocking, and decreased to pre-stocking densities within two months. *K. kelletii* did not show any measurable response to the abalone stocking. Empty shells were sorted into five predation categories: broken shell edges, smashed shell, drill hole, exposed nacre, and no visible damage. The majority of shells had no visible damage, followed by drill holes and chipped edges. The clear response of octopuses to the stocking of juvenile abalone and the impact of predation on the survivorship of these abalone indicate an increased need for predation mitigation to ensure the success of future red and white abalone restoration.

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5. GENERAL SESSION - ORAL PRESENTATIONS

Patterns of predation on gastropod mollusks in rocky shores of the Mexican Pacific

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Predation plays an important role in determining the life strategy and morphology of marine gastropods, since they are part of the diet of different groups of predators including crabs, cephalopods, and even other gastropods. The attacks leave very specific evidence in the shells, so that each type of predator can be identified fairly accurately. Studies on predation and diet selectivity in the Mexican Pacific are relatively scarce, and there are no estimations of the incidence or level of damage caused to gastropods by the various types of predators. To evaluate predation on gastropods and to make an inventory of potential predators, direct manual collections of shells were performed in the intertidal zone of rocky and sandy beaches of four sites at different latitudes along the Mexican Pacific (El Julio, Sonora 30.1°N, -112.7°W; Isla Espiritu Santo, Baja California 24.4°N; -110.3°W; Bahía Chamela, Jalisco, 19.5°N; -105°W; Huatulco Bays, Oaxaca, 15.6°N; -96.2°W). A total volume of three liters of empty shells was collected in each site. The basic hypothesis to test was that in geographic areas with higher diversity of predators (e.g. at lower latitudes), the dominant gastropods have greater variety of types of predation and therefore there will be more shells with repairs (indicating unsuccessful attacks). Also we expect that depending on the latitude, the incidence of different types of damage to the shells should change. The total number of individuals collected was 6,192, from 78 species of gastropods; of these, 16% presented evidence of predation. The most common predators were cephalopods (37% of total dead shells), followed by crustaceans (36%) and gastropod mollusks (17%). Predation by fishes is difficult to assess since they crush the shells completely, however the presence of large numbers of fragments indicate that fishes are important predators, especially in the southern locations. The percentage of shells with evidence of repairs was 4%; also 6% of the dead shells had evidence of attacks from more than one predator. These results confirm our hypotheses: dominant species (e.g. those with higher abundance) had the highest variety of patterns of predation patters; and the percentages of incidence of predation changed according to the latitude.

Review of the taxonomic authorities of marine bivalves and the verification of their presence in the Mexican Pacific coast

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With the objective to generate a catalog of taxonomic authorities for species of marine mollusks belonging to the class Bivalvia reported from the Pacific coast of Mexico, a research program was initiated using



different sources, including the original descriptions from the 17th century; the current classification was verified using recent catalogs. Our preliminary results produced a catalog with two valid subclasses, two valid superorders, 16 orders, 2 suborders, 32 valid superfamilies, one synonymous family, and 58 valid families, 38 subfamilies, 24 synonymous genera and 211 valid genera, 343 synonymous species and 398 valid species. This catalog is being produced in a Database program called BIOTICA 5.0 from CONABIO. Each species is accompanied by environmental information, where the species was reported, the common name, and their uses if relevant. We have found a large amount of information in unpublished documents such as theses, reports of completed research papers, abstracts and presentations in conferences. Currently the catalog includes more than 70% of the species reported for the Pacific coast of Mexico. There are 155 photos associated with their corresponding species. The information contained in the catalog confirms that the Mexican Pacific coast has a wide representation of marine bivalves of the Panamic region.

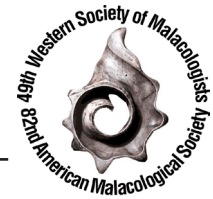
Symbionts, parasites and diseases of the Generous Clam (*Panopea generosa*) from the Pacific coast of Baja California, Mexico

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The Generous Clam (*Panopea generosa*), is distributed along the Pacific coast of the Baja California peninsula, Mexico. Due to its high market value, this species has been under an intensive fishing pressure during the last few years, while its experimental aquaculture production is still in development. The fishery and culture practices point to the movement of clams as a risk factor for dispersal of symbionts, parasites, and diseases. The results of several examinations of clams obtained from producers and facilities that maintain clams alive, prior to marketing, are presented. Blisters and a characteristic darkening and thickening of the surface of the mantle and siphon were observed in some live animals. Histological analysis of the dark lesions showed a dramatic transformation of the periostracum to a cavernous structure with numerous protozoans in different developmental stages. Fungi were occasionally observed. Unusual mortalities were reported by producers in clams affected by the dark lesions. Some weak-flaccid clams were in a post-spawning condition. One pea crab (Pinnotheridae) inside of the siphon was found; additionally, two species of copepods were found, *Pseudomyicola spinosus* and a calanoid species in mantle cavity and gills. A turbellarian species that was not related with tissue damages was also observed in the mantle cavity. *Rickettsia*-like inclusions were found in the digestive gland and gill filaments. *Nematopsis*-like protozoans and trematodes were found in the digestive gland associated with limited damage to the host. One arthropod was observed encapsulated by hemocytes in the connective tissue surrounding digestive gland and unidentified ciliated organism was observed in connective tissue without apparent host reaction. The darkening and thickening of the siphon represents a major issue due to the negative appearance of the clams, which prevents its sale and it is possibly related with unusual mortality episodes. Detailed field and laboratory studies are needed to determine the origin of this pathology, its distribution and its effect on the survival of the host. Moreover field studies on the distribution, prevalence and intensity of the other symbionts and parasites here detected are needed. This data constitutes the first record for organisms associated with *P. generosa* in Mexico and a baseline for future studies.



Tunicate invasion threatens recovery of a population of the penshell *Atrina maura* (Bivalvia: Pinnidae) in the Gulf of California

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The penshell *Atrina maura* is a bivalve native to the Mexican Pacific, including the Gulf of California, which inhabits shallow environments often forming dense banks. This species has sustained a fishery, almost permanently and without official regulation, since 2004 in the coastal lagoon of La Paz, Baja California Sur, Mexico, from which dozens of families depend on fishing. As a consequence of this exploitation, this population of *A. maura* diminished to unsustainable fishing levels, which motivated to Noroeste Sustentable A.C. and the local fishing community to carrying out, since 2011, a population recovery program through aquaculture and non-fishing activities. At present, the results of this program are encouraging and include a significant increase in the abundances of *A. maura* in the lagoon, as well as a socio-cultural change in the community involved in the process. However, now the recovery of this population is at risk due to an invasion of tunicates, first reported in early 2015, that continues expanding in the area. Tunicates are colonial organisms that attach massively on the shells of bivalves, to the point of preventing the opening of valves, affecting negatively their growth, feeding and condition. This work presents preliminary results on the evaluation of the effect of the tunicate invasion in the general condition of *A. maura* in the lagoon of La Paz. A total of 41 specimens of *A. maura* were collected and total weight (bivalve + tunicate), tunicate weight, weight without tunicate, weight without shell and muscle weight were individually recorded. The level of tunicate coverage in *A. maura* was established as the ratio of tunicate weight relative to the total weight: low (<25%), medium (25–50%) and high (>50%). In addition, the general condition index (GCI) and muscle yield index (MYI) were calculated and compared between coverage levels and with data from years preceding the invasion and obtained from the same area. The tunicate species was identified as *Botrylloides violaceus*, and presented a prevalence of 100% in the analyzed sample; 44% of organisms presented low coverage, 18% medium coverage and 38% high coverage. The GCI and MYI had significantly lower values (ANOVA, $P < 0.05$) for the high level of coverage. Similarly, comparisons between years indicate a strong negative effect (ANOVA, $P < 0.01$) of the presence of tunicates in the general condition of *A. maura*. Concerning muscular performance, the interannual difference of MYI values can be explained by the combined effect of the presence of tunicates and anomalous temperature records.



Genetic and genomic resources for the California Butterclam *Saxidomus nuttalli* (Conrad, 1837)

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Two species of *Saxidomus* are native from California, a northern form, *S. giganteus* (Deshayes, 1839), ranging from Alaska to Monterey; and a southern form, *S. nuttalli* (Conrad, 1837) found from Coos Bay, Oregon to San Diego, California (Weymouth, 1921; Schoeder *et al.*, 2013). Furthermore, *S. nuttalli* specimens had been recorded in the Pacific coast of Baja California and Baja California Sur. However, genetic information for these species is limited to only one study for *S. giganteus* (Johnson and Utter, 1973). The main objective of this study is to develop genetic and genomic resources for *S. nuttalli*, a native species that provides an important recreational resource for self-consumption in Baja California, based on next generation sequencing technology (NGS). Specimens were collected from Bahía San Quintín, B.C. and tissue samples from gills were preserved in 96% ethanol. Total DNA was extracted using DNeasy Blood and Tissue Kit (Qiagen). Paired-End DNA sequencing was done in an Illumina MiSeq platform, obtaining a total of 2,759,530 reads. *De novo* assembly was carried out using CLC Genomics Workbench 6.5 software and resulted in 245,050 contigs with an average length of 532 pb covering about 12.12% of *S. nuttalli* genome. Approximately 37.6% of the contigs were annotated using Blastx and the Uniprot database. Annotated genes are described based on their Gene Ontology features as biological process, cellular components and molecular functions. Additionally, a total of 1,312 microsatellite loci were found, but only 407 had flanking regions for primer design. To our knowledge, this is the first study to generate genetic and genomic information for the butter clam *S. nuttalli*, which could be used as valuable tool for research in comparative functional studies, to give insights into phylogenetic and population genetics as well as for conservation and aquaculture purposes.

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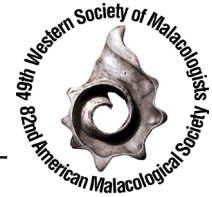
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Hybridization and introgression in cone snails?

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Molecular phylogenetic analyses of several cone snail subgenera have revealed discordant gene trees or relationships that conflict with expectations from patterns of morphological variation. These observations imply that gene introgression through hybridization has occurred in these groups. For example,



in the subgenus *Lividoconus*, some individuals that resemble *Conus lividus* possess mitochondrial gene sequences of *Conus sanguinolentus* and so are suspected hybrid or backcrossed individuals. We examined multiple nuclear gene sequences of members of *Lividoconus* to determine if gene introgression has occurred among these species. In particular, we recovered A-superfamily conotoxin sequences by sequencing multiplexed amplicon libraries of individuals of *C. lividus*, *C. sanguinolentus* and suspected hybrid/backcrossed individuals from Okinawa, Guam and Hawaii. We identified 54 sets of sequences that we interpret to represent distinct conotoxin loci or alleles (i.e., ‘genes’). Of these, 15 and 17 genes occurred uniquely in *C. lividus* and *C. sanguinolentus*, respectively. Only suspected hybrid individuals from Hawaii possessed genes that are unique to *C. lividus*. On the other hand, unique genes of *C. sanguinolentus* occurred in suspected hybrids from all locations. These results suggest that *C. lividus* and *C. sanguinolentus* have hybridized and that recurrent backcrossing occurred predominantly with *C. lividus* in Hawaii and *C. sanguinolentus* in Okinawa and Guam. Because *C. sanguinolentus* is not known to occur at Hawaii, influx of *C. sanguinolentus* genes via migration of hybrid larvae from elsewhere or a selective advantage of these genes may explain their retention in Hawaii.

Growth of black ark from tagging/recapture experiments in La Paz Bay, Baja California Sur, Mexico

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Growth of the black ark *Anadara tuberculosa* (Sowerby, 1833) (Bivalvia: Arcidae) was estimated in El Mogote and El Conchalito mangrove systems in La Paz Bay, Baja California Sur, Mexico. The principal aim was to compare individual von Bertalanffy growth parameters estimated through tagging techniques. Ark individuals were tagged with serial numbers painted or printed (Dymo). A total of 760 arks were tagged at El Mogote and 272 at El Conchalito. Quarterly searches of tagged individuals were made from October 2010 to January 2012. Three other samples were obtained in 2013, 2014 and 2015. The Gulland and Holt plot method was applied to analyze growth increment data, and to estimate L_{∞} and K. For El Mogote black arks, 95 individuals were recaptured with sizes between 44.6 and 90.8 mm. The parameter values were $L_{\infty}=90.0$ and $K=0.189$. For El Conchalito, with 41 recaptured between 38.2 and 80.6 mm, the parameters were $L_{\infty}=83.0$, $K=0.171$. The growth rate differences between both populations are likely due to environmental factors and nutritional deficiency.

Asymmetric genetic introgression of a hermaphroditic invasive sea slug in a native species

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Aplysia parvula is a hermaphroditic, circumtropical species of sea slug that was first found in the Medi-



terranean in 1961. Preliminary data obtained from sequencing two mitochondrial genes (16S and CO1) and one nuclear gene (H3) shows that *A. parvula* is a species complex. Preliminary data also shows evidence of hybridization and asymmetric genetic introgression between *A. parvula* and *A. punctata* (native to the Mediterranean). Mediterranean specimens sequenced showed no mitochondrial gene introgression of *A. parvula* but there was nuclear gene introgression of *A. parvula*. This is evidence of asymmetric genetic introgression, when one organism acts primarily as the sperm donor and the other as the sperm recipient (Yusa, 2008). Future work will include using phylogenetic and morphological data to verify that *A. parvula* is a species complex. Also, sequencing an additional nuclear gene, 18S, will be done to confirm hybridization between *A. parvula* and *A. punctata*.

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New records of marine bivalves for the coast of Baja California Sur, Mexico

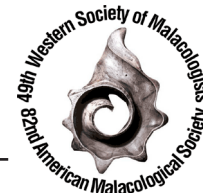
Gurgo Sálice, P., Cáceres Martínez, C., Barrios Ruiz, D. and Rodríguez Trejo, M.

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Samples in two areas of Baja California Sur, Mexico were obtained from the malacological collection *Gurgo Sálice*, which was collected using a trawling net in La Paz Bay (24.28°N, -110.58°W – 24.17°N, -110.30°W) in the Gulf of California and the front beach at *Conquista Agraria* in the Pacific Coast (23.85°N, -110.88°W – 23.94°N, -110.87°W). The trawling was conducted at 2–4 m and 30–40 m depth. The material was sieved through a net 20.0, 10.0 mm using sea water in the field. The gross fraction was dried at sun and stored in plastic bags for macroscopic and microscopic analysis. All mollusks obtained were carefully sorted and classified based on their shell morphology until identification. Bivalves were identified using Keen (1971) in a first attempt and finally identified using Coan and Valentich-Scott (2012). The specimens obtained belonged to different orders of Bivalvia, such as: Arcida, Carditidae, Limida, Lucinida, Myida, Mytilidae, Nuculanida, Nuculida, Ostreida, Pectinida, Pholadomyda, Pholadomyoidea, Pterida, Solemyida and Venerida. A detailed list of specimens and their localities, deep and bottom type is provided in this presentation, some specimens are being recorded for the first time in the sampled sites.

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Larval diversity of gastropods in the Greater Caribbean

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Meroplanktonic marine gastropods include species with larval stages whose duration in the water column vary from hours to months. In this phase, transport processes and larval dispersion occur, and together with the effect of physical, chemical and biological variables affect the gastropods larvae abundance, diversity, and recruitment. In this study, the structure of the larval community was investigated in five locations in the Caribbean during July, August and September (2014). Samples were collected at the localities of Barbados, Guadeloupe, Florida, Dominican Republic and Mexico, under the same sampling protocol in the full moon period and when maximum tidal coefficient happened. At each site, six tows in the opposite direction of the wind were made using plankton nets (30 cm diameter and 200 µm mesh). We had classified a total of 89 morphospecies and identified 1,445 specimens belonging to 13 genera being *Smaragdia*, *Litiopa* y *Rissoina* the most abundant genres which account for 53% of all specimen. On the other hand, there were 30 morphospecies that only appeared once in the samples.

Integrative taxonomy of the *Felimare californiensis* and *Felimare ghiselini* species complex (Mollusca, Gastropoda, Nudibranchia)

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Felimare californiensis and *F. ghiselini* are two nominal species of nudibranch sea slugs known from the warm temperate eastern Pacific Ocean. The phylogenetic relationships among species of *Felimare* were tested; including populations of *F. californiensis* from the North Pacific and the Gulf of California, and *F. ghiselini* from the Gulf of California and Peru; representing their entire known ranges. Sequence data from the 16S and CO1 mitochondrial genes were analyzed using Bayesian and maximum likelihood methods. The Automatic Barcode Gap Discovery analysis was used to test if monophyletic groups correspond to distinct species. Molecular and morphological evidences indicate that the eastern Pacific nudibranch species *Felimare californiensis* and *Felimare ghiselini* are synonyms and an isolated population identified as *F. ghiselini* from the coast of Peru constitutes a distinct species. Morphological comparisons were made using external coloration, reproductive anatomy and radular characteristics. A review of the literature, the result of molecular analyses, and a critical evaluation of the morphological characteristics of other eastern Pacific species of chromodorid nudibranchs confirmed that the Peruvian *Felimare* is distinct; therefore, it is described herein as a new species.

