

*Frontiers of
Biogeography*



*Program
&
Abstracts*

*International Biogeography Society
Inaugural Meeting
4 ~ 8 January, 2003
Oasis Resort, Mesquite, NV*

INTERNATIONAL BIOGEOGRAPHY SOCIETY

INAUGURAL MEETING

**An international and interdisciplinary society
contributing to the advancement of all studies of the
geography of nature**

**4-8 January 2003
Oasis Resort, Mesquite, NV**

**Department of Biological Sciences
University of Nevada, Las Vegas**

Local Committee

Brett Riddle
Connie Herr
Derek Houston
Gary Voelker
Doug Merkler

Lois Alexander
Jef Jaeger
Markus Mika
Zane Marshall

Stacy Mantooth
Garth Spellman
John Klicka
Diana Outlaw
Rob Outlaw

INTERNATIONAL BIOGEOGRAPHY SOCIETY

MISSION STATEMENT 2000

Biogeography, the study of the geography of life, has a long and distinguished history, and one interwoven with that of ecology and evolutionary biology. Traditionally viewed as the study of geographic distributions, modern biogeography now explores a great diversity of patterns in the geographic variation of nature — from physiological, morphological and genetic variation among individuals and populations to differences in the diversity and composition of biotas along geographic gradients. Given its interdisciplinary and integrative nature, biogeography is now broadly recognized as a unifying field that provides a holistic understanding of the relationships between the earth and its biota. Our abilities to develop more general theories of the diversity of life, and to conserve biological diversity may well rest on insights from the field of biogeography. Therefore, the International Biogeography Society (IBS) was founded as a non-profit organization in 2000 with the following mission:

- Foster communication and collaboration between biogeographers in disparate academic fields - scientists who would otherwise have little opportunity for substantive interaction and collaboration.
- Increase both the awareness and interests of the scientific community and the lay public in the contributions of biogeographers.
- Promote the training and education of biogeographers so that they may develop sound strategies for studying and conserving the world's biota.

International Biogeography Society

Interim Officers

The following interim officers have been elected to serve IBS until the close of the inaugural meeting in January of 2003.

President - James Brown

President Elect - Mark Lomolino

Vice-President for Conferences - Brett Riddle

Vice-President for Public Affairs & Communication - Paul Giller

Vice-President for Development & Awards - Larry Heaney

Secretary - Dov Sax

Treasurer - Glen MacDonald

Director-at-large - Vicki Funk

Director-at-large - Robert Hengeveld

Additional IBS founding members of IBS include:

| | | | |
|-------------------------|-------------------------|------------------------|-------------------------|
| Julio Betancourt | John Briggs | Robert Colwell | Michael Donoghue |
| Steven Gaines | Nicholas Gotelli | Chris Humphries | Pablo Marquet |
| David Perault | Klaus Rohde | Geerat Vermeij | Robert Whittaker |

**Project Support Provided by the National Science Foundation and the
National Center for Ecological Analysis and Synthesis.**

Symposia and Speakers

Symposium I: Dynamics of Species Diversity

Conveners: Dov Sax & Rob Whittaker

Robert J. Whittaker

"Reconciling dynamic hypotheses of diversity on islands and continents"

Pablo A. Marquet

"Space, time, and the emergence of diversity"

Stephen P. Hubbell

"Is ecological nature symmetric? Further explorations of the neutral theory of biodiversity and biogeography, and beyond"

Brad. A. Hawkins

"Progress towards understanding latitudinal diversity gradients"

Kaustuv Roy

"Diversity in the sea: past, present and (?) future"

Symposium II: Phylogeography and Diversification

Conveners: Vicki Funk & Brett Riddle

Daniel R. Brooks

"Representing reticulations in historical biogeography"

Vicki Funk

"Biogeography and evolution of the largest flowering plant family (Compositae): A southern hemisphere story."

Bruce S. Lieberman

"From animal origins to the Ice Ages: Macroevolution, biogeography, and the search for congruence."

Craig Moritz

"Historical biogeography and evolution of east Australian rainforest fauna inferred from phylogeography and bioclimatic modeling."

Brett R. Riddle & David J. Hafner

"Phylogeographic and cladistic biogeographic approaches to understanding biotic histories: Working towards a synthesis of perspectives."

Symposium III: Paleobiogeography

Conveners: Julio Betancourt & Rob Hengeveld

Chris Scotese

"Paleobiogeography and plate tectonics"

Paul Sereno

"Analyzing vicariance, dispersal, and regional extinction in deep time"

Steve Jackson

"The ecological niche through time"

Henry Hooghiemstra

"Dynamic Neogene and Quaternary biogeography of the neotropics: time series and time slices"

Julio Betancourt

Late Quaternary biogeography of the Atacama Desert

Symposium IV: Biogeography of the Sea

Convener: Jack Briggs

Brian Bowen, Luiz A. Rocha, D. Ross Robertson

"Phylogeography of Atlantic reef fishes "

John C. Briggs

"The evolutionary engine hypothesis"

J. Alistair Crame

"Pattern and process in marine biogeography: a view from the poles"

Geerat J. Vermeij

"Biogeography: its all about barriers"

Michael Rex

"Biogeographic patterns of species diversity and genetic diversity in the deep-sea benthos"

Symposium V: Biogeography Theory and Conservation Practice

Conveners: Larry Heaney & Mark Lomolino

Larry Heaney

"Biogeography, evolution and conservation in an oceanic island archipelago"

Thomas Brooks

"Conservation biogeography for birds and biodiversity"

Julie Lockwood

"Biogeography, invasions and homogenization of nature"

Victor Sanchez-Cordero

"Biodiversity, geographic variation and conservation of mammals in central Mexico"

Michael Rosenzweig

"Four applications of species-area relationships to diversity conservation"

