

Title: Advancing genetic diversity research in the Indian and Pacific Oceans

Short Title: Indo-Pacific Biodiversity

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Project Summary

Although the Indian and Pacific Oceans (hereafter Indo-Pacific) have long been recognized as containing the majority of marine biodiversity, their vastness poses substantial challenges for empirical research. Syntheses of published data, however, can expand the geographic scope of inference. We plan to examine the recent evolution of Indo-Pacific taxa by drawing upon all available population genetic data. We have two immediate research goals: 1) compile and analyze existing datasets for multiple species using consistent and uniform methods of analysis that represent the best current practice in population genetics to better determine oceanographic and geographic features as well as biological traits correlated with population structure. These results will inform our understanding of evolutionary processes in the region and provide information directly relevant to managers and conservation organizations. We will also: 2) conduct the first large scale multispecies investigation to infer the geography of speciation among Indo-Pacific taxa that incorporates population genetic inferences, thus testing predictions of competing biogeographic hypotheses using a novel approach. These research goals are underpinned by the creation of a database that would become publicly accessible to facilitate future studies. In addition, we plan to develop a virtual collaboration space that will support international collaborations in genetic-based research, training, and education throughout the region.

Public Summary

The greatest concentration of marine species on earth can be found in the coral reefs and surrounding waters of the Indian and Pacific Oceans. Many of these reefs, however, are under increasing stress from human impacts both at the local scale (including eutrophication, pollution, fishing, etc) and the global scale (climate change). Genetic data can clarify connections between reefs that arise from the movement of individual organisms between locations; reef communities that are well connected are likely to be more resilient to local stresses whereas disconnected communities may be more vulnerable. Genetic data can also help reveal the evolutionary processes that have yielded this staggering array of species. Management of coral reef communities should aim to preserve both the connections that maintain persistence in the short term but also the biodiversity-processes that create these biodiverse communities. Although many research groups have independently amassed genetic data that speak to these issues, there have been few coordinated efforts across the entire region, which spans half the globe. We propose to bring together all the available genetic data for this vast region and test specific predictions about how geography and biology influence connections among coral reef communities and how new species are formed. These data will be housed in a virtual collaborative space that will facilitate future research, both synthetic and empirical. The virtual space will also include research tools, instructional materials, and discussion boards. It is our hope that this online presence will nurture international collaborations and improve accessibility of research materials for any investigator or student, regardless of their location.

Introduction and Goals

The patterns and distributions of marine biodiversity differ conspicuously from those of terrestrial biodiversity (Paulay and Meyer 2002; Grosberg et al. 2012). While the fundamental evolutionary processes are probably similar, the specific parameters of those processes are likely very different. Most notably, because gene flow for most marine species is mediated by pelagically dispersing larvae, marine species generally have larger ranges and larger effective sizes than terrestrial species (Kinlan and Gaines 2003; Dawson and Hamner 2008). These large effective population sizes can increase the influence of natural selection relative to genetic drift, which may increase the potential for ecological speciation (Bird et al. 2012). Moreover, large effective population sizes lead to high levels of heterozygosity, which depresses the maximum value of various estimators of F_{ST} (Hedrick 2005; Jost 2008; Bird et al. 2011).

These characteristics make delineating population structure, let alone inferring evolutionary history or connectivity among marine populations (Waples 1998; Hellberg 2009), quite difficult. Theoretical issues surrounding the effect of heterozygosity on F_{ST} and suggested analytical solutions have only come to light within recent years (Hedrick 2005; Meirmans 2006). In addition, there have been important theoretical developments in coalescence for inferring gene flow (Beerli and Palczewski 2010; Hey 2010; Baele et al. 2012), using approximate Bayesian computation to test for shared historical events among co-distributed taxa (Hickerson et al. 2006; Hickerson and Meyer 2008), and landscape genetics for quantifying effects of spatial features on genetic patterns (Lemey et al. 2010; Manel et al. 2010; Selkoe et al. 2010; Storfer et al. 2010; Riginos and Liggins 2013). This expanding tool kit for empirical population genetic research may help illuminate subtle patterns in older datasets. Compounding the difficulty in estimating population genetic parameters for many marine species is the paucity of obvious allopatric barriers in the sea (Rocha et al. 2007), such that *a priori* spatial predictions regarding population structure can be difficult to formulate. Yet, the last decade has seen huge development of oceanographically-informed biophysical models of larval dispersal (Trembl et al. 2008; Kool et al. 2010) and their integration with genetic estimates of gene flow show much promise (White et al. 2010; Crandall et al. 2012; Foster et al. 2012).

As host to the greatest concentration of marine biodiversity on Earth (Roberts et al. 2002), the Indo-Pacific is *the* obvious region to study how biodiversity evolves in the marine realm. It spans nearly two-thirds of the globe, with numerous isolated islands and archipelagos. There is a well-documented “bullseye” pattern of species richness, with the world’s highest marine species diversity for numerous groups occurring at its center in the Indo-Malay-Philippines archipelago. Many species have ranges that span part or all of this distance, meaning that the Indo-Pacific can be considered as a single biogeographic region (Spalding et al. 2007). However, from a practical point of view there are numerous logistical and political challenges created by the sheer size of the region and the fact that it encompasses islands and coastlines of over 50 nations. In our recent (March 2012) NESCent catalysis meeting, “Molecular Ecology and Evolution of the Indo-Pacific”, we identified many structural impediments to comprehensive surveys, including the physical distances, expenses of field work, and the necessity to work in many countries (with differing and often very complex permitting requirements). Many of these obstacles can only be circumvented if research groups from both developed and developing nations work together. In addition, disparities in educational opportunities, particularly in specialist topics, and differing access to molecular lab resources were identified as persistent challenges to widespread regional endeavors. **A primary goal of our working group would be to develop a web-based database and infrastructures to aid collaboration and the cross-dissemination of published data, with the working group and NESCent expertise acting as a spring-board towards developing proposals that would substantially fund education and outreach activities** (including an NSF Research Coordination Network, but also possibly pursuing opportunities through USAID, AusAID and other development funders).

The activities of the proposed working group are closely linked to our recent catalysis meeting and largely arose from activities during that meeting. The emphasis of our catalysis meeting was on developing a framework for collaborative genetic investigations in this geographic region and exploring the utility of genetic data for conservation and management. Whereas we were largely successful in these goals (see attached consensus statement and list of manuscripts being prepared for a special journal issue), it became clear that addressing the big evolutionary questions would require greater effort and focused consideration, which would be better implemented in a small group.

The benefits of archiving published genetic data for re-use by others are obvious (Piwowar et al. 2011). With the advent of second- and not third-generation sequencing technologies, the number of uses of genetic data from a single individual or population probably increases exponentially into the future (although there is no indication that field collecting will become easier). Using only the existing datasets (mostly mtDNA and microsatellites) from most of the major labs working in the Indo-Pacific region, **we are confident that we can address at least two basic research questions in the Indo-Pacific that could not be addressed without region-wide cooperation:**

- 1) **Which geographic features and biological traits affect genetic differentiation in marine environments?** Delineation of population structure continues to be a major problem in marine population genetics (Hellberg 2009; Lowe and Allendorf 2010), but new approaches are revealing subtle patterns that conform to common-sense expectations. For example, a recent paper by Crandall et

al. (2012) demonstrates that realistic population genetic models can be constructed for mitochondrial datasets with the structured coalescent even for species with low and non-significant global F_{ST} (< 0.01). For the four high-dispersal gastropod species they interrogated, a model of stepping-stone gene flow based on predictions from a biophysical model of larval dispersal was favored over several alternatives, including models of panmixia or the island model. We propose to reanalyze published datasets using a suite of population genetic analyses (including coalescent, ABC, and seascape genetic methods - see introduction) alongside biophysical models and other spatial predictors of dispersal to quantitatively evaluate patterns and processes affecting population structure and gene flow for Indo-Pacific species. *A uniform and consistent approach, treating each species as a unit of replication, will allow us to learn about the effects of oceanographic and geographic features as well as biological traits that conform to, or cause deviations from, predicted genetic structure.*