Southern invasion: Population genetics of *Phidiana hiltoni*

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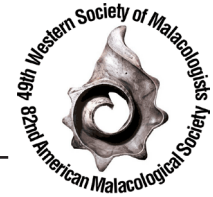
Phidiana hiltoni, a species of nudibranch, is known for its pugnacious behavior (Syn. *Phidiana pugnax*) as it often attacks and eats other aeolids along with its more common diet of hydroids. Its historical range was from the Gulf of California to central California. However, as of the early 1990's, the species has been found as north as the San Francisco Bay area. This dispersal by *P. hiltoni* has already proven a problem for the native species of sea slugs in the Bay area. *P. hiltoni* is not only showing signs of competing with Northern California native sea slugs for hydroids, but has also been observed fighting and consuming these native species when encountered. Collection of specimens of *P. hiltoni* from all along its habitat range, historical and new, and sequencing their DNA will help develop a genetic map of this species. This map will hopefully help to gain an idea of where the new population is deriving from.

Human injuries and fatalities due to venomous marine snails of the family Conidae

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For more than 300 years, gastropods of the genus *Conus* have been known to inflict painful and some-



times fatal injuries on people, but these cases have been studied very sporadically. Many neurotoxic peptides in *Conus* venoms have now been characterized, but as yet little effort has been devoted to how human symptoms relate to their specific chemical and physiological properties, or to use such information to improve treatment of human envenomations. This presentation 1) summarizes the first compilation in more than 30 years of human injuries and fatalities from the predominantly tropical family Conidae, and 2) applies recent advances in knowledge of the physiological effects and molecular genetics of conopeptides. The research goal is to improve our understanding of the human responses to stings by species that normally use their venom peptides to paralyze and overcome prey such as polychaete worms, other gastropod molluscs and fishes. Some data exist on 139 cases accepted as reliably reporting human injuries. A publication in press includes a database of the species responsible, time and place of occurrence, and the sting site on the victim's body, time-course of clinical effects, treatment carried out, if any, and outcome. Members of the hyperdiverse genus *Conus* caused all the injuries, except for two cases due to species from the recently separated genus *Conasprella*. Death occurred in 36 cases, 56 presented with serious symptoms but complete recovery followed, and in 44 cases victims were only minimally affected. Knowledge of conopeptide molecular structure and function is currently burgeoning, permitting initial exploration of relationships between the symptoms and outcomes of human injuries and modes of action of these mainly small, very toxic neuroactive peptides. These relationships are reviewed, especially in regard to the severe and fatal cases, with the aim of making recent knowledge accessible to clinicians and others involved in treating the effects of human stings, which continue to be reported. *Conus geographus*, a specialized predator of fishes, which it paralyzes with its venom and swallows whole, is the most dangerous species to humans. It accounts for about half of the known human envenomations and almost all the fatalities. Children succumb more often to *C.geographus* stings than adults, and stings by larger snails are lethal more often than stings from smaller snails, regardless of the victim's age. Other piscivorous *Conus* species have stung humans, but with non-lethal results. A few species that normally prey on other gastropods have also seriously injured humans, but most of the reported fatalities have not been confirmed. Most Conidae prey only on marine worms; 18 vermivorous species are known to have stung humans, with generally mild effects. Research on the treatment of *Conus* stings has lagged behind that on the application of conopeptides in pharmacological research and drug development. However, improved communication and availability of medical aid in remote tropical areas has likely contributed to reducing mortality rate during the last half century.

Environmental factors affecting holoplanktonic mollusk distribution in the coast of the Mexican Caribbean

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The composition and abundance of holoplanktonic mollusks, as well as the environmental factors influencing their distribution in three locations in the Mexican Caribbean: Cozumel, Punta Allen and Majahual, were analyzed. Zooplankton samples were collected by surface trawls at 45 stations using two conical nets of 333 and 505 μm mesh sizes. Temperature and salinity were recorded at each sampling station. In the



laboratory, zooplankton biomass was quantified by the method of wet weight and the total of holoplanktonic mollusks was also quantified. Six genera and eight species were identified, from which *Creseis clava* and *Limacina trochiformis* were the dominant species in the region. To assess the environmental factors determining the distribution of mollusks, a Regression Tree Analysis was applied, using the density of mollusks as the response variable, and temperature, salinity and zooplankton biomass as explanatory variables. This procedure revealed that the temperature and the zooplankton biomass, viewed as a measure of food availability, were the most important factors influencing the mollusks distribution. The shoreline area recorded the highest density of mollusks, an area where we also recorded the highest zooplankton biomass and moderate temperatures (27.6°C). This study provides important advances in understanding the ecological relationships of this low abundant group within their environment.

Chiton community structure (Mollusca: Polyplacophora) of a rocky shore in Montepío, Veracruz, Mexico

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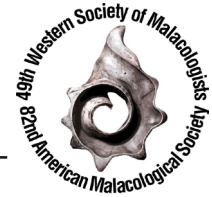
The goal of this study was to analyze the community structure of the class Polyplacophora of a rocky shore in Montepío, Veracruz, Mexico, as well as to examine the morphometric relationships of the most abundant species. Sampling was made in April and October 2014, and chitons were collected by direct methods. There were collected 83 individuals, belonging to four genera and six species: *Lepidochitona bullocki*, *L. rosea*, *L. liozonis*, *Chaetopleura apiculata*, *Ischnochiton kaasi* and *Acanthochitona zebra*. In spite of the similarity in species richness and Shannon diversity index in the two seasons, only two species were present in both months (*C. apiculata* and *L. bullock*), indicating a strong seasonal change on the chiton community composition. The dominant species were *L. rosea*, *C. apiculata* and *I. kaasi*, from which the total length, total width and height was measured in order to analyze their relative growth. Morphometrical data were fitted to a power equation potential ($Y=bX^a$) taking the total length as the independent variable. Results indicated that *L. rosea* and *C. apiculata* had an isometric growth in the form of the body, but negatively allometric for their height. In contrast, *I. kaasi* showed a negatively allometric growth in the form of its body, but isometric for the height. This study provides new knowledge on the community structure of a rocky shore from the southern Gulf of Mexico, and on the morphometric relationships of three chiton species.

Genetic population structure of the Olympia oyster, *Ostrea lurida*, in southern California

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Restoration of the historically impacted Olympia oyster (*Ostrea lurida* Carpenter 1864) is ongoing along



the West Coast but in southern California, where restoration is underway, there is little information regarding the oyster's genetic structure. Previous mtDNA sequence comparisons across the geographic range detected genetic differentiation between Vancouver Island, British Columbia and sites southward, with little to no genetic variation south of the break. In contrast, studies examining microsatellite from oysters collected from Vancouver Island, B.C. to Elkhorn Slough, California found more genetic variation and structure, however nothing is known about genetic variation and structure in microsatellite markers from sites in southern California, thus prompting this study. Oysters were hypothesized to have genetic variation and structure within southern California and between southern California and northern sites and genetic similarity was hypothesized to reflect geographic proximity, as expected for isolation-by-distance (IBD) models. STRUCTURE analyses suggest hierarchical structure with support for one genetic cluster of individuals in California (and possibly a population), separate and distinct from a Washington cluster, with potential subpopulations and site-specific differentiation in each. Significant IBD was found among all sites ($R^2=0.7009$, $P=0.01$), but was not supported among southern California sites alone ($R^2=0.0058$, $P=0.35$). Baseline population genetic estimates and conclusions in this study provide information to enhance our understanding of genetic structure of West Coast North American estuarine invertebrate species and provide new information to successfully restore this and possibly other native estuarine species.

The slug within the bivalve: Reconciliation of shell-based taxonomy and molecular data in Juliidae (Heterobranchia: Sacoglossa)

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Juliidae is a member of the Sacoglossa (Jensen, 1996), a herbivorous clade of heterobranch gastropods. Juliidae has a complex taxonomic history derived from the fact that these gastropods have bivalve shells (Kawaguti and Baba, 1959; Keen and Smith, 1961; Jensen, 1997). The current taxonomy of Juliidae is largely based on shell morphological traits and to a certain extent on internal and anatomical traits, such as the radula and the reproductive anatomy (Jensen, 1997; Baba, 1961). Based on these data, Juliidae is considered to have two extant genera, *Berthelinia* and *Julia*, both with pan-tropical distributions (Jensen, 1997). For this study a species-level molecular phylogeny of Juliidae has been produced using a combination of three genes, 2 mitochondrial (CO1, 16S), and 1 nuclear (H3). Geometric morphometrics were used to quantify and compare the shell morphology of Recent and extinct taxa, based on extant shells as well as fossil shells from the literature (i.e., Baulk *et al.*, 1968; Le Renard *et al.*, 1996). The morphometric data will be integrated with the molecular phylogeny using comparative methodologies.

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It loves me, it loves me not: Counting species of the “rose petal sea slug,” *Polybranchia* (Mollusca: Gastropoda) with a molecular systematics approach

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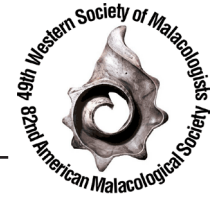
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Polybranchia (Gastropoda: Heterobranchia: Sacoglossa) is a pantropical group of herbivorous sea slugs consisting of eight valid species (Jensen, 1993; Jensen, 2007). One species, *Polybranchia viridis*, can be often overlooked because tends to find shelter under rocks during the day, becoming active mainly at night (Clark, 1994). Nocturnal behavior may apply to all members of *Polybranchia* since they are very difficult to find in the field. As a result, the rarity of this group makes phylogenetic analyses on this genus a difficult task. This genus has been used in large scale phylogenetic studies with only a few species representing the entire group (Crista *et al.*, 2014; Krug *et al.*, 2015) but a detailed phylogenetic study on *Polybranchia* has yet to be conducted. This study investigates the disjunct range of *P. viridis* and whether the species consists of two populations or two species (one from the Caribbean and another from the Eastern Pacific). Secondly, *Polybranchia orientalis* is the most commonly found species in the Indo-Pacific but collecting reports are lacking for the five other described species from the Indo-Pacific. This investigation used nuclear gene H3 and mitochondrial genes COI and 16S. A Bayesian analysis was conducted on the molecular markers to identify clades and cryptic species. Additionally, scanning electron microscopy was used to examine the morphology of the radulae and penis of each clade. Evidence for diversity in obtained specimens was higher than expected.

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Taxonomic revision of the species of the family Atlantidae (Gastropoda: Pterotracheoidea) in the Mexican Pacific using morphological and genetic analyses

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The family Atlantidae is a group of holoplanktonic gastropods that includes *Oxygyrus inflatus*, *Protatlanta souleyeti*, and 22 species of the genus *Atlanta*. These organisms have a right coiled shell with similar morphology within *Atlanta* species, which has complicated their taxonomy and identification. In this study, 426 organisms collected from the Gulf of California and Gulf of Tehuantepec, Mexico; Malpelo Island, Colombia and the Santa Barbara Museum of Natural History collection were analyzed, with the goal of doing a taxonomic revision of the organisms found in the Mexican Pacific using morphological, morphometric and genetic analyses. The shell morphology was the most practical and reliable character for identification. However, the eye type, the shape of the keel and the spire are additional helpful characters to differentiate among species. Using those characters, six groups of morphologically similar species were formed. All species were used in a morphometric analysis to evaluate whether the whorl formula was a useful tool to improve the identification discrimination of species with similar morphologies. However, the analysis showed that the results obtained for the whorl formula vary among organisms of different sizes from the same species, so we concluded that the formula is an inadequate approach for species identification. Alternately, a discriminant analysis using measurements from the protoconch was performed, obtaining species separation but only within groups of morphologically similar species (with the exception of the *helicinoidea-inflata-californiensis* group). The genetic analysis based in sequences from COI and 16SrRNA genes from mtDNA detected species-specific clades. The morphometric and the genetic analyses supported that the species *A. peronii*, *A. gaudichaudi* and *A. pacifica* belong to a single species (*A. peronii* Lesueur, 1817), as well as *A. echinogyra* and *A. plana* belong to another single species (*A. echinogyra* Richter, 1993). With the information above, it is concluded that of the 18 species from the Mexican Pacific, only *Oxygyrus inflatus* and 13 species of *Atlanta* are valid.

Managing conservation of the endangered *Patella ferruginea* (Gastropoda: Patellidae) in a marina about to be enlarged. A potential artificial marine micro-reserve network

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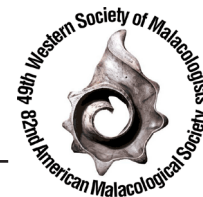
The present study takes place in the Ceuta Marina (Spain), located in northern Africa. In 2005 a tsunami took place in the area, causing huge damage. As consequence, the marina underwent a process of reconstruction and now a new project for enlargement is demanded. However, a conservation problem arises with this: one of the biggest actively reproductive population of the endangered *Patella ferruginea* is located in the Ceuta Marina. This study aims to compare the situation of *P. ferruginea* populations in the different zones of the marina. These zones were defined according to their features regarding currents and grade of exposition to anthropogenic impact. For this purpose, specimens were counted and information regarding morphotype, orientation and other size measurements was recorded. One way ANOVA was performed to test differences regarding the variables 'size' and 'density' of specimens among the different zones. Areas protected against the anthropogenic impact showed a significantly higher density and size of individuals than exposed ones, which is a clear evidence of the reserve effect. To finish with, we propose an alternative design for the enlargement project, since the traditional way of action would cause the death of thousands of specimens of *P. ferruginea*. On the contrary, the following solution would fulfill the requirements of the European port authorities without threatening the survival of this endangered species; and would even be economically profitable. This is the construction of a parallel dock that allows to create a hydrodynamic corridor in the middle, which would act as an artificial marine micro-reserve and thus maintain the genetic flux of the *P. ferruginea* populations. In addition, the construction of a seminatural aquarium is proposed, which could serve as demand for tourism.

Effect of light qualities on the growth and proximal composition of *Amphora* sp.

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Benthic diatoms are the main food used to the nourishment of juvenile abalone, sea urchin and sea cucumber, among other. Also, *Amphora* sp. is a common abalone post larvae food in the natural habitat. The benthic diatoms modify their growth and biochemical composition due their culture conditions. The light quantity and light quality are important factors that modify the metabolism of diatoms. The aim of this study was to evaluate the effect of spectral composition of the light on cultures of *Amphora* sp. and evaluate their growth and proximal composition. Were maintained batch cultures of *Amphora* sp. with different light composition provided by fluorescent lamps of white, green, blue, yellow and GroLux. The growth and proximal composition of cells were obtained from samples collected at exponential and stationary growth phase. Growth and proximate composition of *Amphora* sp. were modified due to the effect of the spectral composition of light and growth phase. The protein content was higher in exponential phase when white light was used; while carbohydrate content increased in stationary phase with GroLux. The lipid content increased in the exponential phase. Organic dry weight and ash content were higher in the exponential phase using yellow light.



Size at first maturity of Squalid Callista *Megapitaria squalida*

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The Squalid Callista *Megapitaria squalida* is an important fishery resource in the state of Baja California Sur, Mexico; thus, knowing the size at first maturity (SFM) is important to provide biological information and define the minimum catch size, necessary to give proper management of the fishery. The SFM — in which 50% of organisms are sexually active — was estimated for two populations of *M. squalida* (La Paz Bay: PB and Magdalena Bay: MB). The organisms were collected monthly from February 2007 to December 2008. Shell length (SL) (± 1 mm) was recorded, and sex and stage of gonadal development stage was identified through histological technique. Data from SL were adjusted to a logistic model to estimate the SFM for each sex, using Somerton's method. The SFM of *M. squalida* was at 64.5 mm SL in PB, and 85 mm PB in MB, for both females and males. Finding organisms in gonadal development from 35 mm and 42 mm respectively, shows that overfishing aimed at larger sizes, shifts the SFM towards smaller organisms.

Benthic diatom culture for abalone nourishment

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Benthic diatoms are the main food used for the nourishment of abalone postlarvae. Different strains of diatoms are used as food of abalone postlarvae on different farms and under experimental culture conditions around the world. The use of different systems and culture conditions cause that the benthic diatom production had differences on the biomass quantity and proximal composition. The aim of this work was an analysis of the different strategies used to the massive production of benthic diatoms, and the main considerations that must be taken when they are used as food to the abalone postlarvae. Presented the results obtained about the growth and survival of postlarvae and juvenile abalone when used different benthic diatoms species and others algae as food. Mentioned different alternatives to the production of benthic diatoms or other strains to be used as food to abalone postlarvae and juvenile.

A seldom traveled path: New marine bivalves in the Perú-Chile Province (western South America)

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The Perú-Chile Province, an area that extends from Punta Aguja, Piura, Perú (5.8°S), and continues south to the southern tip of Isla Chiloé, Los Lagos, Chile (43.4°S), has never had a comprehensive survey of marine bivalve diversity. While preparing a new monograph to be titled *Bivalve Seashells of Western South America* we have encountered a large number of new taxa in this area: nearly 20% of the bivalves documented so far have never been described. These include many new species from waters greater than 300 m, and also many species smaller than 5 mm in maximum length.