Banquet Speaker

Lee Grismer

**"Biogeography in Baja California and the Sea of Cortés:
A Herpetofaunal Perspective"**

Frontiers of Biogeography Capstone

James H. Brown

International Biogeography Society
Inaugural Meeting: 4 - 8 January, 2003

| Time | 4-Jan-03 Day One | 5-Jan-03 Day Two | 6-Jan-03 Day Three | 7-Jan-03 Day Four | 8-Jan-03 Day Five |
|---------------|--|--|---|---|--|
| ? - 8:30 | | Breakfast (NC) | Breakfast (NC) | Breakfast (NC) | Breakfast (NC) |
| 8:30 - 9:00 | | Symposium 1a Dynamics of Species Diversity | Symposium 3a Paleo- biogeography | Symposium 4a Biogeography of the Sea | |
| 9:00 - 9:30 | | Break (C) | Break (C) | Break (C) | |
| 9:30 - 10:00 | | Symposium 1b con't | Symposium 3b con't | Symposium 4b con't | |
| 10:00 - 10:30 | | Poster Session 1 and Lunch (C) | Poster Session 2 and Lunch (C) | Poster Session 3 and Lunch (C) | |
| 10:30 - 11:00 | Arrival and Registration | Symposium 2a Phylogeography & Diversification | IBS Business Meeting II | Symposium 5a Biogeography Theory and Conservation Practice | Field excursion to Gold Butte Area |
| 11:00 - 11:30 | | Break (C) | <i>The Biogeographers</i> <i>Toolbox</i> | Break (C) | |
| 11:30 - 12:00 | | Symposium 2b con't | | Symposium 5b con't | |
| 12:00 - 12:30 | | Informal dinner (NC) | Pre-banquet Cocktail hour | Frontiers of Biogeography capstone speaker | |
| 12:30 - 1:00 | | IBS Business Meeting I | Banquet Dinner (C) | End of formal part of meeting | |
| 1:00 - 1:30 | | | Banquet speaker | | |
| 1:30 - 2:00 | | | | | |
| 2:00 - 2:30 | | | | | |
| 2:30 - 3:00 | | | | | |
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| 4:30 - 5:00 | | | | | |
| 5:00 - 5:30 | | | | | |
| 5:30 - 6:00 | | | | | |
| 6:00 - 6:30 | Opening | | | | |
| 6:30 - 7:00 | Reception (C) Hosted by Blackwell Publishing Ltd | | | | |
| 7:00 - 7:30 | | | | | |
| 7:30 - ?-?? | | | | | |

(C) = Catered

(NC) = Not catered

International Biogeography Society
Inaugural Meeting: 4 - 8 January, 2003

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|--|--|
| Saturday | Day One - 4 Jan 2003 |
| 8:30 AM - 6:00 PM 6:00 PM - 8:00 PM | Arrival and Registration Opening Reception - Hosted by Blackwell Publishing Ltd (catered) |
| Sunday | Day Two - 5 Jan 2003 |
| ? :? ? AM - 8:30 AM | Breakfast (not catered) |
| 8:30 AM - 10:00 AM | Symposium 1a; Dynamics of Species Diversity; 3 invited papers Conveners: Dov Sax & Rob Whittaker |
| 8:30 9:00 9:30 | Robert J. Whittaker "Reconciling dynamic hypotheses of diversity on islands and continents" Pablo A. Marquet "Space, time, and the emergence of diversity" Stephen P. Hubbell "Is ecological nature symmetric? Further explorations of the neutral theory of biodiversity and biogeography, and beyond" |
| 10:00 AM - 10:30 AM | Break (catered) |
| 10:30 AM - 11:30 AM | Symposium 1b; Dynamics of Species Diversity; 2 invited papers |
| 10:30 11:00 | Brad A. Hawkins "Progress towards understanding the global diversity diversity gradients" Kaustubh Roy "Diversity in the sea: past, present and (?) future" |
| 11:30 AM - 2:00 PM | Poster session 1 and Lunch (catered) |
| 2:00 PM - 3:30 PM | Symposium 2a; Phylogeography & Diversification; 3 invited papers Conveners: Vicki Funk & Brett Riddle |
| 2:00 2:30 3:00 | Daniel R. Brooks "Representing Reticulations in Historical Biogeography" Vicki Funk "Biogeography and Evolution of the largest flowering plant family (Compositae): A southern hemisphere story." Bruce S. Lieberman "From animal origins to the Ice Ages: Macroevolution, biogeography, and the search for congruence." |
| 3:30 PM - 4:00 PM | Break (catered) |
| 4:00 PM - 5:00 PM | Symposium 2b; Phylogeography & Diversification; 2 invited papers |
| 4:00 4:30 | Craig Moritz "Historical biogeography and evolution of east Australian rainforest fauna inferred from phylogeography and bioclimatic modelling." Brett R. Riddle "Phylogeographic and cladistic biogeographic approaches to understanding biotic histories: Working towards a synthesis of perspectives." |
| 5:00 PM - 7:00 PM | Informal dinner (not catered) |
| 7:00 PM - ? :? ? PM | IBS Business Meeting I |