- 2) **How does the geography of the Indo-Pacific contribute to its characteristic pattern of species diversity?** Long-standing hypotheses regarding diversification processes (center of origin, center of accumulation, center of overlap, center of survival, Bellwood et al. 2012) in the Indo-Pacific have largely been evaluated based on patterns of species distributions, especially mid range locations. But species with extremely long tails of their dispersal kernel (which probably typifies many marine animals) can decouple range position from location of species origin. Furthermore, range contractions cannot be distinguished from expansions in the absence of other data (Bellwood and Meyer 2009). However, population genetic patterns (e.g. patterns of genetic diversity), are well suited for determining locations of origin (or persistence) within species and coupled with a sister taxon outgroup, can provide information about mode and timing of speciation (Barber 2009). There has been no cohesive effort to test these ideas using genetic data on a cross-section of marine taxa, despite application of genetic information to testing these hypotheses for a few species (for example, Meyer et al. 2005; Drew and Barber 2009; Bird et al. 2011). *We propose to use tools from population genetics to infer locations of species origins and directions of spread and evaluate these results against predictions of classic biogeographic hypotheses.*

Proposed Activities

1) **Gather empirical data for testing hypotheses:** We have already identified the 154 published studies for the region that could provide the necessary data for our goals and assembled these into an online database (summarized at <https://www.google.com/fusiontables/DataSource?snapid=S776307IxC>). We have developed standards for using this same infrastructure to host raw data (using DarwinCore identifiers, see draft version as appendix), and will proceed with the advice of NESCent IT staff and proposed participant Deck, who has extensive experience with biodiversity informatics. For the purposes of the working group, we would populate a database that includes sampling and genetic data (haplotypes and genotypes) from (nearly) all laboratories with large Indo-Pacific collections. PIs of these laboratories are either part of the proposed working group or were part of the Catalysis meeting at which the attached data sharing consensus statement was written (some have also provided an additional letter of support - attached). We would request funds from NESCent to assist with data entry to populate this database, but would also run day-long “data-thons” among participating research groups during which each research group would convene at their home institution (in the USA, Australia, South Africa, etc.) and upload sampling and genetic data from published papers into the database. This type of exercise teaches students how to look at papers in a new light and global camaraderie would be fostered with prearranged video conferencing between research groups. Problematic papers would be identified and pulled aside for expert annotation. The final resultant database would initially be used to address the questions identified above, but also would be available to other researchers in the global community for future investigations.

2) **Clarify and prioritize testable hypotheses:** Two initial study topics are planned as described above. Each of these broad topics is certain to be resolved into multiple delineated studies, thus it will be critical to examine each potential causative process (leading to patterns of population differentiation or species diversity) and to consider how available within-species data would best be combined with other sources of data (phylogenetic, species ranges, biophysical models, etc) to test specific predictions. Some of the proposed working group members are not geneticists and will contribute expert knowledge in larval

dispersal modeling, paleontology, historical ecology, and macroecology. The discussions are likely to lead to one or more conceptual papers and also provide a framework for empirical tests to follow.

3) *Develop a framework for cooperation:* Our ultimate goal is the creation of a virtual collaborative space that is open to any researcher (or student) worldwide with access contingent upon agreeing to certain ground rules for participation and protection of intellectual property. Rules for membership and guidelines for authorship and cooperation may be modeled on NutNet (www.nutnet.umn.edu); although some broad principles were agreed upon at our catalysis meeting, many details are unresolved and need further discussion. We would seek input from NESCent IT regarding development and hosting options.

Potential elements of the virtual collaborative space

1. Information clearing house for
 - a. Collaboration: might include core pre-agreed papers and a clear process for new paper proposals (possibly following NutNet model whereby there are transparent mechanisms for participating in studies)
 - b. Logistics: contacts for regional experts, taxonomic expert group members, collection-permit information (can pull off NESCent wiki), noticeboard for upcoming collections and opportunities for tissue exchanges, local meet ups, empirical works in progress
 - c. Dissemination: paper repository (access to literature is a major impediment to researchers in developing countries), this may include a blog announcing new papers
2. Education and outreach (*long term, likely to require funding and involvement beyond working group*)
 - a. Instructional material (video, written, any format), could range from field techniques and identification, lab methods, analyses/specific programs, scientific writing)
 - b. Remote education course on specific topics, student discussion boards and interactive spaces
 - c. Arena for peer mentoring and inexperienced authors to get feedback
 - d. Announcements for scholarship opportunities

4) *Leverage the working group framework to write an RCN proposal for NSF:* The chance to assemble committed participants in Durham with minimal external distractions would significantly facilitate writing of a Research Coordination Network proposal. Such a proposal would benefit greatly from NESCent staff's input and experience regarding databasing and online material. We anticipate that the major framework could be drafted in 2-3 days and future specific tasks and timelines allocated. The conceptual ideas for the proposal are given above. Under an RCN umbrella, we would also seek to develop teaching and training modules such that could be used to bolster graduate (and undergraduate) experiences, especially in developing countries of the Indo-Pacific region (see above). We are targeting the Aug. 2013 submission deadline for an RCN and have already been in contact with NSF-DEB program officers who are supportive of the concept.

Participating Fields and Partial List of Proposed Participants

Our ideal group composition will include expertise in population genetics, biogeography, paleontology, macroecology, and bioinformatics. Attached (supplementary table) is a list of potential participants reflecting this spread of expertise, all of whom have expressed strong interest in this proposed work. This list includes three NESCent post doctoral fellows: Sbrocco, Harnik, Unmack. If funded, we will select among the list to maximize representation across areas of expertise, career stage, and institutional location.

Rationale for NESCent support

NESCent provides a unique opportunity for international collaboration. We know of no other funding group that will support scientists regardless of their nationality to undertake synthetic work in evolutionary biology. Although some members of our group have previously worked together (see attached documentation), a critical component of the present proposal is to draw in scientists with expertise in traditional biogeography, historical ecology, and macroecology. Getting all these minds in the same room is critical for interdisciplinary integration and cannot be funded through traditional domestic granting agencies. Moreover, we envision the planning input by NESCent IT staff (informed by their extensive experience in dealing with evolutionary questions and collaborative research) as being an absolutely essential guiding influence on our planned activities.

Collaborations with other NESCent Activities

Any opportunities for synergisms will be welcome. NESCent post-doctoral fellows Sbrocco and Unmack participated in our previous Catalysis meeting and will likely participate in the working group. Harnik (currently a post-doctoral fellow) would be a strong addition to this project, contributing expertise in paleontology and phylogenetics.

Anticipated IT Needs

The most crucial IT support will be project-planning advice. Of course we would welcome any additional IT contributions, including hosting a semi-public database, but our exact plans will have to be somewhat flexible in that our plans will obviously change dependant on whether additional funding is obtained from NSF. Usage of free or low-cost infrastructures (including Google fusion tables) would be sufficient to meet our aspirations in a basic if somewhat crude manner, but database and web hosting and affiliation with reliable and appropriate partner (NESCent or a university) would be more appropriate. We may also require funds for time on a computer cluster or cloud-computing instances.

Proposed Timetable

Because many of our participants would have to travel internationally to attend a working group, we would focus on fewer meetings of longer duration (4 meetings, one week duration each). We would also try to schedule a few brief (1 day) virtual meetings to keep the momentum moving.