We have uncovered a minute mussel in the subfamily Crenellinae with the help of two Chilean researchers. As a default, many surveys place small, ovate, infaunal mussels into the genus *Crenella* Brown, 1827. However, this new shallow water Chilean species does not possess the sculpture or the hinge plate characteristic of that genus. Instead, it appears to be closest to *Exospirna* Iredale, 1929, originally described from South Australia. We anticipate describing a new genus and species for this taxon.

However, several other undescribed species are in the families Nuculidae, Nuculanidae, Neilonellidae, and Yoldiidae. Included here are new taxa that are over 10 mm in length and/or live in continental shelf depths, and are not at all uncommon. This leads us to believe that previous studies in the region did not focus on soft bottom sediments, or they potentially lumped the new species in with described taxa from adjacent areas.

The mega-diverse galeommatoidean bivalves will likely yield the highest number of new taxa. These small, frequently commensal, often fragile bivalves are poorly known globally. They often associate with invertebrate hosts, or live in their burrows, making it difficult to adequately sample the group. As of mid-2016, we have found five new species of galeommatoideans.

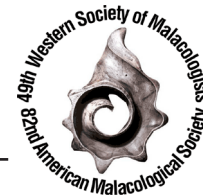
In spite of all of the new taxa we have discovered, the number of marine bivalve species in the Perú-Chile Province is low (<300 species) compared to other eastern Pacific Ocean provinces (>450 species).

Paralarvae of the complex *Sthenoteuthis oualaniensis*-*Dosidicus gigas* (Cephalopoda: Ommastrephidae) in the northern limit of the shallow oxygen minimum zone of the Eastern Tropical Pacific Ocean (April, 2012)

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The three-dimensional distribution of the paralarvae of the complex *Sthenoteuthis oualaniensis-Dosidicus gigas* (Cephalopoda: Ommastrephidae) was analyzed at the northern limit of the shallow oxygen minimum zone in the Eastern Tropical Pacific in April, 2012. The hypoxic water (~44 $\mu\text{mol/kg}$ or 1 mL/L) rises from ~100 m depth in the entrance of the Gulf of California to ~20 m depth off Cabo Corrientes. Most of the paralarvae of this complex, dominated by *D. gigas*, were concentrated in the Gulf entrance, between the thermocline (~20 to ~50 m depth) and the sea surface, in the warmest (>19°C) and oxygenated (>176 $\mu\text{mol/kg}$) layer. The highest abundance of paralarvae was detected in an anticyclonic eddy (~120 km diameter and > 500 m deep), which contained lower salinity water (<35 g/kg), consistent with formation in the California Current. Lower paralarvae abundance was recorded further south off Cabo Corrientes, where hypoxic layers were elevated as water shoaled near shore. No paralarvae were found in the north of the study area beyond the strong salinity front (~34.8–35.4 g/kg) that bounded the anticyclone. These results showed an affinity of the paralarvae for lower salinity, oxygenated water, illustrated by the influence of the mesoscale anticyclonic eddy and the salinity front in their distribution. Based on this study, it can be concluded that the expansion of the depth range of hypoxic water observed in the Eastern Tropical Pacific may be vertically restricting the paralarvae habitat.

Phylogeny, Morphology and Ecology of the Eastern Pacific genus *Ocinebrina* Jousseaume, 1880

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The predatory snail genus *Ocinebrina* Jousseaume, 1880 is poorly understood and species rich in the northern hemisphere. Eastern Pacific species are present in various intertidal and subtidal reefs along the coast of California. Due to apparent phenotypic plasticity and only partly overlapping geographic distributions within California, it is hypothesized that allopatric speciation has had an important role leading to present day species, including those within California. The morphologically diverse Eastern Pacific ocinebrinids are similar to cryptic members of the Eastern Atlantic (Crocetta, *et al.*, 2012; Barco, *et al.*, 2013). Recent phylogenetic studies have detailed subfamilial relationships (Marko *et al.*, 1999) and have shown the necessity to separate the Eastern Pacific species into a new genus (Houart, pers. com.). Anticipated research on genomic DNA sequencing, radulae anatomy, morphometric assessments, anatomical and ecological studies on this group could help delineate species taxa, their distributions and a parsimonious phylogeny. Twenty two known species are currently recognized and additional species are presumed to be new to science. This rapidly evolving group has an extensive Pleistocene record from recent west coast assemblages.

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Using ontogenetic vectors to inform systematic decisions in Isognomoninae Woodring, 1925 [1828]

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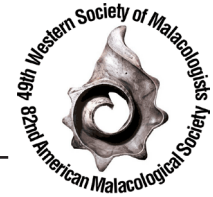
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I carried out a phylogenetic analysis of Isognomoninae Woodring, 1925 [1828] using both mitochondrial and nuclear genes. This phylogeny supports their monophyly but also reveals unexpected structure within this clade. With the relatively recent revision of the Pterioidea Gray 1847 [1820], (Tëmkin, 2010) combining several families into an expanded Pteriidae, the discovery of intermediate structure within *Isognomon* has presented a both a challenge and an opportunity for taxonomic revision. While species assignments can be guided by well-defined and referenced species concepts, intermediate-level clades have no equivalent framework for assigning genera, subgenera, subfamilies, etc. For my revision of the Isognomoninae, I develop a concept by which to judge deeper nodes for taxonomic significance and a novel application of geometric morphometric ontogenetic analysis to generate optimal data for this method.

The criteria I apply is that categories are of maximal utility if they describe only unique information and do not contain information described by a higher or lower taxa. Ontogenetic vectors, high-dimensional algebraic descriptions of whole-animal development are uniquely well suited for this type of comparison, but analogous analyses are possible using nearly any type of data. What ontogenetic vectors allow is a simple, one-dimensional, measure of the redundancy of the information contained in two nodes of the phylogeny - the angle of divergence between the average ontogenetic vector for all specimens within those two clades. At 90 degrees, the developmental pathways of the nodes are independent of each other and describe entirely separate processes of shell-growth. Using this criterion, I find that the Isognomoninae have taxonomically significant changes in shell development at two node levels between the basal node containing the subfamily and the tip-groups containing the species. Therefore, I divide this group into two genera; *Isognomon* Lightfoot, 1786 and *Melina* Philipsson, 1788 each consisting of three subgenera.

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Infection intensity by trematodes in *Megapitaria squalida* (Bivalvia: Veneridae) and its impact on the reproduction

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Bivalve molluscs are intermediate hosts of several types of parasites, being trematodes among the most common. Usually these parasites are located within reproductive tissues inhibiting the formation of gametic cells. Nevertheless, their effect will depend sometimes on the intensity of incidence or infection. In order to determine the occurrence of parasites in the Chocolate Clam (*Megapitaria squalida*) and the intensity of infection, the gonads of organisms from Santa Rosalia, Baja California Sur, Mexico were analyzed. Infection intensity was determined as the area occupied by parasites within the tissue under the following criteria: low (<5% of the tissue is occupied by parasites), moderate (5–25%), high (25–50%) and very high infection (>50%). Gonads presented mainly trematodes larvae (sporocysts, developing cercaria and metacercaria) which displaced gametic cells. In the low intensity, the area occupied by parasites (3%) was lower than the area occupied by gametes (97%). High intensity infection showed a significant increase in coverage of parasites within the follicles (40%) and decreased gonadal area occurred (60%). In the very high intensity stage, most of the follicle was parasitized (78%). The major proportion (56%) of the parasitized clams presented a very high infection intensity (>50% tissue infected). Results suggest that intensity of infection for trematodes larvae inside the gonads of *M. squalida* affects negatively its reproduction.

Epibiont biodiversity from the basibiont *Chiton articulatus* (Mollusca: Polyplacophora) through the Mexican Tropical Pacific

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In the intertidal zone availability of substrate is limited and epibiosis frequently occurs. The epibiotic community of a basibiont (substrate organism) at the intertidal rocky shore depends on the basibiont species, season and region. In mollusks, the main basibionts reported belong to the classes Gastropoda, Bivalvia and



in lesser degree to Polyplacophora. This work compares the local diversity of macroinvertebrate epibionts present on adult chitons (>40 mm total length) of *Chiton articulatus* around the cold season (October 2015 to February 2016) and from three localities along the Mexican Tropical Pacific (MTP): Sinaloa (“SIN” 23°N), Michoacan (“MIC” 18°N) and Guerrero (“GRO” 17°N). About 30 adult *C. articulatus* were haphazardly collected every month and simultaneously from the three localities. The obtained epibionts from each chiton were classified in major categories: crustaceans, mollusks and others. Abundance data of every category were used to estimate some biodiversity parameters of macroinvertebrate epibionts present on each chiton per locality: richness (S , here expressed as categories), diversity ($Shannon H'$) and evenness ($Pielou J'$). Richness values were SIN ($S=2.8$), MIC ($S=2$) and GRO ($S=2$). Diversity values were SIN ($H'=0.51\pm0.19$), MIC ($H'=0.49\pm0.11$) and GRO ($H'=0.47\pm0.06$), and finally evenness values were SIN ($J'=0.52$), MIC ($J'=0.71$) and GRO ($J'=0.63$). A general pattern for the five sampling months was observed, indicating that richness and diversity were slightly higher in the northern locality (SIN 23°N) compared to southern localities (MIC 18°N and GRO 17°N), while, evenness was higher in the middle locality (MIC 18°N). Latitudinally, we could say that apparently the north (23°N) is richer and more diverse in epibionts but with lower evenness, while southwards (18°N–17°N) apparently dominance in abundance of organisms per category shows a moderately even distribution. These values of epibionts on the basibiont *C. articulatus* may serve as a proxy for predicting a general pattern of biodiversity in the MTP as well as its possible loss due to the human consumption of the basibiont observed in the study area.

Diversity and distribution of marine mollusks along the Beaufort Sea shelf and slope: The influence of Pacific and Atlantic water masses

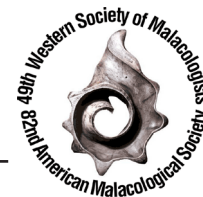
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As an interior Arctic sea with a narrow shelf and a steep slope, the US Beaufort Sea is influenced by complex vertical and horizontal domains of water masses and current regimes. The more than 1,000 species of benthic invertebrates inhabiting that area form communities that reflect the long-term (year to decadal) environmental conditions and water mass sources. During six expeditions over five years, epifauna invertebrates were collected at >150 locations spanning the shelf and slope to 1,000 m across the primary water masses. The >250 species are dominated in species richness by gastropods, especially Buccinidae and Mangeliidae and by crustaceans. At locations deeper than ~350 m, communities increasingly include species common in the Atlantic-influenced Arctic and Atlantic-boreal regions matching roughly the transition from Pacific-origin to Atlantic-origin waters. Over 300 voucher specimens representing 91 molluscan species were identified for these studies. The fauna, particularly large gastropods, is in need of further study and revision.



Gastropod and bivalve mollusks associated with drift plants, transported throughout the freshwater San Joaquin River Delta, California

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Our understanding of benthic invertebrates is mostly tied to sampling hard and soft bottoms; however, drift plants also may provide alternative habitats for many of these organisms, dispersing benthos as adults. In this study we quantified abundance and distribution of benthic invertebrates associated with drifting macrophytes, especially *Egeria densa* (pond weed,) in freshwater portions of San Joaquin River of the California Delta. We used drift samplers to collect and compare drifting invertebrate assemblages associated with sunken and floating drift vegetation, near Stockton, California. Over 42 drift samples were collected above relatively deep (7–13 -m -deep) sandy mud bottoms, using drift sampling nets between August and October of 2015. In addition to extra dip netting, these more quantitative drift samplers were 0.5-m-diameter plankton nets of 500- μ m mesh, weighted on one edge of the bridle and with a small float on the opposite edge, thus suspended vertically in the water above the bottom for ~1-hour intervals, during >1-kt tidal currents. We transported the cooled samples to the lab live for prompt further analysis.

Pulmonate gastropods were found in most drift samples but never in high densities, compared with crustaceans. These pulmonates, reportedly *Physella* (= *Physa*) *gyrena*, commonly occurred even in additional plankton samples near the bottom, without vegetation. Common benthic Asiatic clams, *Corbicula fluminea*, were rare on drift plants, but a native Delta mussel, *Anodonta* “*californiensis*,” (and any future mussel species invasions) might attach to drift plants. Fauna on drift plants appear to speed adult dispersal and help account for separately observed, rapid colonization of recently dredged areas. Our results indicate that drift sampling provides valuable information on such benthic communities, a component often overlooked in conventional benthic sampling.

Community structure of limpets and chitons associated to macroalgal assemblages at the region of Ixtapa-Zihuatanejo, Guerrero, Mexico

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The rocky coastline is an ecosystem that hosts a lot of invertebrates and macroalgae; the latter provide a substrate for some species of mollusks where they live. In Mexico there have been several studies that focused on the biology of mollusks in the intertidal zone, despite this, are the considerable lack of knowledge we have of the associations between the two groups. This study aims to determine the community structure of the limpets and chitons associated with macroalgae along an annual cycle in the region of Ixtapa-Zihuatanejo, Guerrero.

The specimens examined in this study were collected manually on four expeditions in January, May, July and November 2014. The 108 samples (400 cm²) were recorded and environmental variables were taken. The samples were collected in three locations in Ixtapa-Zihuatanejo, Guerrero: Palmar beach, Las Gatas beach, and Municipal Dock.

A total of 71 species of macroalgae were obtained: 17 Chlorophyta, 46 Rhodophyta, and 8 Phaeophyceae; while of mollusks were obtained 608 individuals, 338 limpets and 270 chitons, belonging 11 families and 23 genera. The richness of mollusks was 63 species, of which three are new records for the region of Ixtapa-Zihuatanejo and one for the Mexican Pacific. Palmar beach and Municipal Dock had the highest species richness with 18 and 17 limpets and six and seven chiton, respectively; while in Las Gatas beach had 10 of limpets and five species of chitons.

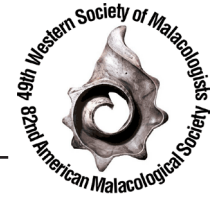
The species with the highest density (individuals/200 cm²) of specimens were *Acanthochitona aragonites*, in the Palmar beach and Las Gatas beach, while *Crucibulum scutellatum* in Municipal Dock. The three localities had highest diversity index ($H' = 3.00$ to 3.63 bits/ind), similar to those reported by other authors. This paper attempts to promote research with a comprehensive approach to biological communities, because in this way you can have full knowledge about the biodiversity of marine communities and create and implement management plans for conservation of these natural resources.

The use of average distinctness index to analyze a freshwater mollusks community in a natural reserve in Southern Mexico

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The worldwide ecological crisis has increased in the last years due to the devastation of rainforests in our planet. Selva Lacandona, a rainforest from Chiapas in Southern Mexico, is one of the regions with the highest biodiversity in this country; therefore it has been recognized as a priority area for conservation. Part of the diversity in this zone has been sheltered in a natural protected area “Reserva de la Biosfera Montes Azules (REBIMA)” which was created in 1978 (INE, 2000). Measures of taxonomic diversity can be used along with species richness and rarity scores in the perspective of conservation (Magur-



ran, 2004). The average distinctness index (Δ^+) is the average taxonomic path length between any two randomly chosen species. This index allows comparing data with different sampling effort, reduces the importance of dominant species and gives information of how taxonomically varied an assemblage is (Clarke and Warwick, 1998). Thus, our aim was to use the average distinctness index to compare the diversity of freshwater mollusks between 11 localities inside the reserve REBIMA using data collected from 2009 to 2015. The values obtained were higher than 50 and lower than 70, with the exception of Río Lacantún which had the lowest value ($\Delta^+=47.22$). Even though Lagarto had the highest number of species (14), its index value was lower ($\Delta^+=63.92$) than the locality with the highest value Arroyo Danta ($\Delta^+=69.05$), where half of those species were found (7). The use of this index is subject to assumptions in relation to comparable taxonomic accuracy, but it is a useful tool that provides another view in contrast with the classic diversity indices and it can help in conservation purposes.

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Climate-driven vicariance and recurrent trans-Arctic migration in the cosmopolitan sea slug *Alderia modesta*

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Understanding the impacts of historical climate change on biogeography can help us predict how species may respond to the rapid human-induced warming currently underway. The temperate sea slug *Alderia modesta* exhibits a remarkably wide circumpolar distribution, inhabiting estuaries throughout the northern Pacific and Atlantic. Phylogeographic analysis of mtDNA previously showed a deep split between the North Pacific and Europe, but no genetic structure across the Pacific. Here we present additional data that produce a reticulated haplotype phylogeny, indicating a pattern of repeated trans-Arctic migration from the Pacific to the East Coast of North America. Both mtDNA and nuclear microsatellite data suggest gene flow has ceased between the western and eastern Atlantic, but high connectivity persists across the entire North Pacific. Colonization of the Atlantic from the Pacific was likely facilitated by opening of the Bering Strait ~5 million years ago, and divergence time estimation suggests Europe-North America isolation began in the mid- to late-Pliocene. In North America, recurrent bouts of Pacific-to-Atlantic trans-Arctic migration followed by isolation were likely driven by Pleistocene glacial cycles, with recent population expansion in the Pacific since the last glacial maximum. Preliminary analyses of radular and penial stylet morphology are congruent with the deep trans-Atlantic genetic split, and may support reclassification of North American populations as a new species distinct from European *A. modesta*.