International Biogeography Society
Inaugural Meeting: 4 - 8 January, 2003

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|---------------------|--|
| Monday | Day Three - 6 Jan 2003 |
| ?:?? AM - 8:30 AM | Breakfast (not catered) |
| 8:30 AM - 10:00 AM | Symposium 3a; Paleobiogeography; 3 invited papers Conveners: Julio Betancourt & Rob Hengeveld Chris Scotese "Paleobiogeography and plate tectonics" Paul Sereno "Analyzing vicariance, dispersal, and regional extinction in deep time" Steve Jackson "The ecological niche through time" |
| 10:00 AM - 10:30 AM | Break (catered) |
| 10:30 AM - 11:30 AM | Symposium 3b; Paleo-Biogeography; 2 invited papers Henry Hooghiemstra "Dynamic Neogene and Quaternary biogeography of the neotropics: time series and time slices" Julio Betancourt "Late Quaternary biogeography of the Atacama Desert" |
| 11:30 AM - 2:00 PM | Poster session 2 and Lunch (catered) |
| 2:00 PM - 3:30 PM | IBS Business Meeting II |
| 3:30 PM - 4:30 PM | The Biogeographers' Toolbox |
| 5:30 PM - 6:30 PM | Pre-banquet cocktail hour |
| 6:30 PM - ?:?? PM | Banquet Dinner (catered) and Lee Grismer - "Biogeography in Baja California and the Sea of Cortés: A herpetofaunal Perspective" |
| Tuesday | Day Four - 7 Jan 2003 |
| ?:?? AM - 8:30 AM | Breakfast (not catered) |
| 8:30 AM - 10:00 AM | Symposium 4a; Biogeography of the Sea; 3 invited papers Convener: Jack Briggs Brian Bowen "Phylogenetic patterns in Atlantic reef fishes" John C. Briggs "The evolutionary engine hypothesis" J. Alistair Crame "Pattern and process in marine biogeography: a view from the poles" |

International Biogeography Society
Inaugural Meeting: 4 - 8 January, 2003

| | |
|---------------------|---|
| 10:00 AM - 10:30 AM | Break (catered) |
| Tuesday | Day Four - 7 Jan 2003 continued |
| 10:30 AM - 11:30 AM | Symposium 4b; Biogeography of the Sea; 2 invited papers |
| 10:30 | Geerat J. Vermeij "Biogeography: its all about barriers" |
| 11:00 | Michael Rex "Biogeographic patterns of species diversity and genetic diversity in the deep-sea benthos" |
| 11:30 AM - 2:00 PM | Poster session 3 and Lunch (catered) |
| 2:00 PM - 3:30 PM | Symposium 5a; Biogeography Theory and Conservation Practice; 3 invited papers |
| | Conveners: Larry Heaney & Mark Lomolino |
| 2:00 | Larry Heaney "Biogeography, Evolution and Conservation in an oceanic island archipelago" |
| 2:30 | Thomas Brooks "Conservation biogeography for birds and biodiversity" |
| 3:00 | Julie Lockwood "Biogeography, Invasions and Homogenization of Nature" |
| 3:30 PM - 4:00 PM | Break (catered) |
| 4:00 PM - 5:00 PM | Symposium 5b; Biogeography Theory and Conservation Practice; 2 invited papers |
| 4:00 | Victor Sanchez-Cordero "Biodiversity, Geographic Variation and Conservation of Mammals in Central Mexico" |
| 4:30 | Michael Rosenzweig "Four Applications of Species-Area Relationships to Diversity Conservation" |
| 5:00 PM - 6:00 PM | Frontiers of Biogeography capstone speaker - James H. Brown |
| 6:00 PM | End of formal part of meeting |
| Wednesday | Day Five - 8 Jan 2003 |
| 8:30 AM - ??? PM | Field excursion to Gold Butte area |

1

GAP ANALYSIS OF THE FLORA OF WYOMING

Fertig W, R Thurston & WA Reiners

Since 1872, nearly 10% of the state of Wyoming has been protected in national parks, national wildlife refuges, wilderness areas, national recreation areas, research natural areas, Nature Conservancy preserves, and other locations categorized as Gap status 1 or 2 lands. Most of these areas were initially protected for their scenic, historic, or recreational values rather than for conserving biodiversity. Gap studies in Wyoming using 445 terrestrial vertebrate species and 42 land cover types have documented high levels of protection for species and cover types from montane and alpine habitats, but minimal protection for taxa from low elevation desert and grassland areas. Vascular plant species were not included in the initial Wyoming Gap Analysis, nor have they traditionally been assessed in other states. We used dot distribution and modeled habitat maps to conduct the first gap analysis of the flora of Wyoming in 2001. Over 208,000 unique location points were derived for 2,764 of the state's 2,803 vascular plant taxa from the digital specimen database of the Rocky Mountain Herbarium, the state natural heritage program, and available checklists for special management areas. These points were overlaid on the state gap land status coverage to determine the number and percentage of points of each species in the four gap land status categories. The same values were calculated with the state's flora subdivided by major biome types and ecoregions and for non-native and rare species. We found that vascular plant data mirrored the findings of previous gap analysis of Wyoming using terrestrial vertebrates and land cover types. Eighty-one percent of the state's flora was represented at least once in gap 1 or 2 areas and 56% of the species had over 10% of their known populations under protection. 88-97% of alpine and montane upland and wetland species were present in gap 1 or 2 lands, while only 72-78% of Great Plains, eastern deciduous forest, and intermountain desert steppe taxa were represented at least once. Only 15-26% of intermountain desert or Great Plains species had at least 10% of their populations protected. All of the state's ecoregions had more than 80% of their species represented at least once in gap 1 or 2 lands, but only the UT-WY Rocky Mountains and Southern Rocky Mountains had more than 40% of their species well protected (with over 25% of their total populations in gap 1 or 2 management). Rare species were twice as likely to be absent from the existing protected areas network as wide-ranging species and were especially poorly represented in the Northern Great Plains, Central shortgrass prairie, Black Hills, and Wyoming Basins ecoregions and grassland and intermountain desert steppe biomes. 57% of the state's non-native plant species were found at least once in gap status 1 or 2 lands. We found that vascular plants may be better suited for gap studies than vertebrates or land cover types because of the high numbers of species available, the mix of habitat generalists in the flora, and the large pool of available location data from herbarium and natural heritage program records and species checklists. By determining the protection status of individual plant species or aggregations of taxa, conservationists have a precise tool for identifying and prioritizing biome types, geographic areas, and suites of species that are underrepresented in the protected areas network.