Meeting 1 – Early 2013:

- Decide on fundamental initial studies and what is needed to achieve them
- Seek NESCent advice on databasing, web structure
- Finalize interim database structure (how to proceed without assuming NSF funding)
- Draft outline of NSF RCN proposal and assign roles for writing

Between meetings:

- Start population database – individual data entry plus global data-thons
- RCN due Aug. 1, 2013

Meeting 2 – ~ June 2013, following SSE

- Finalize RCN proposal
- Work on core concept paper(s)
- Assess status of database, consider contacting authors whose data are not openly accessible
- Plan details of data synthesis work, assign tasks

Meeting 3 (Virtual) – ~ Sept – Oct: 2-3 days with 3 hours meeting time per day to accommodate the wide span of time zones

- Any remaining issues on core concept papers
- Reports by data synthesis leaders, with discussion and brainstorming to follow

Meeting 4 – Late 2013 to Early 2014

- Will know the results of RCN bid
- Work on data synthesis papers
- Decide on pathway forwards pending RCN results: steering committee business or mapping a framework for collaboration and outreach without funding

Meeting 5 (Virtual) – Mid 2014

- Agenda as arises

Meeting 6 – Late 2014

- Finalize data synthesis papers

Agenda as arises

Outcomes

Publications: At least one conceptual and several data synthesis papers. Most likely, several spin-off collaborations among research groups will develop incidentally and result in publications.

Database: The database will facilitate the usage of population genetic data for future synthetic research and will provide a model for how genotyped and georeferenced data can be organized and disseminated. Furthermore, we anticipate that the raw data accessibility will raise the profile of marine biodiversity research by providing easy access to marine data for researchers looking for large population genetic data sets.

Model for international collaborations in spatial genetics: Our proposed virtual collaborative space will extend multi-investigator and international collaborations into the field of spatially explicit genetic investigations (the provenance of population genetics, phylogeography, and some phylogenetic studies). Successful elements from our model could be easily expanded to other habitat types.

Education and outreach resources: The revolution in online communication and education could greatly benefit graduate students in specialized fields who are unlikely to have access to specialists in all topics relevant to their studies. By making content available to any member (or student) in the broader network of collaboration, we seek to equalize the intellectual tools available regardless of home country and to encourage connections among students irrespective of geography.

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Potential working group participants							
Person		Position	Institution	Country	Email	Expertise	Extra skills
Barber	Paul	Associate Professor	UC Los Angeles	USA	paulbarber@ucla.edu	Phylogeography, population genetics	
Bellwood	David	Professor	James Cook University	Australia	David.Bellwood@jcu.edu.au	Paleontology, biogeography, character evolution	
Bird	Chris	Assistant Professor	Texas A&M University - Corpus Christi	USA	cbird@hawaii.edu	Sympatric speciation	Next Generation Sequencing
Connolly	Sean	Professor	James Cook University	Australia	sean.connolly@jcu.edu.au	Macroecology	
Crandall	Eric	Assistant Research Scientist	UC Santa Cruz	USA	eric.crandall@noaa.gov	Phylogeography, population genetics	R, Next Generation Sequencing and some bioinformatics
Deck	John	Biodiversity Informatician	University of California at Berkeley	USA	jdeck@berkeley.edu	Biodiversity informatics	
Fernandez	Iria	Fulbright Postdoctoral Fellow	Hawaii Institute of Marine Biology	USA	iriafernandezsilva@gmail.com	Phylogeography, population genetics	
Harnick	Paul	Postdoctoral Fellow	NESCent	USA	paulharnick@nescent.org	Biodiversity, macroevolution, ecology, paleontology, database	
Karl	Stephen	Associate Research Professor	University of Hawaii	USA	skarl@hawaii.edu	Population genetics	
Lessios	Haris	Director of Marine Research	Smithsonian Tropical Research Institute	Panama	Lessiosh@post.harvard.edu	Phylogeography, population genetics	
Pandolfi	John	Professor	University of Queensland	Australia	j.pandolfi@uq.edu.au	Paleontology, historical ecology	
Riginos	Cynthia	Senior Lecturer	University of Queensland	Australia	c.riginos@uq.edu.au	Phylogeography, population genetics, data synthesis	R, Perl, some data synthesis experience
Saenz-Agudelo	Pablo	Postdoctoral Researcher	King Abdullah University of Science and T	Saudi Arabia	Pablo.SaenzAgudelo@kaust.edu	Parentage, direct measures of dispersal	
Sbrocco	Elizabeth	Postdoctoral Fellow	NESCent	USA	elizabeth.sbrocco@duke.edu	Ecological niche modeling, GIS	niche modelling
Shanker	Kartik	Assistant Professor	Indian Institute of Sciences	India	kshanker@gmail.com	Biogeography, Community Ecology	
Toha	Hamid	Associate Professor	State University of Papua	Indonesia	hamid.toha@yahoo.co.id	Phylogeography	
Toonen	Rob	Associate Professor	University of Hawaii	USA	toonen@hawaii.edu	Larval biology, phylogeography, population genetics, data synthesis	
Treml	Eric	Postdoctoral Researcher	University of Melbourne	USA	eric.treml@unimelb.edu.au	Oceanography, community ecology	spatial databases, R/python scripting, GIS, and ecological modelling
Unmack	Peter	Postdoctoral Fellow	NESCent	USA	peter.web2@unmack.net	biogeography, GIS modeling, phylogenetics	GIS
von der Heyden	Sophie	Lecturer	Stellenbosch University	South Africa	svdh@sun.ac.za	Phylogeography, Population Genetics	
Waples	Robin	Senior Scientist	Northwest Fisheries Science Center	USA	robin.waples@noaa.gov	Theoretical and empirical population genetics	

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ACADEMIC QUALIFICATIONS

Ph.D., Department of Ecology and Evolutionary Biology, University of Arizona (2000)
M.S., Department of Ecology and Evolutionary Biology, University of Arizona (1998)
B.A., Biology (Honors), Haverford and Bryn Mawr Colleges (1993)

PROFESSIONAL APPOINTMENTS

Senior Lecturer, University of Queensland (2012 – present)
Lecturer, University of Queensland (2006 – 2011)
Research Associate / Lead investigator on NSF grant, Duke University (2003 – 2006)
Post-Doctoral Fellow in Molecular Evolution & Comparative Genomics, Duke University (2000 – 2002)

FELLOWSHIPS AND AWARDS

Faculty of Science Teaching Excellence Award, The University of Queensland (2010)
American Association of University Women Post-doctoral Fellowship (2003 – 2004)
Post-Doctoral Fellowship in Molecular Evolution & Comparative Genomics (2000 - 2002)
Duke University

10 SELECTED RECENT PUBLICATIONS

(*graduate student co-author; **undergraduate student co-author)

- Riginos C**, *Liggins L. Seascape genetics: populations, individuals, and genes marooned and adrift. *Geography Compass*. Accepted October 28, 2012.
- Liggins L, Trembl EA, **Riginos C**, Taking the plunge: an introduction to undertaking seascape genetic studies and using biophysical models. *Geography Compass*. Accepted October 28, 2012.
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Ridgway T, **Riginos C**, **Davis J, and O Hoegh-Guldberg. 2008. *Pocillopora verrucosa* genetic connectivity patterns in Southern African Marine Protected Areas. *Mar Ecol Prog Ser*. 354: 161-168.