Molecular description of the intestinal bacterial flora in wild Mexican population of *Haliotis corrugata* and *Haliotis fulgens*

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The guts of abalones (*Haliotis*) contain highly complex bacterial ecosystems, which contribute to food digestion, growth and disease resistance of these organisms, among other factors (Blaut and Clavel, 2007; ten Doeschate and Coyne, 2008; Zhao *et al.*, 2012). To describe the bacterial flora of *H. corrugata* and *H. fulgens*, a 454 pyrosequencing of the 16S bacterial gene was performed. The microflora characterization revealed a high degree of dissimilarity between these the two species. According to the read frequencies, the main differences are: 1) *H. corrugata* organisms have a more heterogenic bacterial flora composition compared with *H. fulgens*; 2) the gut microflora of both abalone species was dominated by different *Mycoplasma* ribotypes; 3) a host-specific adaptation should be considered for many of the detected bacteria. Also, according to the taxa prevalence the dominant bacterial classes were principally uncultured strains belonging to (bacterial frequencies percentage are reported in parentheses): *Mollicutes* spp. (30%); *Gammaproteobacteria* spp. (13%); *Alphaproteobacteria*, and *Fusobacteriia* (0.4%) while around 41% comprised uncharacterized bacteria. Considering the interspecific microbiome differences observed between the two abalones species in this study, the bacteria community harbored by this gastropods should be considered host-specific and may help the abalones in assimilating different alimentary resources or face local environmental factors, among other.

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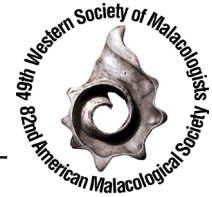
Eocene mollusks from Baja California Sur, Mexico

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The Cenozoic history of Baja California Sur begins with the deposition of marine rocks of the Tepetate and Bateque formations. These are important in the geological record, especially in the North American Pacific region, as they may represent one of the most complete fossil and paleo-oceanographic records of the Paleo-



gene period. The Tepetate Formation is between 70 and 150 km east-northeast of the city of La Paz, while the Bateque Formation is located on the eastern and western of Cuenca Laguna San Ignacio to Arroyo Mezquit- al (between San Juanico and La Purísima). Both formations have been extensively studied for decades, and the first faunal lists of marine macroinvertebrates found in these formations were assembled by Squires and Demetron. However, in recent years there have been new collects and reviewed the localities described by different authors. So far, we have reported 49 localities and 106 collects for the Tepetate Formation and for the Bateque Formation have registered 40 localities and 49 collects. In each of the collects, we have been registered new specimens (unregistered in both formations, but in other formations of the Pacific) and new species, being the phylum Mollusca, which it have more new records. Today, we have reported: 17 new records for the Bateque Formation (bivalves and gastropods), and 25 for the Tepetate Formation (bivalves, gastropods and cephalopods). This faunal assemblage is characteristic of shallow marine water (inner shelf to outer) and tropical to subtropical climates. The abundance and diversity of macroinvertebrates previously reported and new records of mollusks contribute to the understanding of the origin of the different taxonomic groups in Baja California Sur and the Pacific Coast of North America. In addition, the species are indicative of warm waters from the Tethys circumglobal current, which created the conditions for a wide biotic exchange between marine organisms of the Atlantic, Gulf of Mexico-Caribbean, and Pacific.

Gene rearrangement and molecular evolution within vermetid gastropod mitochondrial genomes

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As part of an integrative approach to vermetid systematics using morphological, anatomical, ultrastructural, and molecular data, we have sequenced the complete mitochondrial genomes of 24 ingroup and three outgroup taxa. We used mitochondrial and nuclear ribosomal array nucleotide sequences to generate a robust phylogenetic hypothesis for the Vermetidae. Our phylogenetic hypothesis is, however, at odds with the traditional generic arrangement of vermetids, so we have sought additional support for this novel hypothesis based on mitochondrial gene orders. We find support for many clades in our tree based on shared gene order rearrangement events, suggesting that gene rearrangement events are occurring with greater regularity than typically found in animal mitochondrial genomes. In addition, some gene order changes are further modifications of earlier rearrangements. These nested rearrangements provide an independent marker of evolutionary direction on the tree, and increase our confidence in the phylogeny. These mitochondrial genomes are also useful for investigating mechanisms of molecular evolution and gene rearrangement. Vermetid mitochondrial genomes contain remnants of past rearrangement events, including portions of ribosomal RNA and protein encoding genes, and “extra” copies of tRNAs, some of which appear functional, while others



are pseudogenes. These fragments of genes and extra tRNAs provide support for tandem duplication and random loss as a common, but not the sole, mechanism of genome rearrangement. The extensive movement of tRNAs, as well as the presence of duplicate tRNAs, allow us to investigate tRNA remodeling and recruitment events in a densely-sampled relatively young clade.

Mollusk remains in the offering 125 of the Great Temple of Tenochtitlan

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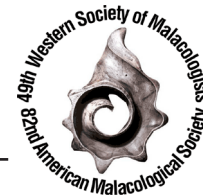
This paper analyzes the shell remains recovered in Offering 125, a ritual deposit found to the west of the Tlaltecuhtli monolith and exactly at plaza level. This offering was buried in a small box made of basalt stones at the front of the stairway of the 6th constructive stage of the Great Temple of Tenochtitlan, at the joint of the temples of gods Tlaloc and Huitzilopochtli. It dates from the reign of Ahuítzotl (AD 1486-1502), and is one of the richest of all, containing a total of 3,899 cultural and organic items. Animal remains were classified in five phyla, of the five extant phyla, Mollusca is the most abundant. Forty-six species were identified, 11 marine species from the Atlantic coast, 33 marine species from the Pacific coast of Mexico, and two freshwater clams (*Nephronaias aztecorum* and *Anodonta chalcoensis*). Twenty-one species are new records for the Great Temple of Tenochtitlan offerings.

Delimiting cryptic species of sea slugs by integrating molecular data with radular characters

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Cryptic species that are morphologically similar to named taxa pose pervasive taxonomic challenges in soft-bodied marine invertebrates. Molecular methods of species delimitation can identify new species; however, morphology may better distinguish cryptic species than DNA in cases of recent radiations, because traits under selection can evolve faster than neutral DNA sequences. A recent species delimitation method (iBPP) jointly analyzes molecular and morphological data, but is limited to continuous traits that are generally lacking for soft-bodied taxa. We applied this method to delimit host-specialized sea slugs that consume invasive “killer” algae, and are traditionally considered species-poor (*Oxyhoe*, 6 recognized spp.; *Lobiger*, 3 spp.). When molecular data from three loci were analyzed for 137 *Oxyhoe* specimens, four delimitation methods yielded incongruent results, but distinguished eight or nine new species from three named taxa. Analyses that integrated six radular tooth characters (standardized for body size) with molecular data supported all 10 new candidate species. Preliminary analyses on 22 specimens representing two nominal *Lobiger* spp. identified four candidate species. Integrative approaches that include radular characters can thus objectively identify putative species in taxonomically challenging sea slugs, even when alleles are shared among recently diverged species.



The *Octopus* commercial fishery in Baja California Sur, Mexico is composed of several species

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In Mexico 10% of the octopus fishery is accomplished in the Pacific Ocean where nine species have been reported: *Octopus bimaculatus*, *O. chierchia*, *O. digueti*, *O. alecto*, *O. fitchi*, *O. hubbsorum*, *O. penicifiller*, *O. rubescens* and *O. veligero* (Lopez-Uriarte *et al.*, 2005). The remaining 90% comes from the Yucatan peninsula, which is mainly composed by *O. maya* reaching 16,000 t per year. In the case of the species from the Pacific Ocean, *O. hubbsorum* is the most common and according to comments by fishermen this species is the most commonly caught for more than 20 years (Aguilar and Godínez-Domínguez, 1995; López-Uriarte *et al.*, 2005). Domínguez-Contreras *et al.* (2013) published a range extension of *O. hubbsorum* to Isla Magdalena, Baja California Sur (BCS). In BCS, the octopus fishery catches have been documented for the last decade (1996–2015), reaching up to 550 tons per year (SAGARPA, 2015). However, in the official fishery records the catches are registered by its common name “Pulpo”. In order to have more information about this resource and elements to regulate the fishery, we studied the species composition of the catches in BCS, on a monthly basis during 2015. We traveled to the different towns of BCS and register the species identification of the *Octopus*, including biometric measurements as well as the fishing gear and methods of fishing. We found that three species of *Octopus* composed the *Octopus* fishery in BCS: *O. hubbsorum* is caught from the Gulf of California in Santa Rosalía and Mulegé through the south of BCS to Isla Magdalena, it is calculated that contributes with 67% of the total catch; *O. bimaculatus* is caught from Isla Magdalena through the Pacific coast of BCS to Sebastián Vizcaíno Bay, and contributes 14%; finally *O. bimaculoides* is caught in the interior of Ojo de Liebre, Lagoon, Guerrero Negro, BCS, and contributes 19%. Each species has different methods of fishing and biometrics measurements.

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Well-traveled chitons on tsunami debris or imported oysters have helped unravel the *Acanthochitona achates* (Gould, 1859) species complex

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Ongoing separate collaborative morphological and molecular studies have involved chitons of the genus,



Acanthochitona Gray, 1821, which are normally absent from the Oregonian province of the northeastern Pacific Ocean but have been arriving by rafting or on oysters. Some began to show up on the West Coast in 2012 and later on Hawaiian shores, attached and obviously healthy on debris as large as floating docks from the earlier devastating 2011 Tōhoku tsunami striking northeastern Honshu Island, Japan. In a separate study led by Rick Harbo (Nanaimo, British Columbia, Canada), we are reporting a new record for western North America first noted in 2014 of an apparently thriving population of *A. achates* within Ladysmith Harbour, British Columbia, Canada, which is on the eastern side of Vancouver Island well within the Salish Sea. These chitons were likely introduced along with imported Pacific oysters, *Crassostrea gigas* (Thunberg, 1793) but, because oysters have not been brought from eastern Asia to our knowledge since 1977 (Bourne, 1979), it is likely that *A. achates* has been present for decades but neglected. Its restricted distribution within Ladysmith Harbour could reflect the anomalously warm temperatures of this locality for the region. Overall, in our DNA sequencing related to these studies, we have found unanticipated species-level diversity in our combined tsunami debris and Ladysmith Harbour samples and those we or others have sequenced from the northwestern Pacific. Only two temperate-latitude species in this genus were recognized for the North Pacific by Saito (2000): *Acanthochitona achates* and *A. defilippi* (Tapparone-Canefri, 1874). Earlier, Taki (1938) had provided a detailed account distinguishing *A. rubrolineata* (Lischke, 1873) from *A. achates*, but he emphasized the perplexing nature of the observed morphological variation. Saito (2000) considered *A. rubrolineata* a junior synonym of *A. achates*. There is also a possibility that some of the relevant type material does not correspond to the names in usage, so more study is needed. The confusion is understandable in retrospect, given that in our studies we have found phylogenetic evidence based on mitochondrial 16S and COI markers, and some morphological distinctions, that *A. achates* is actually a species complex of multiple well supported lineages, including a single available individual representing a distinct lineage that was collected from further south on Okinawa Island, Japan. Surprisingly, the endemic Hawaiian species, *A. viridis* (Pease, 1872), is supported as nested within this species complex, providing evidence that its first appearance in Hawaii was later than the most basal divergence of what is referred to here as the *A. achates* species complex.

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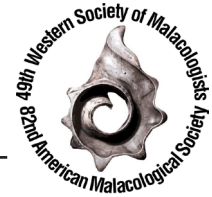
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Phylogenetic reconstruction of the genus *Berthella* using molecular and morphological traits

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Berthella (Pleurobranchomorpha, Pleurobranchidae) is a group of marine side-gilled sea slugs found in tropical and temperate regions of the world. There is much confusion regarding the taxonomy of *Berthella* and its relationship to other pleurobranchids. Recent molecular work on *Pleurobranchus*, another group closely related to *Berthella*, showed *Berthella* to be paraphyletic and some species are sister to *Pleuro-*



branchus. *Berthella* shells are also present in the fossil record. It is however unclear whether these shells belong to *Berthella* or *Pleurobranchus*. Moreover, there are two possible candidates for cryptic diversity in *Berthella*, *B. stellata* and *B. californica*. *Berthella stellata* has a disjunct range including both the Eastern Pacific and the Mediterranean. *Berthella californica* has two different morphotypes with discontinuous ranges in the Eastern Pacific. These uncertainties in the taxonomy of *Berthella* call for a taxonomic revision of this group. The goal of this study is to use molecular and morphological traits of *Berthella* to reconstruct its phylogeny. Two mitochondrial genes (16S and CO1) and a nuclear gene (H3) were sequenced. The sequences were analyzed using the Bayesian and the maximum likelihood analyses. SEM images of the shells and radulae of the available specimens were also obtained and compared. The molecular and morphological analyses indicate *B. stellata* is a complex of at least two species. *Berthella californica*, however, does not appear to be a species complex. Future work will involve the use of geometric morphometrics to determine whether the fossil shells of *Berthella* can be confidently assigned to this group.

Effect of five chemicals on the metamorphosis of Cortez geoduck clam larvae, *Panopea globosa*

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The geoduck clam, *Panopea globosa*, is intensively exploited in Mexico due to its high demand and commercial value in Asian countries. It is a long-lived and slow-growing species, so the replacement of natural populations necessarily requires seed production in the laboratory. One of the most vulnerable stages of mollusks is the settlement/metamorphic larval stage, since they undergo drastic morphological changes, including velum reabsorption and the development and/or disappearance of other organs. All this with a strong energy expenditure that can be reflected in high mortality. The metamorphosis of *P. globosa* is asynchronous and lasts between 2 and 3 days under laboratory conditions. Several organic and inorganic chemicals have been used successfully to induce, synchronize or accelerate the metamorphic process in larvae of different mollusk species. In the present study the effect of 5 chemicals (serotonin, GABA, L-DOPA, epinephrine and KCl) were tested at 3 different concentrations (10^{-6} , 10^{-5} and 10^{-4} M, or 1, 10 and 20 mM in the case of KCl) in order to assess their effect on the metamorphosis of *P. globosa* larvae. Percent metamorphosis and survival was evaluated at 30 hours. In each case 3 phases of metamorphosis were documented (initial, intermediate and completed). No significant deleterious effects were observed on larvae after exposure to the different treatments, except with L-DOPA, where 80% of *P. globosa* larvae died after 24h exposure at the highest concentration (10^{-4} M, 24h). GABA, L-DOPA and KCl failed to induce larval metamorphosis when compared to their control. In contrast, serotonin and epinephrine significantly accelerated the metamorphosis of *P. globosa*. Serotonin rapidly triggered the initiation of metamorphosis, and a highest percent of metamorphosed larvae ($87\% \pm 6.7$) was observed in the combination of 6h exposure and 10^{-6} M. Epinephrine produced the highest percent metamorphosis ($91.4\% \pm 4.0$) after 24h exposure to a concentration of 10^{-6} M. It is concluded that epinephrine was the



best chemical and can potentially be used to accelerate and synchronize the process of metamorphosis of *Panopea globosa* larvae.

Relatedness and differential disease resistance in eastern Pacific haliotids

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Many marine host-pathogen systems are poorly understood, and even less is known about how global climate change will affect the mechanisms of these systems. In the abalone and *Rickettsiales*-like organism (RLO) system, the RLO infects abalone digestive tissues and leads to extreme starvation and a characteristic “withering” of the gastropod foot. First identified in black abalone in California after an El Niño event, the withering syndrome-causing RLO (WS-RLO) has been seen in various sites around the world, and has been found in at least low levels in all abalone species examined, yet not all express WS (Crosson *et al.*, 2014). Some abalone species appear to be highly resistant to the disease, unless held at extremely high temperatures. This suggests that the resistant species possess some physiological resistance to the effects of high temperature. Our goal is to develop a detailed understanding of the abalone digestive system and the mechanisms for differential resistance across the *Haliotis* (abalone) genus. In order to clarify differential susceptibility in geographically neighboring species (such as the highly susceptible red abalone *H. rufescens* and relatively resistant green abalone *H. fulgens*), we are creating a robust phylogeny of *Haliotis* to determine whether certain branches are more susceptible to WS. This phylogenetic tree was created using concatenated data from multiple mitochondrial and nuclear genes, and will result in the most robust phylogeny of Eastern Pacific haliotids to date. Temperature limits are mapped onto the tree to determine whether the evolutionary history of the genus can explain why particular species are more sensitive to temperature.