2

INCORPORATING EVOLUTIONARY PROCESSES WHEN PRIORITIZING AREAS FOR CONSERVATION

Vázquez-Domínguez E, C Moritz, K Richardson & S Ferrier

Diverse efforts have been concentrated in the development of methods that can distinguish intraspecific units or areas for conservation purposes, usually considering richness of indicator taxa, endemics or higher taxa. Quantitative methods have thus been proposed to choose areas for protection that maximize representation of diversity, but few have explicitly address ways of ensuring persistence, i.e. the protection of the processes that sustain diversity. Thus, ways of accounting for those processes must be incorporated into present methods of conservation. One alternative approach is to use phylogeographic data from multiple species to represent patterns of historical isolation and evolutionary processes. We evaluated the performance of different measures of genetic information (Evolutionary Significant Units, ESUs; Phylogenetic Diversity, PD; and Nucleotide Diversity, Da) for the prioritisation of areas. Mitochondrial DNA phylogenies from tropical vertebrate (birds, lizards, frogs) and invertebrate (snail) endemic species from the Wet Tropics, in Australia, were used; analyses considered 12 biogeographical subregions as spatial unit. Subregions were selected iteratively to capture maximum genetic divergence (diversity) for each vertebrates and snail, by applying Ferrier's irreplaceability method to the ESUs and the environmental diversity (ED) algorithm to PD and Da data. ESUs, as expected for their coarser measuring of diversity, perform poorly relative to the other two measures. Da and PD, although moderately similar between them, both perform markedly well for accumulating genetic divergence, and much better comparatively than when using the species counts data. We show that information about phylogeographic and species diversity can be combined for developing strategies for conservation and prioritisation of areas at the level of communities and subregions.

3**ISLAND BIOGEOGRAPHY OF GENES AND SPECIES**

Vellend M

The two most fundamental levels of biodiversity, species diversity and genetic diversity, are seldom studied simultaneously despite a strikingly similar set of processes that underlie patterns at the two levels. Prominent theories of diversity on islands stress the roles of genetic drift and inter-island migration for genetic diversity (within species), and local extinction and colonization for species diversity. Since these processes are jointly dependent on population size (related to island area) and the movement of individuals among islands (related to island isolation), a positive correlation between species and genetic diversity across islands is predicted. Fourteen data sets compiled from the literature on birds, reptiles, mammals and plants in a variety of archipelagos provide strong support for this prediction; the median and weighted mean correlation coefficients between species and genetic diversity for the 14 data sets were 0.63 and 0.56, respectively. Island area appears to be the principal variable through which species and genetic diversity are related. Thus, species and genetic diversity do not vary independently, suggesting that the two levels of diversity are influenced by common processes. The species-genetic diversity correlation (SGDC) introduced here is a general relationship whose examination can enrich our understanding of biodiversity at a broad scale.

4**A FRAMEWORK FOR THE USE OF PHYLOGENIES IN COMMUNITY ECOLOGY**

Webb CO, DD Ackerly, MA McPeck & MJ Donoghue

As phylogenetic hypotheses become available for many groups of organisms, studies in community ecology can be informed by knowledge of the evolutionary relationships among coexisting species. In a recent review, we noted three primary approaches to integrating phylogenetic information into studies of community organization: (i) examining the phylogenetic structure of community assemblages, (ii) exploring the phylogenetic basis of community niche structure, and (iii) adding a community context to studies of trait evolution and biogeography. With this poster, we outline a general framework for incorporating phylogenies into community ecology that helps make explicit the empirical data needed from biogeographic, character evolution, and community structure sources.

5**A PHYLOGENETIC MODEL OF NESTED SPECIES-AREA RELATIONSHIPS USING PACIFIC ISLAND FLORAS**

Price JP & WL Wagner

Volcanic archipelagoes in the Pacific, having arisen de novo in isolation, accommodate biotas derived entirely from long distance dispersal and in situ speciation. Groups of species descended from each colonist thus constitute phylogenetic lineages that have diverged to varying degrees under similar spatial and temporal constraints. Previous work has examined the ecological and biogeographical correlates of species diversity in Hawaiian angiosperm lineages. The most notable trend is that species richness of lineages correlates negatively with the average geographic range size of constituent species. This logarithmic relationship serves as the basis for a model relating phylogenetic processes to species-range distributions and associated species-area relationships. New analyses of the Marquesas and Society Island angiosperm floras are testing this model. These archipelagos represent evolutionary provinces (regions defined largely by in situ speciation) that have similar climates, geologic histories, and source biotas to the Hawaiian Islands, yet differ from one another in total area. By partitioning the floras into lineages as done for the Hawaiian Islands, it is evident that differences in total species richness in these floras are more a function of speciation than colonization. Variation in province area most strongly influences the largest lineages, which account for large proportions of species in each archipelago system. All three provinces exhibit the negative log-linear relationship between average species-range size and species richness of lineages. A more detailed model proposed here links phylogeny with the nested structure of inter-provincial species-area relationships.

6**SPECIES-ISLAND RELATIONSHIPS OF VASCULAR PLANTS IN AN ARCHIPELAGO OF THE GEORGIAN BAY, LAKE HURON, CANADA**

Diver KC

This research analyzes variables other than traditional species-area and species-distance relationships influencing patterns of plant species richness on freshwater islands. Thirty-five islands in Ontario's Massasauga Provincial Park in the Georgian Bay of Lake Huron were sampled for herbaceous and woody species richness, woody species composition, and substrate heterogeneity. The dependent variable, species richness, is calculated for the overall data set and for subsets consisting of forest, shrub, and herbaceous species. Independent variables are tested for their relative impact on species richness using multiple regression models. Independent variables include island area, island perimeter, distance to nearest source pools, "effective distance," topographic variability, island density, island shape, and substrate variability. Richness and composition

of island species are compared across sites and among islands. The modeled relationships demonstrate the role of other variables in modifying the impacts of area and distance on island richness.