5 REPRESENTATIVE SYNERGISTIC ACTIVITIES

- 1) **NESCent Catalysis Meeting** – Co-organized a Catalysis meeting on the Molecular Ecology and Evolution of the Indo-Pacific at the National Evolutionary Synthesis Center in Durham, NC, in March 2012. Thirty-five scientists from around the world met. The groundwork for a collaboration network was agreed upon. I negotiated for a special edition of the Bulletin of Marine Science to host papers arising from the Catalysis meeting and am currently one of two guest editors of this special edition. Bull. Mar. Sci. was selected as a general marine journal with a long-standing reputation, which is also able to accommodate making all submissions open access so that results are open to researchers, NGO's, and managers in all countries of the Indo-Pacific region.
- 2) **Broadening the Participation of Underrepresented Groups in STEM** – Undergraduates that I mentored at Duke University have pursued careers in the biomedical fields (one Hispanic male, one Asian male) and conservation biology (one African American woman is now completed her PhD) and all were co-authors on peer-reviewed papers. At the University of Queensland, women constitute somewhat above 50% of my research group (three female PhD students at present, and one post-doc), with five women having obtained research Honours undergraduate degrees and one Master's degree under my supervision. Undergraduate classes at the University of Queensland contain large proportions of students from Southeast Asia, many with English as a second language. I attempt to promote inclusive teaching practices in my lectures and am currently embarking on project that will develop online teaching materials for first year genetics that will cater to a variety of learning styles and experiences.
- 3) **Graduate writing seminar, University of Queensland** – One of the major challenges facing PhD students is preparing their research results for journal publication. For three years, I co-organized a weekly writing series aiming to 1) give students knowledge and experience in the mechanics of preparing a research study for publication, and 2) to provide a community of peers to provide constructive feedback and emotional support. We structured the writing group around two sets of activities: a) at weekly meetings where the lecturer leads a discussion and sometimes an activity regarding specific aspects of a scientific paper (often with suggested readings as background), and b) students work in small peer groups (2-4 students, typically) to review each other's writing. Students who have completed this workshop series rate the amount of writing time and emotional difficulty as significantly reduced as compared to a control group of biology postgraduates who had written papers but not participated in the workshop ($P = 0.004$ and $P = 0.02$, respectively). In 2010, I was awarded a *Faculty of Science Teaching Excellence Award* for this work.
- 4) **Editorial appointments** – Associate Editor for *Marine Biology* since 2009, currently a guest editor for a special issue of the *Bulletin of Marine Science*.
- 5) **Anonymous reviewing** - Grants from the National Science Foundation (Population and Evolutionary Processes and Biological Oceanography programs: ~3 per year) and the Australian Research Council (~15 per year), external dissertation examination (Griffith University, MacQuarrie University), Manuscripts (including the following journals: Aquaculture, Biol Bull, Biol Invasions, Biol J Linn Soc, BMC Evol Biol, Can J Fish Aquat Sci, Cons Gen, Coral Reefs, Curr Biol, Divers Distrib, Ecography, Evolution, Mol Ecol, Genetica, Heredity, Int J Mol Sci, Invert Biol, J Biogeog, J Exp Mar Biol Ecol, J Mol Evol, Mar Freshw Res, Mar Biol, Mar Ecol Progr Ser, Mol Biol Evol, Mol Ecol, Mol Phylogen Evol, Moll Res, Nature Genetics, Oceanologia, PLOS Biology, Polar Biol, Proc Roy Lond, B; I review ~3 manuscripts per month)

ERIC DARVISH CRANDALL

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Education

1998 B.A. Integrative Biology, University of California, Berkeley
2008 Ph.D. Biology, Boston University

Academic Employment

2012 – present Assistant Research Scientist, Southwest Fisheries Science Center, NOAA/NMFS
2010 – 2012 Assistant Specialist, Southwest Fisheries Science Center, NOAA/NMFS
2008 – 2010 Postdoctoral Research Associate – Old Dominion University-NSF CT-PIRE
2006 – 2007 Palmer-Mcleod Fellow - Boston University Marine Program
2002 – 2005 Teaching Fellow - Boston University Marine Program
2003 – 2004 NSF GK-12 Fellow – Boston University Project STAMP
2000 – 2002 Staff Research Associate – UC Berkeley Dept. of Integrative Biology
1997 Research Assistant – University of Oregon, Oregon Institute of Marine Biology

Grants and Awards

2011 NESCent Catalysis Meeting – “The Molecular Ecology and Evolution of the Indo-Pacific: A Collaborative Research Network ~\$40,000
2007 International Biogeography Society – Student Travel Award - \$1,000
2005 NSF Doctoral Dissertation Improvement Grant : “How do stepping stones of intermediate habitat affect gene flow in neritid snails?” - \$15,000
2004 Boston University – Outstanding Teaching Fellow Award
2004 Lerner-Grey Fund – American Museum of Natural History \$1,500
2004 Conchologists of America – Walter Sage Memorial Grant \$1,500
2003 NSF Graduate Research Fellowship Program – Honorable Mention
2002 Boston University – Outstanding Teaching Fellow Award

Publications

Ackiss, A., Pardede, S., Crandall, E.D., Ablan-Lagman, M.A., Romena, N., Barber, P.H. and Carpenter, K.C. (in press) Pronounced population structure in a highly mobile reef fish, *Caesio cuning*, in the Coral Triangle. *Marine Ecology Progress Series*
Crandall, E.D., Trembl, E.A., Barber, P.H. (2012) Coalescent and biophysical models of long-distance dispersal dynamics in Neritid snails. *Molecular Ecology* 21(22): 5579-5598
Crandall, E.D., Sbrocco, E.J., DeBoer, T.S., Barber, P.H., Carpenter, K.C. (2012) Expansion dating: calibrating molecular clocks in marine species from expansions onto the

- Sunda Shelf following the Last Glacial Maximum. *Molecular Biology & Evolution* 29(2): 707-719.
- Carpenter, K.E., Barber, P.H., Crandall, E.D. Ablan-Lagman, M.A., Ambariyanto, Mahardika, I.G.N., Manjaji-Matsumoto, M. Juinio-Meñez, M.A., Santos, M.D. Starger, C., Toha, A.H. (2011) Comparative Phylogeography of the Coral Triangle and Implications for Marine Management. *Journal of Marine Biology*. doi:10.1155/2011/396982
- Crandall, E.D., J.R. Taffel, P.H. Barber (2010) High gene flow due to pelagic larval dispersal among South Pacific archipelagos in two amphidromous gastropods (Neritimorpha: Neritidae). *Heredity* 104: 563-572
- Crandall, E.D., E.M. Jones, M. Munoz, B. Akinrobe, M.V. Erdmann, P.H. Barber. (2008) Comparative phylogeography of two seastars and their ectosymbionts within the Coral Triangle. *Molecular Ecology* 17: 5276-5290
- Crandall, E.D., M.A. Frey, R.K. Grosberg, P.H. Barber (2008) Contrasting demographic history and phylogeographical patterns in two Indo-Pacific gastropods. *Molecular Ecology* 17: 611-626
- Crandall, E.D. (2008) Isolation and gene flow in Indo-Pacific species with pelagic larvae. Ph.D Dissertation, Boston University. 195 pp.
- Crandall, E.D. (1999) Early life history aspects of amphidromous neritid snails in Moorea, French Polynesia. *Berkeley Scientific* 3:52-61.