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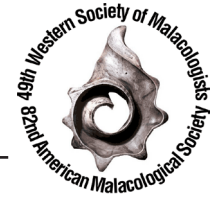
Multivariate selection and the range limit of *Alderia willowi*: Effects of salinity and trait covariance

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For estuarine animals, range limits may be set by complex interactions between abiotic factors, such as geographical gradients in salinity and temperature, and interspecific competition. Further, multivariate



selection can inhibit adaptation to any one stressor. Thus, range limits may occur in different places than would be predicted by considering one environmental factor or trait in isolation. The northern range limit of the sea slug *Alderia willowi* may be set by low salinity following winter rains, and/or competition with its sister species *A. modesta*. We studied multivariate selection on *A. willowi* based on short-term fitness in laboratory experiments. Slugs will be stressed by combinations of low salinity and presence of *A. modesta*, and egg production measured for 1–2 weeks. Analyses of multivariate selection considered the relationship of number of cerata (appendages that circulate body fluid), rate of ceratal beating, and body size on fitness. Preliminary results indicate that lower salinities significantly suppressed initial egg production, but slugs recovered to control levels after a one-week period of acclimation. There was no interaction between body size and fitness in preliminary experiments. Results of ongoing research will provide insight into the basis for northern range limits of estuarine animals along the U.S. West Coast.

Southern California marine shelled gastropod barcode project

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A large portion of the biodiversity of southern California coastal marine fauna is comprised of shelled gastropod mollusks, yet surprisingly few of these (<10%) are currently represented in GenBank by the mitochondrial genes most commonly employed as DNA barcodes, especially COI and 16S. This limits the many potential barcode applications that should be of interest to a broad cross-section of scientists, government agencies, and the public, and also prevents any preliminary phylogenetic or phylogeographic estimates based on comparative DNA analysis. Even those species with sequences in GenBank are not always sufficiently documented by taxonomic experts, referenced museum vouchers, and precise localities. To address this deficiency, we have initiated an informal barcode project specifically for marine gastropods. We have studied available literature to compile a marine gastropod species listing and have assembled a series of working COI and 16S sequence alignments for worldwide members of those gastropod families with species represented on the southern California coast. Already, we have more than doubled the number of shelled gastropod species including still unpublished sequences. Our combined taxonomic, biological, and molecular systematic expertise has allowed us to target the species remaining to be sequenced, including many tiny species that require special sampling and identification methods. With the generous help of cooperating museum staff and others who have contributed previously unrepresented species, or species with sequences available only from outside of southern California, we expect to assemble the first DNA barcode data set representing the majority of common southern California marine gastropods.



Inventory of Southern Californian terrestrial gastropods: A citizen science collaboration between the public and the Natural History Museum of Los Angeles County

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The terrestrial snails and slugs of Southern California are generally understudied and particularly poorly inventoried in the urban and suburban environments of Los Angeles County. This Wallacean shortfall (of native and non-native species) is partly due to the jigsaw puzzle of private land (e.g. backyards) that characterizes LA County's urban sprawl. The Natural History Museum of Los Angeles County has sponsored a citizen science initiative called SLIME (Snail and slugs Living In Metropolitan Environments) that uses the iNaturalist web platform to centralize terrestrial gastropod observations from citizen scientists throughout Southern California. Since November, 2015 the SLIME project has revealed 3 species records for the State of California and six new records for Los Angeles County, including the snails — *Cochlicella barabara* and *Lauria cylindracea*, and the slug — *Arion hortensis*. The success of the SLIME project has been in its person-to-person and virtual collaborations between the public and Museum systematists, creating a genuine citizen science partnership.

Digitization of fossil molluscs at the Natural History Museum of Los Angeles County: Introducing the EPICC TCN

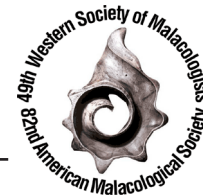
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The Natural History Museum of Los Angeles County (NHM) is a participant in a National Science Foundation (NSF)-funded effort to digitize fossil invertebrates from the Cenozoic of the Eastern Pacific (Alaska to Chile). The Eastern Pacific Invertebrate Communities of the Cenozoic (EPICC) project will mobilize digital image, locality, and associated metadata for Cenozoic marine invertebrate fossil specimens of the Eastern Pacific from eight major collections of the United States. Fossil molluscs are the principal focus of this project, and a major strength of the NHM Invertebrate Paleontology collections.

By making available data from these collections we intend to foster increased accessibility, efficient analysis to understand past climate and geologic change, the identification of factors involved in that change, and enable predictions for how current biodiversity may be impacted by future change. In digitizing these fossils they will become available and useful to the malacological and paleontological communities of



North and South America, as well as researchers around the world. This wealth of data will also provide resources to researchers, K-16 educators, and interested parties in government, industry, and the general public through iDigBio. Virtual fieldwork experiences are also being developed to guide educators in understanding how field data and fossil collections are used to infer past ecosystem and environmental conditions.

Challenging a paradigm of gastropod macroevolution: Species selection favors dispersive life histories in sea slugs

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Lineages benefit from species selection if they express a trait that increases net diversification (speciation minus extinction). A textbook example is the supposedly greater diversification of marine snails that produce short-lived lecithotrophic larvae, which have reduced gene flow compared to related lineages with dispersive planktotrophic larvae. For 40 years, paleontological studies have argued that species selection favors lecithotrophs, which speciate more and accumulate over time in some neogastropod families. However, lecithotrophs also have elevated extinction rates, and molecular phylogenies of diverse groups instead suggest lecithotrophs accumulate without diversifying due to frequent life-history shifts from planktotrophic ancestors. We present updated results using a 5-gene phylogeny for 256 species of sea slugs in clade Sacoglossa, showing at least 27 origins of lecithotrophy in this group. Contrary to long-standing assertions, maximum-likelihood methods support models in which species selection strongly favored planktotrophy. Most lecithotrophic lineages originated through recent character change and did not subsequently diversify, indicating extinction outpaces speciation for lineages with limited dispersal. Thus, selection below the species level frequently favors life-history shifts to lecithotrophy, but above the species level, short-lived larvae yield short-lived lineages. These findings challenge long-standing assumptions about gastropod macroevolution.

Larval and post-larval growth, and spat production of the clam *Chione cortezi* (Carpenter, 1864)

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Bivalve molluscs are an important part of fisheries production in the world. In Mexico in 2012, clams were positioned in place 13 of national fisheries production. In Baja California, México, a state with a long coastline, fishing and aquaculture activities are very important. State fisheries department SEPES-CA-BC, reports that during 2015 were caught a total of 1,430.12 tons of bivalve molluscs, and 2673.82 tons were cultured. Within the group of clams that are exploited for human consumption in Baja California, it is found *Chione cortezi* (Carpenter, 1864), an endemic clam of the Gulf of California. This clam, commonly known as “sand clam” or “mud clam”, has been caught by some groups of fishermen in San Felipe, Baja California, but the growing demand has led to overfishing. Given the current consumption of these clams, the increase in demand for human consumption and its overfishing in waters of Baja California, the objective of the work was to describe the larval, postlarval and juvenile development cycle of *Chione cortezi* clam, in the hatchery for producing spat. As result of the broodstock spawn (n=29), we get a total of 5.70 million larvae with an average size (\pm standard deviation) of $93.11 \pm 2.82 \mu\text{m}$, 24 hours post fertilization. Larvae were cultured in 2000 liters tanks with a density of 5 larvae/mL, and nursing of postlarvae was done placing the organisms in rectangular containers fiberglass mesh in background. Culture conditions were performed at $24^\circ\text{C} \pm 2$, and salinity of 33 ppm. Pediveliger larvae (height $233.2 \pm 8.52 \mu\text{m}$, wide 244.6 ± 7.96) were observed after 11 days. Metamorphosis was epinephrine induced at day 13 after fertilization, and postlarvae reached the 2 mm at day 60 (height $2119.00 \pm 245.90 \mu\text{m}$, wide 2350.00 ± 300.40). Larvae organisms were fed a mixture 1:1 of *Isochrysis galbana* and *Chaetoceros calcitrans* at an initial algae concentration of 15,000 cells/mL and a final concentration of 50000 cells/mL; postlarvae were fed with the same algae mixture starting at 50,000 cells/mL, divided into two servings per day, and finished at 180,000 cells/mL. Under the above culture conditions, we had a spat production of 2.20 million of healthy juvenile *Chione cortezi* clams (survival of 38.60%); 1.5 million of these juvenile clams were donated to San Felipe producers as aquaculture spats. We conclude that *Chione cortezi* culture it is possible under semi-industrial laboratory conditions, and knowledge of its biological cycle until they would be useful for aquaculture activities, it is important as an option to generate productive and sustainable fisheries in Baja California.

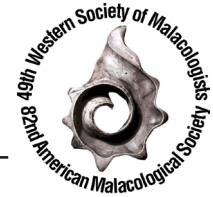
Temperature effect in males of *Octopus maya* and their sperm quality

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Octopus maya is an endemic species found in Yucatan Peninsula, where is subject to large climatic variations both in short and long term. The temperature in Yucatan continental shelf water varies between 21°C in January and 30°C in September with oscillations up to 4°C in summer. Octopuses are exposed to significant annual thermal variations and daily and weekly variations. This research aims to assess the effect of the exposure to three fixed temperatures (24°C, 28°C y 30°C) for 30 days by evaluating zootechnical variables as the final weight, weight gain, digestive gland index, and total count hemocytes among others; as well as some indicators of sperm quality. Octopuses were maintained in individual ponds for 30 days in each experimental temperature. They were fed twice a day at 8% of their weight. At the end of the exposure, the corresponding measures were realized. We obtained that the 30°C exposure has a significant effect on the final and gain weight of the octopuses. The Digestive gland index showed that the exposure to 28°C and 30°C has a significant effect in comparison to the octopuses exposed to 24°C. We observed a significant increase in total hemocytes count in the hemolymph of the octopuses exposed to 30°C. The hemocyanin concentration was affected in the octopuses exposed to 28°C. We did not observed significant differences in the octopuses osmoregulatory capacity at the three different temperatures. As for sperm quality, it was observed that the total sperm count and the number of live spermatozoa were not affected by exposure to different temperatures. However, the number of spermatophores showed a highly significant increase in temperature of 30°C. Temperature is a factor that plays a determinant role in reproduction of these organisms. According to the results, exposure to high temperature has an effect in the spermatophores production in these octopuses. However, it is important to carry out further tests such as sperm motility, viability, among others, to fully evaluate the effect of high temperature exposure on sperm quality of this species.

Survival and growth of geoduck clam larvae (*Panopea generosa*), reared at different densities in a flow-through seawater system

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A flow-through seawater system based on Sarkis *et al.* (2006) was designed and tested for rearing geoduck clam larvae, *Panopea generosa* in triplicate 45-L conical fiberglass tanks under three different densities (5, 10 and 15 larvae/ml). A head tank located above the culture tanks maintains constant the hydrostatic pressure and incoming flow. Water renewal rate was 1.5X the total tank volume/d, while instantaneous algal concentration (*Isochrysis spp* clone T-ISO, 37.5 ml/min) reaching the experimental tanks ranged between 4,300 and 208,174 cel/ml, depending on larval size. Survival and growth of *P. generosa* was evaluated every 4d during 17d. The flow-through system was very stable and allowed to maintain constant the temperature (ca. 18°C) and seawater inflow (53±1.7 ml/min) throughout the experiment. Cumulative percent survival decreased linearly in all treatments during the first days, reaching stable minimum values of ca. 50% in the lowest density treatments (5 and 10 larvae/ml) and 20% in the highest density (15 larvae/ml). However the mean larval size reached by experimental geoduck larvae at



the end of the experiment (243 ± 1.78 to 270 ± 0.7 $\mu\text{m/d}$) was not statistically different among treatments, even though a trend for greater growth rate was observed in the lower density treatment (9.5 $\mu\text{m/d}$) when compared to larvae from the two higher experimental densities (8.5 $\mu\text{m/d}$). Survival of geoduck larvae was comparable to that reported for *Pecten maximus* (47%) reared in tanks of 3,500L (Magnesen y Jacobsen, 2011) and *Argopecten gibbus* reared in 200-L tanks with daily water renewal rates of 3.4X the tank volume (Sarkis *et al.*, 2006). With these results it is concluded that *P. generosa* larvae can be cultured in flow-through systems at optimal densities of 10 larvae/ml, and the system design is reliable to maintain the flow water constant in the experimental tanks without the need of pumping.

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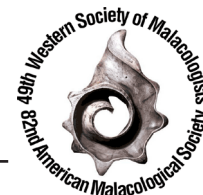
Effect of stress by decreasing the pH in the expression of genes in geoduck larvae *Panopea globosa*

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The increase in atmospheric CO₂ concentration, the absorption of this by the ocean and the hydrolysis of carbon dioxide has resulted in lowering the pH of seawater (Haugan and Drange, 1996) causing the decline of the availability of carbonate to the process of biomineralization of organisms such as echinoderms and mollusks (Watson *et al.*, 2009; Chapman *et al.*, 2011; Hüning *et al.*, 2012; Shi, *et al.*, 2013; Evans and Watson-Wynn, 2014) This effect has been evaluated by physiological parameters such as growth rate, gene expression analysis and evaluation of the metabolic rate which has seen an increase in oxygen consumption in organisms exposed to low pH (Thomsen and Melzner, 2010). *Panopea globosa* has a distribution in the upper Gulf of California and its fishery is economically important in northwestern Mexico, extracting more than 1,000 tons per year, generating profits of up to \$223,623.00 (Gonzalez-Pelaez and Luch-Cota, 2010). During their larval development is undergoing important processes (such as organogenesis, cell differentiation) and one of singular importance is the calcification and consequent formation of the shell.

In this experiment was exposed to larval stage D and Umbonated at pH of between 7.3 and 7.5 against a control group in pH 8.0, finding effect on growth from the third day in the larva D, and from the second day in umbone larva, reducing growth in larvae exposed to more acidic pH to comparison which were developed in pH of seawater. the effect of exposure to this pH was evaluated by respirometry (consumption oxygen) and the effect on the expression of genes involved in calcification be evaluated by quantitative real time PCR (q-PCR).



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6. GENERAL SESSION - POSTER PRESENTATIONS

Will it be possible to rear the larval stages of queen conch *Strombus gigas* from the Caribbean sea (Mollusca Gastropoda) under near-future predictions of ocean temperature?

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As the planet warms due to increased atmospheric CO₂, so does the ocean. The estimated increase in mean sea-surface temperatures by 2100 will be 1.1 and 6.4°C. The magnitude of change is differing markedly between regions. Atmospheric CO₂ concentrations were previously increasing at a rate of 1% per year in the 20th century. Now, they are increasing ~3% per year and may exceed 800 ppm by the end of this century (Byrne *et al.* 2013). An increase in temperature and acidification of ocean waters can be negatively effects on many marine organisms, in particular those with calcified parts, like mollusks. In this work we show the influence of near-future predictions of ocean temperature on larval development, survival rate and calcification of *Strombus gigas* under temperatures of 28.0 and 31.0°C and pH of 7.6 and 8.1. Shell length, development and survival rates were measured every two days for each treatment. For analysis of calcification, imaging and chemical mapping (proportion, wt) were performed on 30-day-old larvae using a High Resolution Scanning Electron Microscopy (HR-SEM) and X-ray Photoelectron Spectroscopy (XPS). A temperature of 31°C was advantageous for larvae growth (27.33±2.96 μm d⁻¹) and development. However, Calcium showed no significant difference between treatments (at 31°C, 25.4±4.7% wt Ca versus 28.0°C, with 24.9±0.7% w Ca)

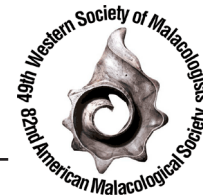
Pomacea flagellata Say, 1827 as basibiont of *Acineta tuberosa* Ehrenberg, 1838 (Ciliophora: Suctorina)

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Molluscs of epicontinental water bodies have been studied mainly for diversity. Also they are known to be a substrate and a mechanism of transport for various invertebrates. However, no studies have been conducted to know the epibiotic protists, *i.e.* suctorians (ciliates). The goal of this study was to provide a new record of the gastropod *Pomacea flagellata* as a basibiont (substrate organism) of a suctorian which has been recorded for some other substrates. We obtained some *P. flagellata* individuals from Tzisco, Chiapas, and suctorians were removed from the shells and identified as *Acineta tuberosa*. Free-living and stained observations of ciliates showed the attachment structure (stalk). This is the first record of suctorians on *P. flagellata*.



The Solenogastres, Caudofoveata and Monoplacophora classes in México: The current state of knowledge

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This work is a review of members of the Solenogastres, Caudofoveata and Monoplacophora classes reported for Mexico. The research was performed in ten Mexican biological collections, as well as in fifteen malacological databases records from the United States of America. In addition, an exhaustive investigation of specialized literature that reports records of such classes was performed. A total of four Solenogastres (Scheltema, 2000) and four Monoplacophora species were found (Menzies and Layton, 1962; Warén and Gofas, 1996), and not a single record of Caudofoveata has been reported. Records were found only for the Pacific Ocean, specifically in the states of Baja California, Baja California Sur, Sinaloa, Nayarit (Levin and Lonsdale, 1983); and five unidentified individuals of Solenogastres were found in the state of Guerrero, which are being analyzed yet. This work represents the first effort to gather information about this three classes of Mollusks in México and it expects to set a precedent for future investigations.