7

ARTHROPODS OF THE GRAND STAIRCASE - ESCALANTE NATIONAL MONUMENT: SURVEY METHODS, EFFORT CURVES, AND DISPERSAL TENDENCIES

Nelson CR, JC Shields, E Ahlstrom, H Barber & RW Baumann

We have been surveying the arthropods and other invertebrates of the Grand Staircase - Escalante National Monument (GSENM) in southern Utah near the site of these meetings in Mesquite, Nevada. Our major goal has been to assemble a baseline list of taxa for managers and researchers working on the GSENM. Additionally, the isolated and dissected nature of the many microhabitats there have allowed us to consider the distribution and dispersal tendencies of many taxa on the nearly 2 million acres which comprise GSENM. We have plotted species-effort curves for a variety of collecting techniques and have been summarizing local distributions in the total range for some taxa. With this poster we will introduce the Grand Staircase - Escalante National Monument as a study area, illustrate some of the more striking invertebrate taxa, and give indications as to which techniques are most successful in surveying the invertebrates of this biogeographically important area.

8

ASSEMBLY OF WOODY PLANT COMMUNITIES: PATTERNS IN FUNCTIONAL TRAIT DIVERSITY

Cornwell WK & DD Ackerly

A common model of community assembly posits that all species with the ability to disperse to a community pass through a series of filters. Those species that can pass through the filters form the observed community, and patterns in these species relative to the pool are used to infer information about the filtering process. Many studies have focused attention on the role of functional traits in allowing some species and not others to pass through these filters. A simple model suggests that if habitat tolerance structures communities, only species that possess a narrow range of traits can tolerate the conditions. Therefore, trait values will be under-dispersed relative to a null model. Alternatively, if competition structures communities, species with similar trait values will be excluded and the trait values will be over-dispersed. Here, we use such a community assembly framework to examine the patterns in functional trait diversity across a landscape. We compare several neighboring woody plant communities in the Santa Cruz Mountains, California spanning a wide topographically-mediated gradient in water availability. We measured and gathered from the literature nine functional traits for each species in the larger pool. The distribution of trait values for species in the observed community are compared to a null model of the trait values associated with species drawn at random from the larger pool. Functional trait diversity is greater at the more exposed, south-facing sites. This result could be indicative of alternative strategies for persisting through drought, suggesting that a simple dichotomy between competition and tolerance influencing the levels of functional trait diversity may be too simplistic.

9

SCALE MATTERS: THE CHANGING RELATIONSHIP BETWEEN DIVERSITY AND PRODUCTIVITY

Scheiner SM

The relationship between diversity and productivity remains a contentious issue in ecology. While some have asserted that the relationship is always hump-shaped, a comprehensive literature survey found no single relationship. This study extends those results by a comprehensive examination of the components of scale (grain, focus and extent) across a geographic hierarchy (e.g., spatially defined) and two, overlapping ecological hierarchies defined by formation and community types. I examined how species richness of terrestrial vascular plant varies with net primary productivity in 901 stands scattered across the state of Wisconsin, U.S.A. I found no single relationship between species richness and productivity. Instead, the relationship depends on the components of scale (grain, focus and extent) and hierarchy (ecological or geographic). For the state as a whole, the relationship was U-shaped. Increasing the grain resulted in the opposite pattern, the relationship went from U-shaped, to negative, to hump-shaped. With increasing focus, the relationship became negative. For the ecological hierarchy among community types, increasing the grain changed the relationship to negative, while for the among-formation hierarchy, increasing the grain eliminated any relationships. In contrast, increasing the focus among community types strengthened the U-shaped relationship, but similarly eliminated it among formations. Decreasing the extent – examining individual formations or communities types – generally eliminated the relationship, although a negative relationship was found for northern upland forests. These results have implications for how we study the effects of scale, its components, the effects of sampling bias, and the scale at which various causal mechanisms might be operating.

10**CITIES ARE NATURALLY SPECIES RICH?**

Kuehn I, S Klotz & R Brandl

Several analyses on different scales in different areas of Europe and North America show that cities harbour more plant species than their surroundings or non-urbanised areas. This is usually ascribed to be an effect of global change, namely (1) a high number of introduced alien species in cities, (2) a response to the intermediate disturbances theory due to human land use and (3) an increased habitat heterogeneity due to human influence. However, it is also very well documented that plant species richness is determined by natural environmental heterogeneity. We argue that cities are naturally species rich by answering the following questions: (1) Are native or just alien species more abundant in cities than to expect by random? (2) Which parameters influence these species richness patterns? (3) Are cities randomly distributed regarding these parameters? (4) Is there an additional city effect on species richness?