5 Representative Synergistic Activities

- Co-organized and funded a Catalysis meeting for an international group of 35 scientists on the Molecular Ecology and Evolution of the Indo-Pacific at the National Evolutionary Synthesis Center in Durham, NC, with the goal of developing a collaborative network for Indo-Pacific Ecology and Evolution
- Lead Instructor, Co-instructor or T.A. for Molecular Ecology course developed by Paul Barber and myself and taught to graduate and undergraduate students at Boston University, Old Dominion University, University of the Philippines and Udayana University
- Mentor in molecular ecology theory and methodology for nine graduate students from the Philippines, Indonesia and the United States: Amanda Ackiss (USA), Samantha Cheng (USA) Adam Hanson (USA), Jeremy Raynal (USA), Inggat Casiligan (Philippines), Maria Lourdes Docoy-Boucher (Philippines), Rita Rachmawati (Indonesia), Tri Komala Sari (Indonesia), Shinta Pardede (Indonesia). Mentor to fifteen US undergraduates from underrepresented minorities as part of REU program - The Diversity Project.
- Wrote, co-organized and taught teaching laboratories (BIOBUGS) for Boston area high schools, reaching over 300 students. Numerous similar outreach activities in collaboration with US Peace Corps, UC Berkeley Lawrence Hall of Science, UCSC Institute for Scientist and Engineer Educators
- Reviewer for BMC Evolutionary Biology, Conservation Genetics(3), Evolution(4), Journal of Applied Ichthyology, Journal of Biogeography(2), Journal of Evolutionary Biology, Journal of Experimental Marine Biology(2), Fundamental and Applied Limnology, Journal of Fish Biology, Journal of Marine Biology, Marine Biology(2), Marine Ecology Progress Series(4), Marine Genomics, Molecular Ecology(5), Molecular Ecology Resources, Molecular Phylogenetics and Evolution(2), US National Science Foundation(2), South Africa National Research Foundation(2), Geography Compass

Robert John Toonen

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Phone: (808) 236-7401 Fax: (808) 236-7443 Email: toonen@hawaii.edu

Education:

Ph.D. Population Biology. Center for Population Biology, University of California, Davis, CA. (2001)
M.Sc. Marine Sciences. University of North Carolina, Wilmington, NC. (1993)
B.Sc. Honours Zoology. University of Alberta, Edmonton, AB. (1991)

Professional Appointments:

Associate Research Professor: July 2008 – present, Hawai'i Institute of Marine Biology, School of Ocean and Earth Sciences and Technology, University of Hawai'i at Mānoa
Assistant Research Professor: June 2003 – June 2008, Hawai'i Institute of Marine Biology, School of Ocean and Earth Sciences and Technology, University of Hawai'i at Mānoa
Research Associate: 2002 – 2003, Center for Population Biology, Section of Evolution & Ecology, University of California, Davis.

Awards and Recognition:

2012 Peter V. Garrod Distinguished Graduate Mentorship Award
2011 finalist for UH Regents Distinguished Graduate Mentoring Award
2010 finalist for UH Regents' Medal for Excellence in Research

10 Selected Recent Publications (N = 114):

*denotes graduate student co-author

1. Karl, SA, **RJ Toonen**, WS Grant, BW Bowen (2012). Common misconceptions in molecular ecology: echoes of the modern synthesis. **Molecular Ecology: Invited reviews and meta-analyses**. [Online Early](#)
2. **Toonen, RJ**, K Andrews*, I Baums, C Bird, G Concepcion*, T Daly-Engel*, J Eble*, A Faucci*, M Gaither*, M Iacchei*, J Puritz*, J Schultz*, D Skillings*, M Timmers * & BW Bowen (2011). Defining boundaries for ecosystem-based management: A multispecies case study of marine connectivity across the Hawaiian Archipelago. **Journal of Marine Biology** [#460173, 13 pp.](#)
3. Selkoe, KA, J Watson*, C White*, T Ben-Horin*, M Iacchei*, S Miterai, D Siegel, SD Gaines & **RJ Toonen** (2010). Taking the chaos out of genetic patchiness: seascape genetics reveals ecological and oceanographic drivers of genetic patterns in three temperate reef species. **Molecular Ecology** [19:3708-3726](#).
4. White C*, KA Selkoe, J Watson*, D Siegel, D Zacherl & **RJ Toonen** (2010). Ocean currents help explain population genetic structure. **Proceedings of the Royal Society Series B** [277:1688-1694](#).
5. Bird, C., I. Fernandez-Silva, D. Skillings* & R.J. Toonen (2012). Sympatric Speciation in the Post "Modern Synthesis" Era of Evolutionary Biology. **Evolutionary Biology**. 39:158-180.
6. Puritz, JB * & **RJ Toonen** (2011). Coastal pollution limits pelagic larval dispersal. **Nature Communications**. [2:226, 8 pp.](#)
7. **Toonen, R.J.** & A.J. Tyre. 2007. If larvae were smart: A simple model for optimal settlement choices of competent larvae. **Marine Ecology Progress Series**. 349: 43–61.
8. **Toonen, R.J.** & J.R. Pawlik. 2001. Settlement of the gregarious tube worm *Hydroides dianthus* (Polychaeta: Serpulidae) I. Gregarious and nongregarious settlement; II. Testing the desperate larva hypothesis. **Marine Ecology Progress Series** 224:103-131.
9. **Toonen, R.J.** & J.R. Pawlik. 2001. Foundations of gregariousness: A dispersal polymorphism among the planktonic larvae of a marine invertebrate. **Evolution** 55:2439-2454.
10. **Toonen, R.J.** & J.R. Pawlik. 1994. Foundations of gregariousness. **Nature** 370:511-512.

5 Representative Synergistic Activities:

- **Broadening the Participation of Underrepresented Groups in STEM:**

Minority students supervised to date (name, nationality, dates in our lab): Saipologo Toala, Am. Samoa (2004); Houston Lomae, Marshall Islands (2004); Megan Lin, Hawaii (2004); Greg Concepcion, Filipino (2004-present); Sierra Isalias, Palau (2005); Alexander Alfonso, Pohnpei (2005, 2007); Senifa Annedale, Am. Samoa (2005), Laurie Soerenson, Hawaii (2005-2006); Van Nicholas Valesco, Hispanic (2005-2006); Damien Cie, Hawaii (2006), Shelley Remengesau, Palau (2007), Bethany Kimokeo, Hawaii (2008-2011), Ngedikes Benedict, Palau (2008), Nikita Adachi, Palua (2009), Ale'alani Dudoit, Hawaii (2009-present), Eric Tong, Hawaii (2009-present), Pauleen Fredrick, Pohnpei (2010-present), Paulino Balagot, Pohnpei (2011), Miguel Vaca, Hispanic (2011).

- **Representative Invited Presentations to the Public (Last 5 years, N=31):**

Marine Aquarists Roundtable Conference, 2010, Sacramento, CA.
Marine Aquarium Conference of North America, 2009. Atlanta, GA.
Fourth International Days of Saltwater Aquarists, 2005. Strasbourg, France.
International Marine and Reef Aquarium Conference, 2003. Chicago, IL.

- **Popular Literature Publications:**

Over 100 popular literature articles for *Advanced Aquarist Online Magazine*, *Freshwater & Marine Aquarium (FAMA) Magazine*, *Tropical Fish Hobbyist*, *Marine Fish & Reef USA Annual*, *Koralle (German)*, *Les Lettres Récifales (French)*, *Practical Fishkeeping (UK)*, and *ReefArt (Italian)* - complete list online at

<http://www2.hawaii.edu/~toonon/publications.html#aquarium>

- **Editorial Appointments**

Marine Ecology Progress Series Anonymous Review Staff Referee (2002 – present); Guest editor for *Journal of Marine Biology*, special issue on Ecosystem-based Management of Pacific Islands. (2010–2011); *Conservation Genetics*, Associate Editor (2011 – present), *Pacific Science*, subject editor marine invertebrates and population genetics (2011 – present); *PLoS ONE*, Academic Editor (nomination pending).

- **Anonymous Referee Service**

Reviewed manuscripts for *African Journal of Marine Science*, *American Naturalist*, *Aquaculture*, *Aquatic Conservation*, *Auk*, *Biofouling*, *BioTechniques*, *Biological Bulletin*, *Biological Invasions*, *Bulletin of Marine Science*, *BMC Ecology*, *BMC Evolutionary Biology*, *Canadian Journal of Fisheries and Aquatic Science*, *Coral Reefs*, *Ecological Applications*, *Ecology*, *Ecology Letters*, *Ecography*, *Evolution*, *Gene*, *Genome*, *Israel Journal of Ecology and Evolution*, *Journal of Applied Ecology*, *Journal of Experimental Biology*, *Journal of Fish Biology*, *Journal of Heredity*, *Journal of Experimental Marine Biology and Ecology*, *Journal of Plankton Research*, *Limnology and Oceanography*, *Marine and Freshwater Research*, *Marine Biology*, *Marine Biotechnology*, *Marine Ecology Progress Series*, *Molecular Ecology*, *Molecular Phylogenetics and Evolution*, *Nature*, *New Zealand Journal of Marine and Freshwater Research*, *PLoS ONE*, *Proceedings of National Academy of Sciences USA*, *Proceedings of Royal Society B: Biological Sciences*, *Pacific Science*, *Quarterly Review of Biology*, *Sarsia*, *Science*, *Sea Grant*, the National Science Foundation, National Geographic, Natural Environment Research Council (UK), Natural Sciences & Engineering Research Council (NSERC) of Canada, Australian Research Council (ARC), L'Agence Nationale de la Recherche (ANR), and several edited book volumes. (currently ~ 24 / yr).