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Preliminary characterization of hemocytes in the Geoduck, *Panopea globosa* (Dall 1898)

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The Geoduck *Panopea globosa* (Dall 1898) is one of the two species that sustain the fishery of geoduck clams in the Mexican Northwest. Revenues from this fishery reached \$21 million in 2015, but profits between 18 and 30 millions have been previously reported. Despite the economic importance of this species for the region, the knowledge about parasites, diseases and immune response of *P. globosa* is nonexistent. Hemocytes are the circulating cells of the hemolymph and are involved in shell repair, uptake of nutrients but also, are the first line of defense against pathogens. They phagocytose foreign particles and destroy them inside the cell with reactive oxygen species (ROS). Characterization of hemocyte quantity and type of subpopulations present in the hemolymph helps to understand the defensive capabilities of wild and cultured organisms. Hence, the aim of the present study was to characterize morphologically the hemocytes of *P. globosa*. Preliminary analyses with light and transmission electron microscopy revealed two types of hemocytes in the hemolymph of *P. globosa*: granulocytes and hialinocytes. Granulocyte diameter measured $16 \pm 1.6 \mu\text{m}$ in average, showed round nucleus, abundant basophilic and acidophilic granular cytoplasmic inclusion and some vacuoles. In contrast, hialinocytes diameter measured $13 \pm 0.8 \mu\text{m}$ in average, round eccentric nucleus, exhibited scarce basophilic inclusions in the cytoplasm without vacuoles. Ultrastructural characterization of hemocytes is still undergoing, while differences in granularity, size and shape of nuclei are expected to be confirmed.

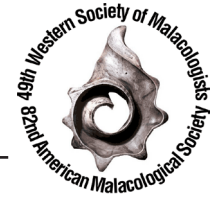
Structure of rocky intertidal community of gastropods associated to macroalgae in Ixtapa-Zihuatanejo, Guerrero, México

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The rocky intertidal is exposed to the sun and the wind during the lowest tides, however it is covered or splashed by waves during high tides, causing extreme conditions (Lalli and Parsons, 1997). The rocky intertidal is mainly habited by seaweeds and different animals. Seaweeds not only provide shelter and protection to animals, their morphology gives complexity to the substrate, increasing the number of niches and allowing the coexistence of a greater number of species (Dean and Connell, 1987; McConnaughey, 1978). The main organisms that inhabit the rocky intertidal molluscs, especially gastropods, which are a very stable community, due to the fact that they can live under these extreme conditions (Fernández and Jiménez, 2006). Although there have been several studies of mollusks and seaweeds, both taxonomic and ecological, but always these have been studied each group individually and very few its association, moreover the aims of this work are to extend the biological knowledge association between gastropods and macroalgae in an annual cycle.

This study was conducted in three locations in Ixtapa-Zihuatanejo, Guerrero: Palmar beach, Las Gatas beach, and Municipal Dock, where 71 species of macroalgae were found: 17 Chlorophyta, 48 Rhodophyta, and 8 Phaeophyceae; while for gastropods were observed a total of 7,034 organisms, included in 133 species. Macroalgae and gastropods have 7 and 8 new records for the area of Ixtapa-Zihuatanejo, respectively.



The diversity of macroalgae was between 0.90 and 1.05 bits/individual, which are the first reports on diversity in the area. The diversity of gastropods was between 0.06 and 0.93 bits/individual, being lower than that reported by other authors. A close relationship between *Oxynoe panamensis* and *Caulerpa sertularioides* was found, while *Littorina modesta*, *Littorina zebra*, *Littorina* sp1 and *Nerita funiculata* were found generally associated with the high intertidal zone. The presence of gastropods with different eating habits in different areas of this study is strongly marked by the presence or absence of sediment in algae, this generates a greater number of microhabitats and more favorable conditions against drying. However, more studies are needed to separate the abiotic and biotic effects and therefore establish the macroalgae-gastropods relationship with accurately.

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Mollusks associated the seaweed *Sargassum horridum* and the exotic species *Acanthophora spicifera* in Punta Roca Caimancito, La Paz, Baja California Sur

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Mollusks are organisms associated with a variety of rocky substrates, coral reefs, seagrasses and macroalgal assemblages. In the Gulf of California *Sargassum horridum* is an ecologically important habitat that provides shelter to diverse organisms of importance ecology, economic and fisheries, shares habitat with *Acanthophora spicifera* is an exotic species. So a comparison of the structure of associations epibionts mollusks associated with *S. horridum* and *A. spicifera* in Punta Roca Caimancito, Bahía de la Paz, Baja California Sur was performed during April and May 2014. In *S. horridum* 4,771 organisms were quantified in a total of 120 cm² of algal tissue representing 23 species, 8 genera and 1 organism identified to family level. In *A. spicifera* 1,937 were quantified in the same area, including 17 species, 2 genera, 1 organism identified to family level and 1 organism identified to class. The most abundant species associated with *S. horridum* were *Barleeia carpenteri* accounting for 60% of individuals in April and *Diffalaba opinosa* accounting for 43% in May. In *A. spicifera* the most abundant species was *Elachisina grippi* comprising 68% and 78% of individuals in April and May, respectively. There were significant differences in species richness between the two host algae. So we conclude that both algae have a different structure of this community is that present a different morphology that allows epibionts specificity to each.



Morphometric and genetic comparison of the bivalve *Spondylus princeps* in the Baja California Peninsula

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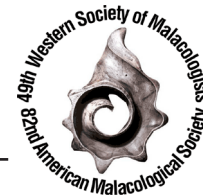
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Species of the genus *Spondylus* (Linnaeus, 1758) are of great economic interest. Thus, knowledge on their biology and ecology is important. *Spondylus princeps* is a bivalve distributed from the west coast of the Baja California Peninsula (BCP), Mexico, to Paita, Peru and its bathymetric distribution is commonly between 3 and 28 m. In this study, genetic and geometric morphometric analyses were used to examine the population structure along the coast of the BCP. The samples were collected from one site located on the west coast (Laguna Ojo de Liebre) and from three sites on the east coast of BCP (Bahía de los Ángeles; Santa Rosalía, and Agua Verde-Isla Danzante). Genetic analysis ($n=119$) were based on a fragment of cytochrome oxidase subunit I (COI) and the morphometric analyses ($n=104$) on shell landmarks. Our results indicate values of haplotype and nucleotide diversity relatively similar among sites. Pairwise Φ_{ST} was significantly different only between Laguna Ojo de Liebre and Agua Verde-Isla Danzante sites ($\Phi_{ST}=0.037$, $P=0.035$); however, no significant genetic differences remained after the Bonferroni correction. The morphometric analyses supported the existence of different morphs associated to the shape of the shell. Two canonical variates indicated significant differences between groups (Lambda Wilk's=0.0133, $P<0.01$, CV1; Lambda Wilk's=0.0870, $P<0.01$, CV2). Assignment *a posteriori* based on the Mahalanobis distances supported a high percentage of discrimination among the three groups (96% for Santa Rosalia, 97% for Agua Verde and 97% for Laguna Ojo de Liebre). Our data do not support the existence of genetic differences in *Spondylus princeps*, which might be due to larval dispersal influenced by oceanographic currents, contributing to the homogenization of populations. Alternatively, limited gene flow could occur, but not detected due to a recent isolation or to the low-resolution of the molecular markers used. The morphometric results support this idea. Further studies using more polymorphic molecular markers (mtDNA Control Region, microsatellites or SNPs) should be conducted to have a better understanding of the population structure of this species.

Hybrid abalone larvae of *H. rufescens* ♀ × *H. corrugata* ♂ production using male gonadal biopsies

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Worldwide, the abalone industry has been facing problems derived from the loss of genetic diversity in organisms produced in captivity (Evans *et al.*, 2004; Li *et al.*, 2004; Liu *et al.*, 2013). Given that, most of the abalone farms do not have selective breeding programs, and crossbreeding between related organisms often occurs. This has generated high levels of close relationship among culture individuals (Roodt-Wilding, 2007), which ultimately results in a decrease in fecundity, hatching and survival rates, as well as an increase of deformities during larval development (Deng *et al.*, 2005; Park *et al.*, 2006; Kobayashi and Kijima, 2010). On the other hand, it is well documented that some abalone interspecific crosses has shown “hybrid vigor” in commercial traits, such as growth, survival, as well as an increase in the immune response and thermal tolerance (Lafarga-de la Cruz and Gallardo-Escárate, 2011; Liang *et al.*, 2014; You *et al.*, 2015), and the hybridization process is considered a viable tool for genetic improvement of abalones (Elliot, 2000). In abalone interspecific crosses, there are two critical factors that affect fertilization and hatching success: the oocyte-age (time from its release to the *in vitro* fertilization) and the sperm concentrations (oocyte-sperm ratio). Depending on which species are being crossed, an oocyte-age greater than 5–20 min significantly lowers the fertilization rates, and sperm concentrations from 10 to 100 times higher than those required for homospecific crosses are necessary to achieve heterospecific fertilization (Leighton and Lewis, 1982). Therefore, the availability of sperm is crucial to carry out hybridization. However, the traditional H₂O₂ method used to induce spawning in some domesticated species as red abalone (*H. rufescens*), does not work well in other species of wild origin such as pink abalone (*H. corrugata*). So, there is no standardized method that allows natural spawning of different abalone species and subspecies. The main goal of this study was to evaluate the use of male gonadal biopsies to obtain viable sperm for interspecific crosses between red (cultured) and pink abalone (wild). Future applications of this techniques for abalone industry will be discussed.

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Identifying bivalves associated with the oxygen minimum zone: Not an easy task!

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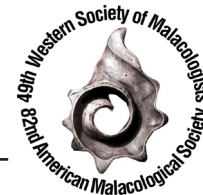
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The class Bivalvia in the deep sea has been intensively studied worldwide (e.g., Zamorano *et al.*, 2006; Krylova, 2010; Gracia and Valentich-Scott, 2012; Oliver, 2015; Güller and Zelaya, 2015; Schwabe *et al.*, 2015). Still, many issues have remained unsolved when attempts are made to identify material at species level. This is often due to the lack of abundant material or to the availability of damaged specimens or empty valves. Besides, regional comprehensive identification keys are lacking. A similar situation occurs with the mollusks fauna inhabiting the continental slope off the west coast of Baja California in Mexico. During the TALUD project, material was collected below the Oxygen Minimum Zone (OMZ) that characterize the west coast of the Baja Peninsula. In this environment, species experience adverse conditions due to the lack of oxygen (concentrations < 0.5 ml/l or lower). A total of 28 species of Bivalvia were collected, some of which presented a taxonomic challenge. Material of *Ennucula panamina* and *E. taeniolata* was very similar, but some of their characteristics overlapped, including the shape of the valves and the number of hinge teeth. Their identification is considered tentative and it has been suggested that these species could be synonyms. *Nuculana cf. hamata* was represented in the samples by a single valve hence it was tentatively identified with this species. Specimens of *Limatula* were close to *L. saturna* but smaller than the known size of this species. Some differences in the shell sculpture were noted when compared to *L. saturna*, and the material available came from a significant deeper locality (2,285 m vs. 675 m), thus suggesting it might represent a new species. *Policordia* is close to *Dallicordia*. Our material features an elongate shell, not subquadrate, and the arrangement of gills and of the exhalant siphon tentacles is characteristic of *Policordia*. A juvenile of *Propeleda* sp. featured a variation in the arrangement of the hinge teeth (orientated both horizontally and obliquely). Although only one juvenile specimen was collected, it is considered to be close to *P. loshka* or *P. extenuata*. In all the cases, further studies are needed including comparison with the type material of close-species and resort to other taxonomic tools.

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Benthic mollusk community on the continental platform of the SE Gulf of California, Mexico

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A large series of benthic mollusks were collected between 27 and 127 m on the continental shelf off the coast of Sinaloa, in the SE Gulf of California, Mexico. Specimens were captured with the R/V “El Puma” of the Universidad Nacional Autónoma de México” using three different gear: an Otter trawl, an oyster dredge and a Van Veen grab. Three cruises were organized: SIPCO I (April 1981), SIPCO II (August 1981), and SIPCO III (January 1982). A total of 4936 specimens belonging to 205 species (141 Gastropoda, 56 Pelecypoda, 4 Polyplacophora, 3 Cephalopoda y 1 Scaphopoda) were collected and this fauna has been reported in details by Hendrickx *et al.* (2014). The collection data were analyzed considering period of sampling, gear, depth, and environmental parameters measured at bottom level (i.e., temperature, dissolved oxygen, sediment composition). Average species diversity was higher during the SIPCO III, followed by SIPCO I and SIPCO II. Highest average diversity was obtained with the Otter trawl (2.492 bits) vs. 1.914 bits with the oyster dredge and 0.938 bits with the Van Veen grab. Average diversity when combining gear and cruise was obtained for the Otter trawl samples of the SPCO III cruise (2.882 bits). An ANOVA using diversity data indicated significant difference between the Otter trawl and the Van Veen grab sample composition, and between SIPCO I and SIPCO II, and SIPCO II and SIPCO III cruises. Average species richness was higher during the SIPCO I and when using the Otter trawl. Considering the 23 samples obtained with the Otter trawl, 16 form a cluster at 13% similarity (Bray-Curtis). Spearman correlation between diversity (H') and the environmental variables indicated a significant association only with depth ($R=-0.358$, $p=0.018$). An ANOVA using different depth strata (each 20 m) did not show any significant difference in diversity (H') ($F_{3,43}=2.5702$; $p=0.0667$), although highest diversity was observed in the 40-59 m interval (2.705 bits) and the lowest in the deeper interval (0.913 bits) where there is a significant decrease of dissolved oxygen concentration.

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Relationships of mollusks to oxygen concentrations in Todos Santos Bay, Baja California, Mexico

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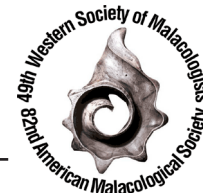
Oxygen depletion in seawater is sometimes a consequence of human impacts that affect the abundance and distribution of benthic infauna. Mollusks have been considered reliable indicators of human impacts; however, there is little information on how these organisms are associated under natural conditions with oxygen concentrations. The aim of this work is to determine the relationship of mollusk abundance with physicochemical properties of seawater and sediment granulometry under natural conditions of low impact. We analyzed the mollusk database of the oceanographic cruise from October 1994 in Todos Santos Bay. Sediment samples were taken with a Van Veen grab (0.1 m²) and sediments sieved using 1mm mesh size, organisms were sorted and identified to genus level. Additionally, temperature, salinity, and dissolved oxygen (DO) were measured with a CTD; organic matter content and sediment grain analysis were determined in the laboratory. A total of 836 mollusks were collected, Gastropoda (52%), Bivalvia (41%) and Scaphopoda (7%). Gastropoda was the most abundant and diverse class with 27 genera, followed by Bivalvia with eight genera and Scaphopoda with only one genus. According to CCA analysis dominant mollusks were related significantly with DO concentrations. Thirteen genera were dominant: *Donax*, *Natica*, *Acteocina*, *Bulla*, *Anachis*, *Odostomina*, and *Crucibulum* can be classified as sensitive genera because they were found in high oxygen concentrations (3.1-5.6 ml l⁻¹); on the other hand, *Cardiomya*, *Nuculana*, *Laevicardium*, *Chione*, *Trucantella*, and *Dentalium* can be classified as tolerant genera (1.0–5.6 ml l⁻¹). Four genera were related to DO with a negative binomial generalized lineal model; the model explained 22–39% of the total variance. In conclusion, Todos Santos Bay hosts a diverse malacological fauna (36 genera), our results showed that the dominant genera were strongly related to high dissolved oxygen concentrations. Mollusca can be a useful tool in environmental monitoring programs related with oxygen depletion as mariculture and other human activities can favor eutrophication in coastal environments.

Digitization of molluscan biodiversity at the UMMZ

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The Mollusk Division of the University of Michigan Museum of Zoology (UMMZ) is currently involved with two NSF Thematic Collections Network (TCN) projects that aim to advance digitization of biological collections. The Great Lakes Invasives TCN is a collaborative effort involving more than 25 institutions and approximately 1.73 million specimens representing 2,550 species of exotic fish, clams, snails, mussels, algae, plants, and their congeners. For this project, the UMMZ Mollusk Division is currently digitizing data and imaging approximately 25,000 catalogued lots that roughly comprise 390,000 mollusc specimens. We are also participants of the InvertEBase TCN which seeks to database and geo-



reference over 3 million specimens of terrestrial and freshwater mollusks and arthropods of eastern North America. Specimen data, high-resolution images and georeference data will be available through a national resource (iDigBio.org). Aside from considerably advancing digitization efforts in our collections, contributions to these projects will improve the ability of both experts and the general public to more accurately distinguish invasive species from their native congeners and provide information to evaluate changes in distributions of species over time due to large-scale perturbations (e.g., climate change and land-use changes).