11**FREQUENCY DISTRIBUTIONS OF SPECIES' RANGES: ESTIMATING THE GEOGRAPHIC EXTENT OF HUBBELL'S METACOMMUNITY FOR NEW WORLD PLANT ASSEMBLAGES.**

Weiser MD, BJ Enquist, B Boyle, S Reddy & CO Webb

Understanding large-scale patterns of diversity is fundamental to disentangling the effects of local ecological interactions from larger-scale processes (e.g., ecological drift). The concept of the metacommunity, defined as "...all trophically similar individuals and species in a regional collection of communities" (Hubbell 2001, p. 5) is essentially synonymous with the concept of species pools, the species potentially present in a given sample area. While it is in practice impossible to create a global tally of all individuals of all species found within a given sample area, it is possible to estimate the geographic extent (species ranges) of species found within a given assemblage. Here we estimate the range sizes for species found within several New World plant assemblages collected by the late Alwyn Gentry. Specifically, we focus on latitudinal variation in the frequency distribution of range sizes of species found within samples. The geographic extent of species ranges are the spatial context of b-diversity, and the shape of the frequency distribution of species distributions should, all else equal and given neutral processes, not vary across latitude or species richness. To estimate species ranges we use Specimen.DQ, a Java utility which uses a series of distributed queries and data parsers to access on-line taxonomic and specimen locality information for a given list of plant species.

12**THE BIOMAPS PROJECT: GLOBAL PATTERNS OF VASCULAR PLANT DIVERSITY**

Mutke J, G Kier, H Kreft, A Hostert, D Rafiqpoor, W Küper & W Barthlott

Quantitative maps of spatial biodiversity patterns at continental to global scales are still scarce. Within the BIOMAPS project (www.botanik.uni-bonn.de/system/biomaps.htm) we produced continental to global maps of species richness of vascular plants, gymnosperms and mosses. Contrasting and correlating these with maps and data concerning the geodiversity (the diversity of the abiotic environment), close relations to, e.g., topodiversity and climate diversity are evident. Comparing global latitudinal gradients of vascular plant species richness at different longitudes we show possible influences of climate. Global centres of vascular plant species richness are Chocó-Costa Rica, the Tropical Eastern Andes and North-West Amazonia, Atlantic Brazil, Eastern Himalaya-Yunnan, Northern Borneo, and New Guinea. This is in contrast to the patterns found for the gymnosperms, where global maxima are concentrated in China, South-East Asia, Western and North-Eastern North America, and the Mediterranean.

13**CONTINENTAL PATTERNS OF PLANT DIVERSITY IN AFRICA**

Küper W, J Mutke, G Kier, H Sommer, D Rafiqpoor, H Kreft, & W Barthlott

The economic and scientific exploitation of biodiversity -but also its protection- requires an intensive knowledge about its spatial distribution and the underlying mechanisms. We aim to map continental patterns of plant species richness and endemism in Africa. Patterns of plant diversity are compared with geodiversity (e.g. precipitation, topography, temperature). Our analysis bases upon a unique dataset of African plant distributions. With far more than 4000 taxa, it is the actually largest and most representative dataset in respect to its taxonomic spectrum and its geographical representation. For the first time, analyses cover the Sahel and Sahara region. The distribution of these taxa has been modelled based on abiotic characteristics of the species habitats and were overlaid in a GIS. For the first time, the results from this taxon based approach have been validated in respect to their representativity using an inventory based dataset on the species richness of more than 420 African geographical units. Centers of species richness and endemism in Africa have been identified. Species richness patterns are highly correlated with waterbalance, seasonality and topodiversity, resulting in a clear latitudinal zonation of species diversity and very high values for afro-montane regions. Mean range size rarity (a proxy for

endemism) corresponds significantly to topographic diversity, as in the case of the Albertine Rift and especially the Cape region. Research is conducted within the new BIOTA Africa framework project (www.biota-africa.de).

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SPATIAL PATTERNS OF SPECIES RICHNESS AND GEOGRAPHIC RANGES IN AFRICAN PROTEACEAE: BAYESIAN HIERARCHICAL MODELS

Silander J, A Schmidt, A Latimer, S Wu, A Gelfand, T Rebelo & R Cowling

Understanding spatial patterns of species diversity and the distributions of individual species is a consuming problem in biogeography and conservation. The Cape Floristic Region of South Africa is a global hotspot of diversity and endemism, and the Protea Atlas Project, with some 60,000 site records across the region, provides an extraordinarily rich dataset to model biodiversity patterns. Model development focuses spatially at the one minute grid-cell scale (~37,000 cells total). We report on results for a subset of the Proteaceae (of ~330 species total). Using a Bayesian framework, we developed two stage, spatially explicit, hierarchical logistic regression models. The first stage models the potential probability of presence/absence for each species at each cell, given species attributes, site-level environmental data with species-level coefficients, and spatial random effects. The second level models the probability of occurrence given the human altered nature of the extant landscape. The posterior probability distributions for the model parameters were obtained via Gibbs sampling and MCMC methods. Results are mapped as the probability of presence/absence for each species across the domain. Summing yields the predicted species richness over the landscape. In a novel twist we introduce methods for integrating phylogeographic components to the modeling. Our results describe biogeographical patterns over the region remarkably well. The modeling takes into account heterogeneity in areal sampling intensity, provides quantification of uncertainty for all parameters, and accounts for spatial autocorrelations. The result is a more informative specification for the range or distribution of a species: a probability surface for an areal grid. This specification incorporates gaps in ranges and declining probabilities of p/a near distributional limits, yielding greater biogeographic realism. This approach provides predictions that can be tested empirically. We show which of the modeled response variables contribute significantly to the patterns of species presence/absence and richness. Finally by taking into account human transformations of the landscape one can predict how this has altered patterns of species distributions and richness, which has important conservation implications. The approach we develop has broad application to modeling biogeographic patterns elsewhere.