Consensus statement on data collaboration from March 2012 Catalysis meeting

Addressing competing hypotheses regarding the generation and maintenance of biodiversity in the Indo-Pacific marine realm will necessitate syntheses of genetic data obtained by many different research groups. To advance this goal, we advocate that data from published studies be made openly available.

We encourage best-practices in collecting and data management, including:

- Local involvement and sustained collaboration with area scientists
- Collection of voucher specimens, including photo-vouchers, and one whole individual per population (when feasible) followed by deposition of vouchers in museum collections
- Upon publication, open access material that explicitly links individual genotype (sequence and/or multilocus genotype), georeferenced location of collection, and affiliated voucher specimens
- Long-term maintenance of tissues and DNA's; if not sustainable in individual labs then depositing them with museums of other public repositories (such as ocean genome legacy)

Draft fields for database – each genotyped individual appears as a single entry.
 Developed by Riginos, Crandall, and Meyer

Essential fields

ScientificName	Putative ident	Apogon doederleini
ColloquialName		Doederlein's cardinalfish
IdentifiedBy	Person iden	E Trembl
BasisOfID	morphology, I	morphology
Specimen_Num_Collec	ID from the	ET100
OrigInstitution	University of	
Latitude	Name of lat	Queensland
Longitude	Decimal De	-23.445300
Genetic Data Location	NCBI, BOLD	NCBI
Accession number (Genbank, BOLD)		JF717878
Data Collectors Names		A Mirams
Head of Research Group		Riginos
Locus type	mtDNA sequ	mtDNA sequence
Loci	list of loci in	COI
Genotype	sequence(s)	TTCGTAAT...
Genbank Acc. No.		JF717878
Publication Reference	DOI	10.1007/s00338-011-0767-x
EnteredBy		C Riginos
DateFirstEntered	dd/mm/yea	6/22/2012
Additional field		
HoldingInstitution	Physical loc	University of Queensland
ProjectCode	Any code as	ARC-WWF
Voucher ID	Museum Accession #	or Database ID if present
Photo		photo if available
Sample Collectors Names		Trembl
GeneticTissueType	type of tissue	muscle
VerbatimCollectingLabel		
VerbatimIDLabel		ET100
CollectingLabelNotes		
Country	Where collect	Australia
Province	Where collect	Queensland
Locality Name	Where collect	Heron Island
Permit_Info	Permitting ag	Queensland Government: G08/28114.1
specimen_Habitat		lagoon
specimen_MicroHabitat		sand with coral bommies
YearCollected		2008
MonthCollected		11
DayCollected		17
Collection_Method		Snorkel
specimen_MinDepthMe	min collecting depth	
specimen_MaxDepthM	max collecti	3 m
coll_eventid		if applicable
preservative	EtOH?	DMSI 95% EtOH
fixative		
relaxant		
DNA Sample Location	Where DNA	University of Queensland
DNA Extraction Type	Chelex? Dneasy? Qiagen?	
IdentifiedInstitution	Institution i	University of Queensland
YearIdentified		2008
MonthIdentified		11
DayIdentified		17
Kingdom		Animalia
Phylum		Chordata
Subphylum		Vertebrata
Superclass		ata
Class		Actinopterygii
Order		Perciformes
Family		Apogonidae
Genus		Apogon
PreviousID	is it a type sp	no
TypeStatus		
LifeStage		Adult
Parts		whole fish
Weight		
WeightUnits		
Length		
LengthUnits		

Special issue of Bulletin of Marine Science arising from March 2012 Catalysis Meeting

Manuscripts in progress (submission deadline is Jan 1 2013)

Conceptual/synthesis papers arising directly from the workshop:

- 1) Integration of genetic data into marine conservation and management in the Indo-Pacific: a review and case studies – S. von der Heyden, M. Beger, Rob Toonen, Rachel Ravago-Gotanco, Cecile Fauvelot, Marie Antonette Juinio-Meñez, Christopher E. Bird, Giacomo Bernardi – **submitted**
- 2) Using population genetics in spatial planning for conservation – Lead author: Maria Beger, other authors: K. Selkoe, E. Crandall, C. Riginos, H. Fox, C. Favelot, R. Toonen
- 3) Advancing Biodiversity Research in Developing Countries: the Need for a New Paradigm - Paul H. Barber, Ambariyanto, Menchie Ablan, Eric Crandall, Rachel Gotanco, Ngurah Mahardika, Annette Junio-Menez, Craig Starger, Hamid Toha, Michele Weber, Demian Willette
- 4) Phylogeography unplugged: the relevancy of mtDNA sequencing – Lead author: Brian Bowen, other authors: L Rocha, G Pauley
- 5) Scope and breadth of published genetic studies in the Indo-Pacific - Jude Keyse, other authors: E. Crandall, E. Trembl, C Riginos, C Meyer
- 6) Coincidence of Late Quaternary climatic gradients and marine species boundaries in the Coral Triangle - Elizabeth Sbrocco
- 7) Integrating biophysical models and genetics – E. Trembl, S. Mitharai, J. Kool, K. Selkoe
- 8) So you want to use Next Generation Sequencing for marine science research. - Demian Willette, William Cresko, Elisa Meyer, Daniel Barshis, Mikhail Matz, Eric Crandall, Paul Barber, Iria Fernandez-Silva, Fred Allendorf, James Seeb, Kent Carpenter

Articles with new empirical data contributed from research groups

- 1) What can geographic ranges tell us about genetic connectivity? The comparative phylogeography of *Halichoeres ornatus* and *Halichoeres claudia* - Moisés A. Bernal, William B. Ludt, Matthew T. Craig, Brian W. Bowen and Luiz A. Rocha.
- 2) Population genetics of the reef corals *Pocillopora damicornis* and *Seriatopora hystrix* in the Philippines – Craig J. Starger, Kent E. Carpenter, Rebecca S. Hersch, Ma. Carmen Ablan Lagman, November Romena, Paul H Barber – **submitted**
- 3) Strong genetic structure among coral populations within a conservation priority region, the Bird's Head Seascape (Papua and West Papua, Indonesia)- Craig J. Starger, Paul H. Barber, Mark V. Erdmann, Abdul H. Toha, Andrew C. Baker
- 4) Comparative phylogeography of commercial scombrids in the Indonesian Archipelago - Alexis Jackson, Paul Barber, Ambariyanto, Mark Erdmann, Hamid Toha, Luke Stevens, Alyssa Brayshaw
- 5) Small scale population differentiation detected in *Dascylus aruanus* in the Coral Triangle using mitochondrial and nuclear sequence data – Jeremy Raynal, Eric Crandall, Ngurah Mahardika, Menchi Ablan-Lagman, Paul Barber, Kent Carpenter
- 6) Speciation times in Indo-Pacific sharks and rays - M. Hickerson, Chen and C. Riginos
- 7) Concordant phylogenetic patterns inferred from mitochondrial and microsatellite DNA in the giant clam *Tridacna crocea* – DeBoer, Naguit, Erdmann, Ablan, Ambariyanto, Carpenter, Barber
- 8) Extreme phenotypic polymorphism in *Pocillopora* across the Pacific; corallite morphology corresponds to genetic groups, while taxonomy based on colony morphology does not. Marti-Puig P, Forsman ZH, Haverkort-Yeh RD, Maragos JE, Toonen RJ. – **submitted**
- 9) Population structure of the commercially harvested sea cucumber *Holothuria atra* (lollyfish) throughout the Central Pacific, with implications for management. Skillings D, Bird CE, Toonen RJ.
- 10) Szabo Z., et al. Phylogeography of the Manybar Goatfish, *Parupeneus multifasciatus* reveals moderate structure between the Central and North Pacific and a cryptic endemic species in the Marquesas.