The effect of El Niño year in the reproductive cycle of *Mytilus galloprovincialis* in Bahía de Todos Santos, Baja California, NW México

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In the Bahía de Todos Santos (BTS) the culture of the blue mussel *Mytilus galloprovincialis* is done commercially by the company “Aqualap”, through the use of submerged long lines. This company produces 300 t/year. While the cultivation of mussels in this area is important, only a single study on the reproductive cycle of this species has been conducted. The objective of the present study was to determine the reproductive cycle of *M. galloprovincialis* in the BTS for period from October 2014 to March 2016. Each month 30 mussels of market size (7.55 ± 0.43 cm) were extracted from the culture area. Once in the laboratory, the condition index (CI) was determined by measuring the total wet weight of the body (TWB), as well as the total wet weight of meat (TWM), $CI = TWM/TWB * 100$. The results of the reproductive cycle of *M. galloprovincialis* from the period of 2014-2015 show that in November a CI of 41.75 is achieved, decreasing to 38.79 in December, indicating a first spawning. Subsequently, CI increased to 41.91 in February followed by a decrease to 38.00 in March, second spawning. CI increased again until reaching its maximum in May (50.35) and decreased in April to 41.92, third spawning (with longer duration and intensity). While in the period of 2015–2016 (El Niño year), CI increased in September to 43.29 and decreased in October to 42.07, registering the first spawning. Then the CI began to increase and reached its maximum of 49.82 in December, and decreased to 45.41 in February, indicating a second spawning. As described above, we can conclude that the BTS under normal temperature conditions (not El Niño year) reflects three periods of spawning (November–December, February–March and May–August), while in an El Niño year, the periods and the intensities of spawning events change, and are registered in the periods of September–October and December–February.

Growth, survival and proteolytic activity of *Octopus bimaculatus* paralarvae fed with enriched *Artemia franciscana*

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Studies of the digestive system development and its ability to digest and absorb nutrients from diet are indispensable to understand the nutritional physiology of the octopus paralarvae; in the future, the results of these investigations could lessen the problems that limit the cultivation (Hamlin *et al.*, 2000). *Octopus bimaculatus* is an important economic food resource and a potential candidate for aquaculture diversification in the pacific coast of Mexico, however, knowledge on the paralarvae nutritional requirements of this species is nil. For this reason we evaluated the growth, survival and the proteolytic activity of the *O. bimaculatus* paralarvae with two diet; live *Artemia franciscana* (8.2±1.20 mm of total length) enriched with the tuna orbit oil (TOO group) and *Isochrysis* sp. (ISO group). The experimental cultivation of paralarvae fed with TOO group ended 17 days after hatching (DAH) with a survival of 1.93% and the number of suckers increased from 5 to 9 in each arm, while those fed with the ISO group ended at 11 DAH with a survival of 1.77% and 6 suckers. Acid and Alkaline proteolytic activity of paralarvae were detected at hatching which tended to increase accordance with the age. Total acid proteolytic activity of paralarvae range from 0.38±0.03 to 1.23±1.23 where the maximum value was registered at 8 DAH in paralarvae fed with TOO group. While total alkaline proteolytic activity range from 0.61±0.01 to 2.61±0.15, the maximum value was registered at 14 DAH in paralarvae fed with TOO group. TOO group only had a significantly influence on acid proteolytic activity of paralarvae at 8 and 11 DAH, however the final survivor obtained in this treatment was higher compared with paralarvae fed with the ISO group. Based on the shape and cell structure of the organs that constitute the digestive system of the newly hatched of *O. bimaculatus* paralarvae (López-Peraza *et al.*, 2014) and the level of proteolytic enzyme activity reported in the present study, could indicate that the newly hatched paralarvae have the initial capacity to ingest and digest the food, although it is not possible to specify in which degree. For these reasons, we recommend to accomplish specific studies on the digestive capacity of the newly hatched of *O. bimaculatus* paralarvae to determine the maturity level of the digestive system more accurately.

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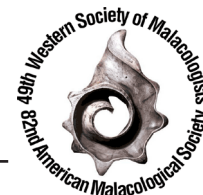
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Joint likelihood function based on multinomial and normal distributions for analyzing the phenotypic growth variability of geoduck clam *Panopea globosa*

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A frequent assumption in stock assessment models is that individual growth in marine organisms can be described adequately through mean growth parameters. However, these parameters are usually estimated from length-at-age data, and they are highly variable (Sainsbury, 1980). This means that the growth models are commonly fitted to average trajectories that ignore intrinsic biological variability about individual growth. In age and growth studies the individual growth variability is recognized as a source of bias, if it is not taken into account in the analyses it can lead to overestimates or underestimates of the mean length at age of a cohort (Chen *et al.*, 2003). In this study, a new approach for analyzing individual shell length-at-age variability was developed for *Panopea globosa* using a joint negative log-likelihood where both shell length frequency distributions (0.053–7.04 mm) and shell length-at-age (100–160 mm) data sets were combined. Six candidate growth models were analyzed that included assumptions about the variance for each age in the population, and the best growth model was selected using a multi-model inference approach. Growth modeling including phenotypic growth variability showed that estimates of t_0 were better than those computed from conventional growth models. We found that the Johnson model was the best candidate growth model for fitting both data sets.

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Diversity of terebrid snails (Neogastropoda: Terebridae) off the coast of Jalisco and Colima, Mexican tropical Pacific

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An analysis on the diversity of species in the Terebridae family found in the soft ocean bottom off the coast of Jalisco and Colima (Mexican tropical Pacific) is presented. The importance of this group of gastropods resides in the fact that some of these species use venoms as their main feeding and defense mechanism, which can be potentially used as biologically active compounds with pharmacological use. The analyzed data are from three different periods in the past twenty years: 1) Drags with shrimp nets realized between 1994 and 1996 in seven different collection sites at four different depths in the coast of Jalisco and Colima (140 drags), 2) Similar drags in two different sites previously researched, and at two depths between 1997 and 1999 (64 drags), and 3) Drags using a biological dredge in the Bay of Navidad, Jalisco, between 2011 and 2013 (12 drags). The analysis of the database in the first periods of the study, and the review of the collected organisms in the third period, allow to establishing a richness



of 17 species and 104 organisms in the Terebridae family on the soft ocean bottoms. The species that presented the highest abundance on the three different periods was *Oximeris strigata*. From the samples collected on the Bay of Navidad, there were collected a total of 67 organisms distributed on the following way: *Euterebra puncturosa* (1), *Oximeris strigata* (13), *Pristiterebra tuberculosa* (1), *P. glauca* (5), *Terebra allyni* (3), *T. armillata* (6), *T. brandi* (4), *T. crenifera* (1), *T. formosa* (1), *T. guayaquilensis* (7), *T. intertincta* (2), *T. larvaeformis* (3), *T. lucana* (6), *T. ornata* (1), *T. robusta* (1), *T. specillata* (4), and *T. variegata* (8). Finally, data are presented regarding the characteristics of the collection sites, and the depths at which the species were found.

Ecological aspects of *Conux nux* Broderip, 1833 off the coast of Jalisco, Mexican tropical Pacific

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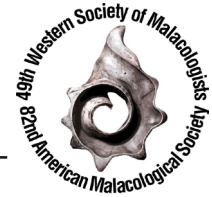
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As part of a project developed between Mexican Universities for the study of shellfish of the Conidae Family on the Coast of the tropical Mexican Pacific, this study is presented on *Conux nux*. The preliminary results indicate that this particular species is the most abundant on the coast fringe of Jalisco. This work seeks to determine some of the ecological aspects of the species, such as the relative abundance, spatial distribution, preference relative to the substrate, and the bathymetric distribution. There were collected in 5 different beaches, covering the substrate from shallow subtidal from 1 to 5 meters depth (accessible with free diving) and deep subtidal from 6 to 20 meters (accessible with autonomous scuba diving). The abundance presented values between 1 and 15 snails per dive. The average diving time was 47 minutes. Based on the previous observations, the relative density is computed as 13.2 snails per diving hour. A clustered spatial pattern was determined using the nearest neighbor index, and the variance-to-mean ratio. The registered sizes go from 7.0 to 26.1 mm with an average of 16.6 mm. The underwater pictures analysis show a preference of the snail *Conux nux* to reside on a rocky substrate covered by brown algae. As for the bathymetric distribution, there was no tendency observed on an increase in numbers or clusters by sizes; however, it must be taken into consideration that these only constitute preliminary data.

Changes on the community structure of paralarvae off the southwestern coast of Baja California Sur in relation to water masses

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To identify the changes in the community structure of cephalopod paralarvae (PL) off the southwestern coast of Baja California Sur (CSO), zooplankton samples (surface and oblique tows made simultaneously) corresponding to spring and autumn 2003 were analyzed. The collection of samples was performed with a CalCOFI net, in 85 sampling stations located from Magdalena Bay to Cabo San Lucas. At each station CTD casts were made. The community of PL was significantly different between types of tows and seasons, registering a significantly higher abundance in surface tows of spring than in autumn ($p < 0.0024$), but higher in the oblique tows of autumn than in those of spring ($p < 0.0027$). The richness, diversity, and the number of tropical-subtropical taxa were higher during autumn in both types of tows. The species accumulation curves of the CSO showed greater similarity to those in the Gulf of California and Tehuantepec but were different from the recorded north of the study area. The canonical correspondence analysis showed that chlorophyll-*a* concentrations and zooplankton volumes were the variables best correlated with the abundance of PL, forming two groups of few species in a cold and productive environment with Subarctic Water in spring, and one with higher richness present in a warm and less productive environment with Subtropical Surface Water in autumn. Environmental factors associated with the prevailing water masses in each season, modulate the presence, abundance, and biogeographic affinity of the PL present in the CSO.

Multivariable suitability habitat model for Pinto Abalone (*Haliotis kamtschatkana*) in San Diego County, California

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Habitat modeling aids in conservation biology by providing a snapshot of where a species occurs based on field sampling extended to predict where it could occur in order to assist restoration efforts. Based on a data set from a separate study by one of us (AB) we are using bathymetric data associated with pinto abalones (*Haliotis kamtschatkana* Jonas, 1845, alternatively treated as a southern “threaded abalone” subspecies, *Haliotis kamtschatkana assimilis* Dall, 1878) in ArcGIS for Desktop (v. 10.3.1) to create a suitable habitat model for pinto abalone (*Haliotis kamtschatkana*) in southern California. Specifically, we have emphasized a subtidal portion of this species’ field-sampled range between La Jolla to Point Loma in San Diego, California. Habitat-based modeling allows for physical data to be represented spatially to show habitat preference for a particular species. This can be an important tool for conservation and restoration efforts. Our model for the pinto abalone could be useful in predicting habitat and more generally as a first step in making a predicative habitat model that could help survey pinto abalone abundances in a broader region or could help restoration planners assess available suitable habitat. In our ongoing study, information including substrate type, kelp coverage, and bathymetry is used to calculate environmental correlations for this species. All data sets are converted into rasters, which are images containing elements of habitat characteristics associated with observational data. Habitat preference parameters are then established, and an ArcGIS spatial analyst tool (Map Algebra) is used to highlight preferable habitat characteristics. Using the Benthic Terrain Modeling extension, created by ESRI and NOAA for ArcGIS, rugosity will be calculated to characterize surface type for seafloor habitat, as well as aspect and slope. After all variables have been selected, raster images are calculated using the Model Builder extension



and the Raster Calculator for ArcGIS. The most important variables are given proportionately higher ranking, or weight, and the resulting calculation is a map of estimated habitat preference. These methods can be used to inform similar recovery efforts for another abalone species.

Implementation of two strategies of enrichment in *Macrocystis pyrifera* using epiphytes microalgae and nutrients as alternative to feed juveniles of red abalone (*Haliotis rufescens*)

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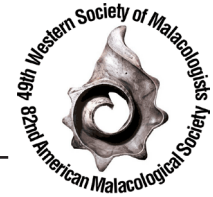
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On the abalone farms in México the main species of macroalga used to feed juvenile and adult abalone is *Macrocystis pyrifera*, due their abundance, fast growth rate, low economic cost and easiness to harvest. The aim in this research was to measure the growth rate and survival of juveniles of red abalone (*Haliotis rufescens*) fed with *Macrocystis pyrifera* enriched with epiphytic microalgae and nutrients. The enrichment treatments of *M. pyrifera* were carried out using four different species of microalgae that were isolated epiphytes of *M. pyrifera* blades (*Sellaphora* sp., *Phormidium* sp., *Grammaphora angulosa* and *Komvophoron* sp.) and two nutrient concentrations with two N:P ratios (14:0.87 μM (L) and 200:12.05 μM (H)). The *M. pyrifera* blades were maintained in 18 L white plastic buckets with 15 L of filtered and disinfected seawater. For the treatments were measured the proximal composition of the blades at different times. Based on the increment of the proximal composition of the blades, were selected one treatment of enrichment with microalgae epiphytes and other one of enrichment with nutrients. The select treatments were used to massive production of enrichment algae biomass to feed juvenile abalone. The strain of *Grammaphora angulosa* was chosen due to its higher content of proximal composition of lipids (18%), proteins (33%), carbohydrate (11%) and low ash content (16%). In the enrichment with nutrients the higher ratio of N:P (200:12.05 μM) was select due its highest proximal of lipids (11%), proteins (19%), carbohydrate (9%) and low ash content (13%). The results indicate that the two strategies to enrichment *M. pyrifera* appears to be a potential source of increase the nutritional value of the blades. The biomass of the blades enrichment with the selected treatments were used to feed juveniles of red abalone. The abalone were maintained by triplicate on 18 L plastic buckets with seawater and air bubble, were feed *at libitum* with the enriched blades of the two selected treatments. As control of feed was used *M. pyrifera* blades without any treatment. Survival (%) and specific growth rate of abalones were measured to evaluate the effect of the treatments.

Investing in biodiversity collections for the future: A new century at the UMMZ

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The University of Michigan Museum of Zoology (UMMZ) is a recognized leader in biodiversity research and education. It houses approximately 13 million specimens organized in six divisions (Birds, Insects, Fishes, Mammals, Mollusks, and Reptiles and Amphibians). All collections rank in the top 10 in size for their discipline and most rank in the top five nationally. As collections associated with a university, some of the collections rank first in the world. In 2009, UM addressed storage limitations and safety issues for the UMMZ's enormous ethanol-preserved collection by relocating the collections to a newly renovated facility, referred to as Varsity Drive. In August 2015, an additional renovation at Varsity Drive, which also included space for the UM anthropological, botanical, and paleontological collections, increased total renovated space to approximately 97,000 gross square feet with new 1) environmentally-controlled collection space, 2) preparatory laboratories, 3) research offices and laboratories, 4) compact storage for paper collections and libraries, 5) administrative support offices, and 6) a demonstration room for teaching and public programs. The installation of new archival specimen cabinets will be completed by June 2016, and the relocation of specimens will begin May 2016 with an expected completion date within 12-18 months. Solutions for public transportation and a new building name are under consideration. Total university investment is ~\$44,450,000.

Three-dimensional distribution of paralarvae of the complex *Sthenoteuthis oualaniensis-Dosidicus gigas* (Cephalopoda: Ommastrephidae) and other cephalopods in relation with mesoscale structures in the Gulf of California and adjacent Pacific

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Cephalopods are an important link between trophic levels, and an emerging target for global fisheries, given the collapse of many pelagic resources. However, studies of early life stages are lacking, and spawning zones and nursery habitats are virtually unknown. The aim of this study is to assess the three-dimensional distribution of the paralarvae of the complex *Sthenoteuthis oualaniensis-Dosidicus gigas* ("SD complex"; Cephalopoda: Ommastrephidae) and other cephalopods in relation with mesoscale dynamics in the Gulf of California and adjacent Pacific waters. Based in two oceanographic cruises, in which a cyclonic eddy and an oceanic front were sampled, it was found a preferential habitat for the SD complex is in the mixed layer and thermocline, in the warm and oxygenated layer. The highest abundance of the SD complex occurred in convergence zones in both cruises. In the inner Gulf, the pyroteutids



prefer the high-productive central zone of the cyclonic eddy, under the thermocline, as a nursery habitat; while the enoploteuthids used the mixed layer as the main nursery habitat. The presence of octopods in the cyclonic eddy was scarce. In the adjacent tropical Pacific, the octopods were the most abundant taxa with a high relation with hypoxic water. The SD complex differ in their vertical habitat with other omastrephids, that inhabit under the thermocline. It was concluded that the SD complex has a high sensitivity to convergence zones, and their spawning is related to dynamic conditions, more than stationary conditions.