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DIVERSITY AND BIOGEOGRAPHY OF NEOTROPICAL VASCULAR EPIPHYTES - A GIS BASED APPROACH

Kreft H, W Küper, N Köster, J Nieder & W Barthlott

The present knowledge about structure, diversity, and phylogeography of neotropical forests is mainly based upon studies on woody plants, although non-woody plants contribute much to the high species richness and ecological complexity of these ecosystems. Epiphytes are an extraordinarily diverse life form and contribute up to 50 % of vascular plant species richness on a local scale. Biogeographical studies about this life form are scarce and based on insufficient data. Based on our own field studies and data compiled from literature the diversity and biogeographical relationships of 16 neotropical local epiphyte inventories with comparable size and collecting effort were analyzed. Floristic similarity was calculated among all local inventories using Sorensen's Index. Basic spatial parameters (e.g. altitudinal difference, distance, sum of altitudinal changes) were determined and included in the analyses. Floristic similarity shows strongest correlation with the difference in altitude between local floras. Mean floristic similarity is highest among lowland floras, whereas it is 44 % lower among montane floras and 78 % lower between montane and lowland epiphyte floras, respectively. Floristic overlap of epiphytes between local floras is about 20 % higher than of other life forms, probably due to the higher dispersal ability of epiphytes. Pteridophytes contribute significantly more to floristic overlap among local floras than Orchidaceae. Cluster and factor analyses reveal four distinct biogeographical groups. Lowland floras are clearly distinct from montane floras. Central and North Eastern Amazonian floras differ from other lowland floras which are situated in regions with high precipitation close to Andean foothills of Central America, Ecuador, and Bolivia. Northern Andean epiphyte floras are clearly separated from the four other examined montane floras, which are situated slightly higher above sea level. In an inventory based case study for Ecuador we show a strong altitudinal gradient with highest species richness and endemism in mid-elevation cloud forests. There is also a positive correlation between altitude and species-per-genus ratio. Species richness of epiphytes is positively correlated with annual precipitation in lowland epiphyte floras. We conclude that Andean orogenesis and the heterogeneity of abiotic factors are a major force in driving speciation and causing high alpha-diversity as well as high floristic heterogeneity in montane epiphyte floras. Data show that modern taxa with high evolutionary plasticity, such as Orchidaceae, contribute most to floristic heterogeneity. The lack of geographical barriers in Amazonia together with the comparatively high dispersal ability of epiphytes cause lower speciation rates and higher floristic similarity. We also conclude that the "explosive adaptive radiation" of Andean epiphytic taxa increases epiphyte diversity in adjacent lowland regions with high annual precipitation.

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MATHEMATICAL RELATIONSHIP BETWEEN RANGE SIZE AND SPECIES DIVERSITY

P Rodríguez, HT Arita, A Christen & J Sóberon

We show a fundamental mathematical relationship between the two basic units of biogeographic and biodiversity studies: geographic range and species diversity. In most studies, the structure of presence-absence matrices is analyzed using the marginal totals calculated either horizontally or vertically, that is, either concentrating on species diversity or on the distribution of species. We show that such procedures waste a great deal of information contained in the matrix and that can be retrieved only by considering simultaneously its row and column structure. It can be shown that for any collection of N sites in which S species distribute, the average proportional range size (p) of all species must equal the average proportional species diversity (q) of all sites. Moreover, the inverse of p or q equals beta diversity if this is measured using Whittaker's formulation. We show that biological and mathematical restrictions constrain the range of values that diversity and range size can acquire when analyzing the matrix by species and by sites. For example, species with restricted distributions can be present in sites with low or high species diversity, but the average species diversity within the ranges of widespread species is always low. Similarly, low-diversity floras and faunas can be formed by any combination of restricted and widespread species, but the range of species occurring in high-diversity sites are always, on average, small. We present empirical data for the North American fauna of mammals and show that: (1) areas of high diversity in general coincide with areas of concentration of species with restricted distribution, (2) consequently, beta diversity is higher in areas with high regional diversity. The mathematical constraints that we present have important implications for conservation programs based on the identification of hot-spots, on the assignment of value based on the rarity of species, or on the use of complementarity algorithms.

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THE EVOLUTION OF BETA DIVERSITY AMONG LESSER ANTILLEAN ANOLIS LIZARDS

Buckley LB & JE Roughgarden

We compare habitat use by Anolis lizard species pairs on two Lesser Antilles islands with differential topography using new GIS methodology. St. Kitts anoles segregate habitat with respect to perch height. Grenada anoles exhibit some local microclimate habitat partitioning, but observations over an expanded elevation breadth suggest that this partitioning is less pervasive than previously thought. Grenada exhibits a greater degree of broad scale horizontal habitat segregation than St. Kitts, with the larger species predominantly occupying mesic, higher elevation sites and the smaller species predominantly occupying xeric, lower elevation sites. Grenada's more equal distribution of habitat types may induce the evolution of habitat specialization, whereas St. Kitts' predominance of a single habitat type may result in local habitat partitioning rather than broad scale habitat specialization. An individual based model of anole population dynamics that includes thermal physiology offers a starting point to determine to what extent the evolution of beta diversity can be traced to physiological adaptation.

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SPATIAL AND TEMPORAL VARIATION OF ARTHROPOD COMMUNITIES ON THE COLORADO PLATEAU: IMPLICATIONS FOR USEFULNESS OF INVERTEBRATES AS INDICATORS OF ECOSYSTEM CONDITION

Graham TB, WI Williams, LJ Lingenfelter & KE Plengemeier

Pitfall, colored water, and flight interception traps are being used at a number of sites in southern Utah to collect invertebrates at riparian and upland sites. Sites have been sampled for two to four years, and most at least twice a year. Samples from a few sites have been sorted to order, and for some, species have been assigned to morphospecies as well. Large differences in the relative abundance of arthropod orders are evident between sites during the same sampling period, and at the same site in different months and different years. The implications of this variation in time and space of arthropod communities is discussed in relation to ecological functions.