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November 29, 2012

Dear Rob, Cynthia, and Eric,

Thanks for contacting me regarding the continuation of the NESCent working group on the Molecular Ecology and Evolution of the Indo-Pacific. Participating in this working group earlier this year was very valuable and will lead to long overdue integration of much of the research that has been conducted in this region. I am very interested in your idea to create a virtual collaboration space that would make existing genetic data from the Indo-Pacific available for, training, and education throughout the region.

Having worked in the Coral Triangle for fifteen years, we have data sets on 40-50 different marine invertebrates and fishes. About half of this has been published, and much of it will be published soon. These data sets would be an excellent addition to this database.

I am happy to participate in your proposed working group and understand that we will develop guidelines for data sharing and co-authorship as part of the workshop. If this proposal is funded and we develop an acceptable model for data and authorship sharing, I plan to contribute our available datasets and archive the raw data from published studies as part of this effort.

I look forward to working with you all on this project

Sincerely,

A handwritten signature in black ink, appearing to read "P. Barber", with a long horizontal line extending to the right.

Paul Barber
Associate Professor
Ecology and Evolutionary Biology
University of California Los Angeles



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November 30, 2012

Dr. Rob Toonen
Hawai'i Institute of Marine Biology
PO Box 1346
Kane'ohe, HI 96744

Dear Cynthia, Eric and Rob

I am definitely interested in your proposed idea to create a database of all available genetic data from throughout the Indo-Pacific as part of a virtual collaboration space to support international collaborations in genetic-based research, training, and education throughout the region.

As you know, my lab has datasets on Pacific-wide mitochondrial and nuclear DNA sequences from sea urchins, such as *Diadema*, *Tripneustes*, *Pseudoboletia*, *Echinometra*, and *Eucidaris* and also teleost fishes, such as *Stegastes* and *Mulloidichthys*. We are also working on compiling such data for a number of genera present in the eastern Pacific but absent from the Indo-West Pacific, such as the sea urchin *Arbacia*, and the brittle star *Ophioderma*. These unpublished datasets are expected to be completed within the next calendar year and could become part of the future effort.

I am very interested in your proposed working group and pledge to participate. I understand that we will develop guidelines for data sharing and co-authorship as part of the workshop. If this proposal is funded and we develop an acceptable model for data and authorship sharing, I plan to contribute our available datasets and archive the raw data from published studies as part of this effort.

I look forward to working together on this exciting initiative.

Sincerely

H.A. Lessios
Senior Scientist



UNIVERSITEIT • STELLENBOSCH • UNIVERSITY
jou kennisvennoot • your knowledge partner

30th November 2012

Dear Cynthia, Rob and Eric,

Many thanks for your email.

Yes, I am definitely interested in your proposed idea to create a database of all available genetic data from throughout the Indo-Pacific as part of a virtual collaboration space to support international collaborations in genetic-based research, training, and education throughout the region.

As you know, my lab has data sets from around southern Africa, which spans various vertebrate and invertebrate groups. I am also able to facilitate exchanges with colleagues along the east African coastline.

In addition, we have several unpublished datasets in the works, but that are expected to be completed within the next calendar year that could become part of the future effort. These include phylogeographic and phylogenetic data sets across a variety of taxa.

I am very interested in your proposed working group and pledge to participate. I understand that we will develop guidelines for data sharing and co-authorship as part of the workshop. If this proposal is funded and we develop an acceptable model for data and authorship sharing, I plan to contribute our available datasets and archive the raw data from published studies as part of this effort.

I look forward to working together on this exciting initiative.

Sincerely,

Dr Sophie von der Heyden

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100 SHAFFER ROAD
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SANTA CRUZ,

Santa Cruz, 30 November 2012

Dear Cynthia, Rob, and Eric,

I am very happy to be part of a database with the pooled genetic information from the different labs from the Indo-Pacific. This will be a fundamental basis of collaboration between all our labs and labs of the region, that will be used for training, education and research.

My lab has genetic samples and studies from the Philippines, Indonesia, Micronesia and a lot from French Polynesia. We mostly focus on Pomacentrids (damsels and clownfishes) but also have parrotfish, and a large number of miscellaneous samples that we will provide to the researchers that can use them.

We also have about 8-10 datasets that are pretty much ready to go, and those will be added to the pool of information that we will be able to contribute.

I am very interested in your proposed working group and pledge to participate. I understand that we will develop guidelines for data sharing and co-authorship as part of the workshop. If this proposal is funded and we develop an acceptable model for data and authorship sharing, I plan to contribute our available datasets and archive the raw data from published studies as part of this effort.

All my best, and looking forward to working on this great project with you

A handwritten signature in black ink, appearing to read "G. Bernardi", with a stylized flourish at the end.

Giacomo Bernardi
Professor of Biology
University of California Santa Cruz



University of Hawaii at Manoa

Brian Bowen, Research Professor

Hawaii Institute of Marine Biology

P.O. Box 1346 • Coconut Island • Kaneohe, Hawaii 96744-1346

Phone: (808) 236-7401 • E-mail: bbowen@hawaii.edu • Fax: (808) 236-7443

November 28, 2012

Dear Cynthia, Eric, Rob;

I am hugely supportive of continuing the NESCent working group. This group has already demonstrated tremendous success in linking collaborations across the Indo-Pacific. I am currently cooperating on projects with at least 10 members (Planes, Rocha, Bernardi, Barber, van Herwerden, Lessios, Fauvelot, Toonen, Crandall, Riginos), and have plans to collaborate with others (Von der Heyden, Edwards, and more) as a direct outcome of the NESCent workshops and networking.

The proposal of a virtual work space to support international collaboration and training is a very worthwhile extension of this success story, and I will dedicate my time and resources to this effort. I have genetic data sets, including mtDNA sequences, intron sequences, and microsatellite data, on some 25 Indo-Pacific reef fishes. Further, I have data in the can or in production for at least 15 more. This data will be available to the NESCent working group for international collaborations and explorations.

The Indo-Pacific Ocean, spanning over half the planet, is the wellspring of most of the world's tropical marine biodiversity. This area holds the answers to many urgent issues about biodiversity production and maintenance, especially in a conservation context. Yet the area is too large for any one research program to survey adequately. The only solution is an international network of researchers working in cooperation and coordination, and the NESCent group has filled this important research need. We absolutely have to continue.

Sincerely,


Brian Bowen

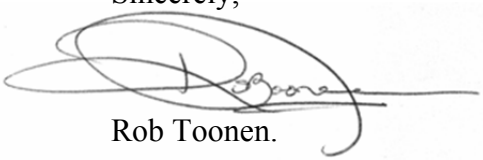
Dear Cynthia & Eric,

I am writing this letter to confirm my participation in compiling a database of all available genetic data from throughout the Indo-Pacific as part of this proposal. I am very excited about the proposed project and will commit my time and lab resources to the effort.

As you know, my lab has generated population genetic data from a suite of coral reef species, primarily focused on the Hawaiian Archipelago (Table 1). To date we have 44 species completed and expect to add another 16 to that dataset by the end of 2013. At that point, we expect to have genetic data for roughly 60 species across the Hawaiian Archipelago, and for some of those species, we also have some samples collected from throughout selected Central Pacific (e.g., *Acanthaster planci*, *Calcinus* spp.).