Composition and community structure of soft bottom mollusks in Isla Santa Cruz, Gulf of California, México

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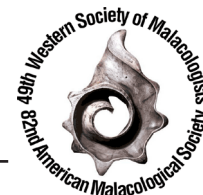
The composition and structure of the soft bottoms mollusk community of Santa Cruz Island (25°18'N, 110°45'W) was analyzed. On the summer of 2010, 32 samples were collected; 16 correspond to biological samples and 16 to sediments. The composition, abundance and diversity of the benthic malacological community were analyzed as ecological indicators. A total of 695 individuals were recorded, they were grouped in 2 classes; Gasteropoda with 446 organisms (5 orders, 11 families and 19 species), the most abundant species was *Siphonaria maura* (18%), the class Bivalvia with 249 organisms (8 orders, 14 families and 25 species), the most abundant species for this class was *Tellina eburnea* (10%). The class Gastropoda represented higher abundances than Bivalvia with 64.17% and 35% respectively. The species with major abundances and relative frequencies were the gastropods *Siphonarua maura* and the bivalve *Septifer seteki*. Four trophic categories were identified, filterers were the most abundant group (73%), followed by the herbivores (20%), carnivores (5%) and ectoparasites were the rarest group (2%). In this site the specific richness (44 taxa) were lower compared to other sites from different latitudes of the western Gulf of California possibly due to that the study site is a high energy environment were only juvenile mollusks and micromollusks were found.

Efficacy of calcein as a growth marker in molluscan biomineralization studies

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Current methods for growth and age determination of Mollusca have specific limitations. Length frequency distribution analyses need well-defined age cohorts and relatively large sample sizes, invasive tagging-recapture methods promote physical disturbance and uncharacteristic growth rates, whereas



quantification of shell growth rings are frequently affected by erosion and other disturbance events (Hermann *et al.*, 2009).

Calcein is a non-toxic fluorescent dye with excitation and emission wavelengths of 495/515 nm respectively. This dye is incorporated into newly mineralized calcium carbonate structures such as mollusk shells, polychaete tubes, echinoderm plates, corals; providing a green fluorescence reference growth mark visible under ultraviolet light (Saderne and Wahl, 2013). Calcein is considered an effective marker for tagging newly formed biogenic calcite or aragonite, the two polymorphs of calcium carbonate. Newly settled larvae of bivalves are not adversely affected by this dye (Moran and Marko, 2005), we also found no detectable negative effects on serpulid larvae and juveniles. Riascos *et al.* (2007) after testing different dyes conclude that calcein was the best growth marker because it produced a long lasting mark.

The calcein solution was prepared using filtered seawater at a concentration of 70 mg/l using magnetic stirrers to dissolve the dye and sodium borate to adjust the pH. Organisms were placed in the calcein solution for 48 h and fed with the microalgae *I. galbana ad libitum*. Measures of growth using Image J allow use to evaluate the shell growth as well as the impact of ocean acidification in calcification and shell growth.

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Effect of incubation temperature on the thermal tolerance of newly hatched juvenile *Octopus bimaculoides*

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Thermal tolerance of organisms is used as an indicator of their ability to adapt to heat stress conditions (Paladino *et al.*, 1980). In this research, the use of this indicator is proposed to determine the effect of different temperature incubation on the condition of juvenile octopus hatchlings *Octopus bimaculoides* a species with potential for mariculture. In this study, the thermal tolerance of newly hatched juveniles was evaluated with three incubation temperatures of 16, 18 and 20°C. The incubation period of the eggs of *O. bimaculoides* showed significant differences ($p < 0.05$) between treatments. The duration of incubation for eggs held at 20°C was 63 days as opposed to the eggs incubated at 18°C and 16°C, which lasted 102 and 108 days respectively. The thermal tolerance was evaluated by the dynamic method (Beitinger *et al.*,



2000), which consisted of placing a newly hatched octopuses in an aquarium and the water temperature was increased at a constant rate until reaching an endpoint or sublethal. Thermal tolerance was in the range of 29.7°C to 31.9°C with differences between treatments ($p < 0.05$), indicating that for every two degrees of increase in the incubation, the thermal tolerance increased by 1°C. The difference between the value of the CTMax and incubation temperature of organisms showed that juvenile hatchlings incubated at 16°C tolerated a greater increase in temperature (13.7°C), while in the octopuses incubated at 18 and 20°C were 12.7°C and 11.9°C respectively. The information presented in this study contributes to the knowledge base about the species, in order to be able to target the right conditions for the development of an experimental culture.

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InvertEBase: Providing access to 200 years of land and freshwater mollusk data from eastern North America

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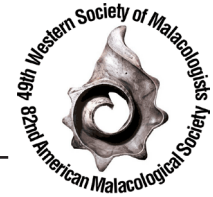
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Understanding the scope of biodiversity change projected to occur in North America in the coming decades requires a high-resolution picture of preexisting biodiversity levels. Natural history museums in the US have collecting legacies that go back hundreds of years, but for most invertebrate taxa, the information is difficult to access by a broad variety of end users.

To address this concern, the InvertEBase Thematic Collections Network (TCN), part of the iDigBio National Resource for Advancing Digitization of Biodiversity Collections, has been digitizing terrestrial and freshwater mollusks and arthropods of eastern North America for the past two years. The goal is to complete the data entry, georeferencing, and some imaging of millions of new and legacy records, and to provide public access to these data through portals such as Symbiota.org and iDigBio.org.

This poster summarizes the biodiversity data that has been digitized and made publically available by the collaborating institutions as we approach the end of grant year 2. In addition, we describe the development of a shared exhibit that will introduce the general public to the value of natural history collections, why digitization is important, and highlights from the collections of collaborating institutions.

This collaborative National Science Foundation award (NSF EF 14-02667, EF 14-02697, EF 14-04964,



and others), is made as part of the National Resource for Digitization of Biological Collections through the Advancing Digitization of Biological Collections program and all data resulting from this award will be available through the national resource (iDigBio.org).

Effects of global change on the reproductive cycle of *Crassostrea virginica* at Tamiahua Lagoon, Veracruz, Mexico (historical data: 1965-2014)

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Marine life is currently under threat because of changes to the environment. Anthropogenic emissions of greenhouse gases are causing ongoing change to global marine systems, particularly through ocean warming and acidification. We reviewed the state of the knowledge of the reproductive cycle of *Crassostrea virginica* in the context of global environmental change. In particular we focused on the response to Tamiahua coastal lagoon warming; observations of the gonadal condition of naturally established oyster populations demonstrate a dependence on water temperature. Recently, *C. virginica* in Tamiahua lagoon had continuous reproduction stages with high proportions of growing, maturation and multiple spawning events during most of the year (Robles-Hernandez, 2006; Arias de León *et al.*, 2013; Aldana-Aranda *et al.*, 2014; Ascencio-Aguirre *et al.*, 2014). Nevertheless, Sevilla and Mondragon (1965) reporting a seasonal reproductive cycle with well-defined rest, gametogenic, spawning and post-spawn periods, coinciding with Ortega and Arroyo (1987) and Argüello (1986) observed that spawning is limited to July and August. This could be influenced by temperature changes, during the 1980's the average of temperatures recorded were 26.2°C, however for the period 2000-2010 the average increased to 26.9°C. Recently the water of Tamiahua lagoon remains warmer longer and influences the frequency and intensity of reproductive cycles and overlapping all gonadal stages throughout the year.

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To move or not to move, is that the question?: Preliminary results from acoustic tracking of Pinto Abalone (*Haliotis kamtschatkana*)

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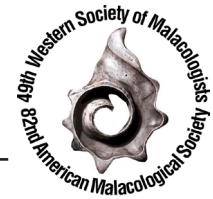
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Following overfishing and potentially other anthropogenic impacts, pinto abalone (*Haliotis kamtschatkana*) populations in the Southern California Bight fell to alarmingly low levels. The pinto abalone was listed as a U.S. Species of Concern in 2004, which means that the National Marine Fisheries Service (NMFS) has concerns regarding status and threats, but does not have sufficient information indicating a need to list the species under the Endangered Species Act. Monitoring the population demography, behavior, and habitat requirements of this species not only helps focus conservation efforts for it, but also informs recovery strategies for the highly endangered white abalone (*H. sorenseni*), a close relative of pinto abalone. In this study, SCUBA, in-situ cameras, and acoustic telemetry are being used to provide critical time-series information for pinto abalone over a variety of temporal and spatial scales (point-in-time – months and ~1–100 s of m², respectively). SCUBA surveys have led to the discovery of rare, cryptic, and patchily distributed pinto and white abalone in some areas where they had not been observed for a decade or more (pinto: N=151; white: N=30). The size range of pinto abalone observed (13-190 mm SL) suggests that recent recruitment events have occurred despite very low densities. In-situ camera observations revealed that over a period of months, adult pinto and white abalone (N=6 individuals) fed primarily on drift *Macrocystis pyrifera* kelp and rarely left an area larger than 1 m². Acoustic tags were placed on 25 pinto abalone (95–142 mm SL) within a 100 x 70 m acoustic receiver array to help determine whether movement and aggregative behavior could help explain the discrepancies between evidence of recent recruitment, densities below suspected thresholds for successful reproduction (~0.2/m²), and short-term lack of movement. Nearest neighbor distances ranged from 1-14 m, with the majority of animals (52%) being ≥5 m from a nearest neighbor. In-situ camera observations revealed that acoustic tag application had little or no effect on pinto abalone (N=2) behavior or movement over a 6 week period. The acoustic array has been collecting data since November 2015, a time frame that happened to coincide with strong El Niño conditions. Six, tagged empty shells (100–126 mm SL) and 56 untagged empty shells (36–132 mm SL) have been collected since the start of the study. Preliminary data suggests that acoustic telemetry in combination with time lapse cameras may be useful in tracking the survival, movement patterns, behavior, habitat needs and long-term viability of abalone in the wild both prior to and following enhancement.



Local public opinion of Baja California's mollusk production

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Sonora, Baja California Sur, Baja California and Sinaloa are the most important producers of commercial mollusks in Mexico, even though the majority of the public has little or no knowledge of production methods or how to access them.

The results show how familiar are people with these organisms and the attitudes towards the increase of production in the state; all of this with the purpose for taking it to a regional scale. It is important to highlight the need of promotion and information regarding the consumption and aquaculture of mollusks. The most effective means to deliver information would be social media, TV, radio, mobile applications, newspapers and county fairs.

This study reveals the public supports policies that increase the quantity of seafood domestically produced. The people surveyed were also asked about how the local production impacts employment, regional economy and stress on natural reserves. These study hopes to bring the essential information for the public, politicians and entrepreneurs for further development of this sector and its incorporation into society.

Comparison between two Red Abalone (*Haliotis rufescens*) tagging methods

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In this experiment, PIT (Passive Integrated Transponder) tags were compared to conventional plastic ones that were attached to red abalone (*Haliotis rufescens*) seeds (26 mm SL), with cyanoacrylate based glue. PIT tags were placed in previously made grooves in the shells to improve retention and avoid potential problems reported with other tagging methods (Hale *et al.*, 2012) The 180 tagged juveniles (half of these tagged only with plastic tags (P) and half with plastic and PIT tags (P+PIT) were released in three tide pools conditioned with food and boulders, located at the touristic resort of Bajamar, 30 km north of Ensenada. Four evaluations were made, the first on February 26th and the last on May 1st of 2014. Surveys consisted on searching tagged organisms, with the help of Google lenses and using a racket-shaped antennae (18 cm diameter) connected to a HPR Plus (Biomark) reader. Searches were conducted before and after removing the boulders used for the tide pool conditioning as well as other obstacles like algae or animals. On the second survey, performed 24h after seeding, 4.2% of P organisms and 41.6% of P+PIT organisms were found before removing the rocks (out of the total of organisms found with the two survey



methods). The third and fourth surveys were performed one and two months after seeding, but due to storms, predation, food unavailability, refuge removal and to the cryptic habits of this species, most of the abalones were not found. Even though, the percentage of organisms found before removing the rocks was 88.2% for P+PIT abalones against a 33% of P abalones (out of the total of organisms found with the two survey methods). These results suggest that the PIT technology might improve the efficiency of the evaluation of abalone restocking efforts, but more studies are required to improve the detection distance and to adapt this technology for subtidal use (Searcy-Bernal *et al.*, 2013).

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Commercial spat production of *Panopea globosa* in México in Acuacultura Robles Hatchery

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The geoduck *Panopea globosa* is found in México on the Pacific coast of the Baja California peninsula south of Bahía Magdalena Bay and throughout the Gulf of California. It sustains a very important fishery, but due to its extremely long life cycle, overexploitation of the stock presents a significant risk, while aquaculture of the species is still in an early experimental stage. Here we present the most important results for the production of spat from the Aquacultura Robles laboratory in La Paz, Baja California Sur, from 2014 - 2016. Breeders were obtained in the months of January and February from Magdalena Bay, Baja California Sur by the company MARSEL, and transferred to the hatchery. There, the breeders were stimulated to spawn by injection of serotonin and by the stripped gonad method. Oocytes and sperm were collected to carry out fertilization and developing larvae were maintained at 22±1°C during 12–14 days. D larvae had a size of 122.94±2.9µm shell length and 95.32±1.8µm Shell height, while the pediveliger larva had a size of 346.22±29.7 µm shell length and 317.68± 3.9µm height. Culture density started at 3 larvae / ml and ended at 0.2 larvae/ml. Pediveliger settlement was carried out in downwelling systems normally used for Pacific oyster. The spat was placed in upwelling systems and grown to a shell length of approx. 3mm, when spat was placed in sand systems for juveniles. Spat production in the three years was one million spats. The species presented high survival rates for all stages of culture, but to increase production it is necessary to improve the sediment system used in the final nursery stage. The results are very encouraging and commercial spat production may become feasible in the near future, enabling significant aquaculture production of the species and even re-population of depleted geoduck banks in the wild.

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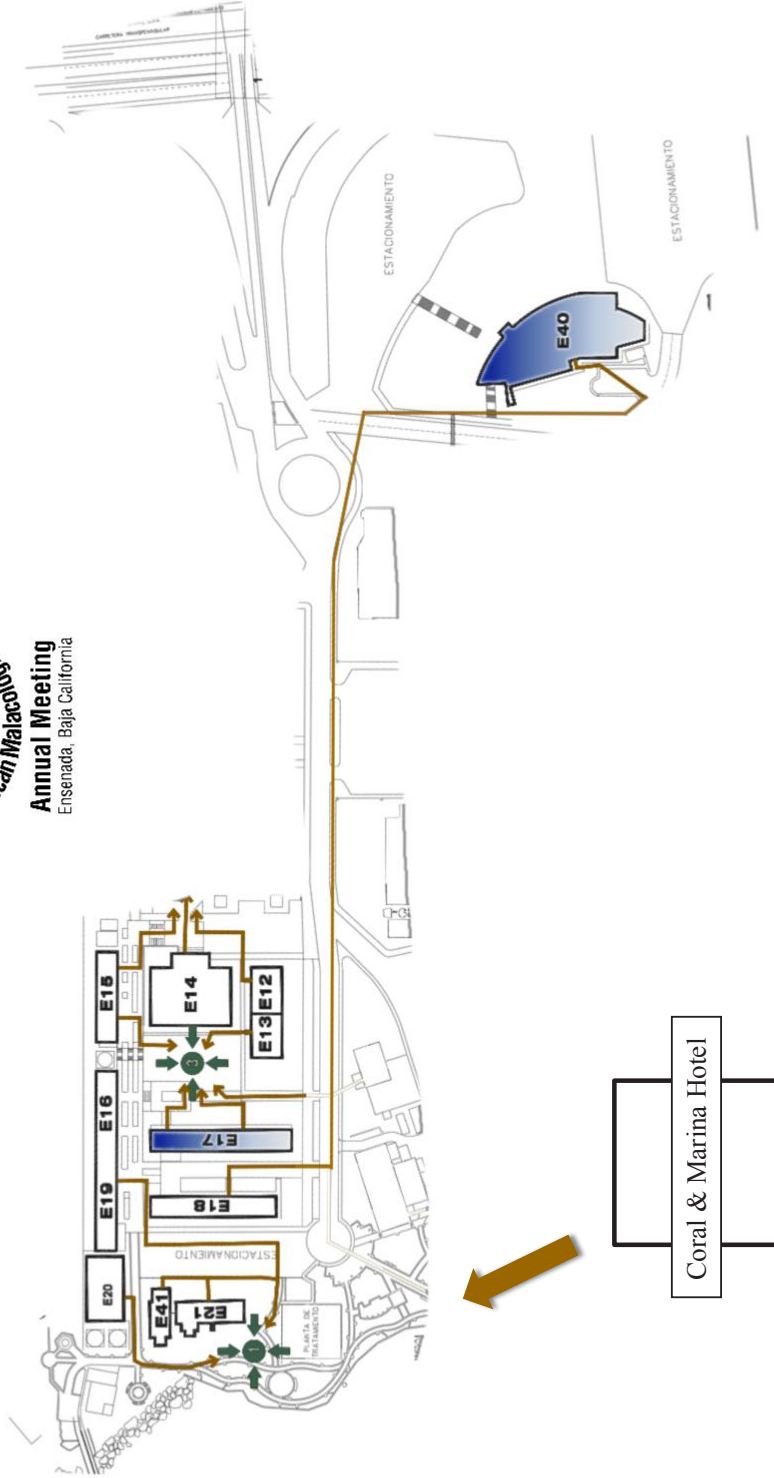
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