I look forward to working together on this exciting initiative.

Sincerely,

A handwritten signature in black ink, appearing to read 'Rob Toonen', with a large, loopy initial 'R' and a horizontal line extending to the right.

Rob Toonen.

Table 1. Genetic datasets for 59 species: data complete for 43; 16 more expected in 2013. Markers are M=microsatellites - #loci, NS=nuclear sequence, CB=cytochrome b, CI=cytochrome oxidase, CR=control region, RAD~10,000 SNPs; 'Mean, rge' refers to mean, range of sample sizes in the Hawaiian Archipelago.

Taxon	Species, Footnoted Source	Markers	Sites	Mean,rge	Taxon	Species, Footnoted Source	Markers	Sites	Mean,rge
Coral	<i>Monitpora capitata</i> , 1	M-9	12	45, 25-51	Urchin	<i>Heterocentrotus mammillatus</i> , 9	CB, AFLP	7	28, 3-50
Coral	<i>Porites lobata</i> , 2	RAD,M-9	10	25, 16-40	Butterfly	<i>Chaetodon fremblii</i> , 10	CB	10	35, 20-48
Coral	<i>Pocillopora damicornis</i> , 1&2	RAD,M-10	10	45, 9-50	Butterfly	<i>Chaetodon miliaris</i> , 10	CB	14	29, 10-46
Coral	<i>Pocillopora meandrina</i> , 1&2	M-8	13	47, 16-50	Butterfly	<i>Chaetodon multicinctus</i> , 10	CB	10	28, 14-41
Coral	<i>Fungia scutaria</i> , 1&2	M-8	10	42, 10-50	Damsel	<i>Dascylus albisella</i> , 11	CR	6	15, 7-28
Coral	<i>Pavona varians</i> , 1&2	M-8	9	41, 29-50	Damsel	<i>Stegastes fasciolatus</i> , 11	CR	7	31, 15-49
Coral	<i>Acropora cytheria</i> , 1&2	M-7	5	38, 12-50	Goatfish	<i>Mulloidichthys flavolineatus</i> , 12	CB	5	29, 21-41
Limpet	<i>Cellana exarata</i> , 3	RAD, CI	14	25, 11-41	Goatfish	<i>Mulloidichthys vanicolensis</i> , 12	CB	5	33, 18-42
Limpet	<i>Cellana sandwicensis</i> , 3	RAD, CI	12	22, 8-42	Grouper	<i>Hyporthodus quernus</i> , 13&14	M-8, CR	10	29, 9-44
Limpet	<i>Cellana talcosa</i> , 3	RAD, CI	10	35, 24-43	Grouper	<i>Cephalopholis argus</i> , 15	CB	9	29, 9-54
Snail	<i>Dendropoma gregaria</i> , 4	CI	11	16, 5-53	Moray	<i>Gymnothorax flavimarginatus</i> , 16	CB,CI,NS-2	5	16, 3-53
Snail	<i>Dendropoma platypus</i> , 4	CI	12	12, 5-40	Moray	<i>Gymnothorax undulatus</i> , 16	CB,CI,NS-2	4	27, 19-34
Snail	<i>Dendropoma rhyssconcha</i> , 4	CI	5	18, 5-29	Shark	<i>Squalus mitsukurii</i> , 16	CR	3	35, 7-91
Snail	<i>Serpulorbis variabilis</i> , 4	CI	4	15, 8-25	Shark	<i>Triaenodon obesus</i> , 18	CR	9	17, 5-30
Octopus	<i>Octopus cyanea</i> , 3	CI, NS	5	22, 5-52	Snapper	<i>Etelis marshi</i> , 13	CB	9	44, 10-76
Octopus	<i>Octopus oliveri</i> , 3	M-9,CI,NS	8	20, 18-21	Snapper	<i>Etelis coruscans</i> , 13	CB	11	59,10-104
Crab	<i>Calcinus hazletti</i> , 2	CI	8	21, 7-34	Snapper	<i>Lutjanus fulvus</i> , 15	CB	4	33, 10-41
Crab	<i>Calcinus seurati</i> , 2	CI	4	40, 9-78	Snapper	<i>Lutjanus kasmira</i> , 15	CB	10	37, 9-50
Crab	<i>Calcinus haigae</i> , 2	CI	3	48, 21-71	Snapper	<i>Pristipomoides filamentosus</i> , 15	M-13	9	55, 17-81
Shrimp	<i>Stenopus hispidus</i> , 5	CI	8	23, 5-50	Squirrel	<i>Myripristis berndtii</i> , 19	CB	8	18, 5-31
Lobster	<i>Panulirus marginatus</i> , 5	CI	13	46, 18-63	Surgeon	<i>Acanthurus nigrofuscus</i> , 20	CB	9	31, 20-40
Lobster	<i>Panulirus penicillatus</i> , 5	CI	10	29, 5-52	Surgeon	<i>Acanthurus nigroris</i> , 21	CB	12	34, 27-46
Lobster	<i>Scyllarides squammosus</i> , 5	CI	4	50, 50-50	Surgeon	<i>Acanthurus olivaceus</i> , 15	CB	15	23, 8-33
Brittle star	<i>Ophiocoma erinaceus</i> , 6	16S	14	26, 10-30	Surgeon	<i>Ctenochaetus strigosus</i> , 20	CB	16	33, 25-40
Brittle star	<i>Ophiocoma pica</i> , 6	16S	14	27, 10-30	Tang	<i>Zebrasoma flavescens</i> , 20	M-14, CB	16	46, 29-55
Cucumber	<i>Holothuria atra</i> , 6	CI	11	24, 5-37	Wrasse	<i>Halichoeres ornatus</i> , 19	CB,CR	13	25, 4-72
Cucumber	<i>Holothuria whitmaei</i> , 6	CI	8	33, 22-57	Wrasse	<i>Thalassoma ballieui</i> , 19	CB	10	30, 10-55
Sea Star	<i>Acanthaster planci</i> , 7	CR	7	44,13-106	Jack	<i>Caranx melampygus</i> , 22	NS-2	4	14, 4-26
Sea Star	<i>Linckia multifora</i> , 8	M-8,CB,CI	11	41, 10-50	Dolphin	<i>Stenella longirostris</i> , 13	RAD,M-10	9	56,32-119
Urchin	<i>Eucidaris metularia</i> , 8	CB	10	28, 6-50			CR		

1. G. Concepcion, 2. I. Baums, 3. C. Bird, 4. A. Faucci, 5. M. Iacchei, 6. D. Skillings, 7. M. Timmers, 8. J. Puritz, 9. H. Bolick, 10. M. Craig, 11. Ramon, 12. I. Fernandez, 13. K. Andrews, 14. M. Rivera, 15. M. Gaither, 16. J. Reece, 17. T. Daly-Engel, 18. N. Whitney, 19. L. Rocha, 20. J. Eble, 21. J. Debattista, 22. S. Santos

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November 30, 2012

To Whom It May Concern:

I am deeply committed to the principles of open data access and strive to make all published data from my research group publically available. Thus, there is no impediment to making the data from my research group available to the Indo-Pacific research community.

We have collections from numerous locations in tropical Australia (Great Barrier Reef, Coral Sea, Mooloolaba, Torres Strait, Ashmore Reef, and Ningaloo) and from Timor L'Este, Papua New Guinea, Fiji, and Tonga. Samples include a cross spectrum of reef fishes and invertebrates, with many species selection purposefully to complement existing research programs in Indonesia (close coordination with Paul Barber's group) and the central Pacific. We have sequenced mtDNA loci and are starting to genotype some fishes with microsatellites.

Much of our unpublished or "in press" results can be made available once an acceptable model for data and authorship sharing has been agreed upon.

Sincerely yours,



Cynthia Riginos
Senior Lecturer