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COMPARISON OF MICROCRUSTACEAN COMMUNITY ASSEMBLAGE IN EPHEMERAL WETLANDS AMONG THE ECOREGIONS OF OKLAHOMA

Cosyleon GB & S Schwartz

Isolated ephemeral wetlands are ubiquitous and provide habitat for many unique invertebrates. By definition these habitats are highly fragments in space and time and without connection across the landscape so that inhabitants exist in metacommunities. In spite of their global distribution, our knowledge of local and regional patterns of species distribution and richness within these habitats is weak. Given the intimacy of the terrestrial landscape with those shallow (<1 m) habitats we tested the hypothesis that terrestrial ecoregions can be used to predict community assemblages of aquatic microcrustaceans. Oklahoma's heterogeneous landscape (11 level III ecoregions) provides an excellent opportunity to assess this approach. In so doing we hope to determine the quantitative criteria with which to formulate protocols for protecting ephemeral aquatic ecosystems. In the spring of 2001 and fall of 2002 we samples 146 ephemeral wetlands

across Oklahoma. Species richness of the zooplankton was determined for each habitat and compared within and between ecoregions. Across all ecoregions there were 6.0 ± 0.23 species/pond with significant differences across ecoregions. A mean of 6.0 species/pond were found in the Central Oklahoma Plains ecoregion whereas 4.7 species/pond were found in the Southwestern Tablelands. Similar to other studies of species richness, common species were rare and rare species were common. Of the 95 species identified, 33% were unique to single habitats, another 10% to two habitats. Of the 146 wetlands sampled only two possessed as many as 15 species, while 88 wetlands had four to eight species, indicating limiting factors to community assembly. Invertebrate assemblages were distinctive among ecoregions based on a Bray-Curtis presence-absence similarity analysis. Although each of the 11 ecoregions could not be clearly discriminated, four geographically distinct assemblages could be readily distinguished: southeastern, northeastern, central, and far west. Data analysis continues but it is clear that terrestrial ecoregions can be a useful tool to classify and delineate ephemeral wetland invertebrate fauna. Invertebrates to monitor condition of ecosystems will be discussed.

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A BIOGEOGRAPHIC SURVEY OF NORTHEAST PACIFIC FISHES

Smith KF & M Behrens

Although the study of large-scale species distributions has traditionally focused on terrestrial systems, recent advances in technology have allowed biogeographers to also search for general patterns and processes in the marine realm. We compiled distributional data and life history information for 1035 species of coastal marine fishes native to the northeast Pacific Ocean between 0° and 75° N (Froese and Pauly 2002). Here we document patterns of body size, trophic position, and geographic range along gradients of depth and latitude. Although median geographic range size increased with increasing latitude, the pattern appeared to be a direct consequence of the disproportionately high number of shallow water species in tropical latitudes and the loss of these species from extratropical latitudes. All trophic levels exhibited a relatively high frequency of range endpoints around two prominent biogeographic boundaries, Punta Eugenia (27° N - 28° N) and Point Conception (34° N - 35° N). Herbivores, however, appeared to be more localized to tropical-mid temperate latitudes, while carnivorous species were ubiquitous across all latitudes. Teleost fishes exhibited an increase in maximum body length with increasing latitude while elasmobranchs did not, a pattern that may be explained by the differential number of carnivorous teleosts at high latitudes. Although it is beyond the scope of this report to uncover the mechanisms that drive these patterns, preliminary analyses suggest that the latitudinal distribution of coastal marine fishes is not a direct consequence of the annual range in contemporary sea-surface temperature or the presence of marine algae.

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HIGH VARIABILITY IN DIVERSITY AND ABUNDANCE OF VASCULAR EPIPHYTES WITHIN AMAZONIA

Köster N, H Kreft, V Schmit-Neuerburg, W Küper, J Nieder & W Barthlott

This study provides the first direct comparison of the epiphytic vegetation of two Amazonian lowland rain forests, situated more than 1000 km apart from each other. At Western Amazonian Tiptutini Biodiversity Station, Ecuador (220 m a.s.l.; $0^\circ 38' S$, $76^\circ 9' W$), we carried out a complete survey of all individual plants of vascular epiphytes in a 0.1 ha plot. Regarding the systematic composition, diversity, and abundance of vascular epiphytes, the results are compared to those of an equivalent survey of the 1.5 ha plot at Northern Amazonian Surumoni Crane Project, Venezuela (100 m a.s.l.; $3^\circ 10' N$, $65^\circ 40' W$). Additionally, structural parameters of host trees as well as the occurrence of epiphytic mosses and lichens, canopy soil, and ant gardens on epiphyte growing sites are analyzed. Centers of altitudinal distribution of all species are determined using collecting locality data of $> 30,000$ herbarium specimens. At Tiptutini, 8762 epiphytic individuals of 146 species and 24 families are found on 0.1 ha, facing only 1760 individuals of 80 species and 14 families on 1.5 ha at Surumoni. Calculated for quadrants of 25 m², an average of 241.8 individuals and 20.6 species is found in Tiptutini, whereas the average in Surumoni is 2.9 individuals and 1.2 species. Comparing individual and species numbers with various other neotropical 0.1 ha plots reveals an extraordinarily high alpha-diversity and abundance of epiphytes at Tiptutini. Araceae with 49 species (33.6 %) is the most diverse family at Tiptutini, whereas ferns with 7357 individuals (77.3 %) represent by far the most abundant taxonomic group. At Surumoni, Orchidaceae with 33 species (41.3 %) are most diverse, and Araceae with 949 individuals (53.9 %) are most abundant, represented predominantly by ant garden species and secondary hemiepiphytes, which begin their life cycle with contact to the ground. The vast majority of epiphytic individuals at Tiptutini is found on old, structurally diverse upper canopy trees with large dbh, whereas most of the individuals in the late successional forest of Surumoni grow on smaller trees. Most individuals in Tiptutini grow on humus accumulations or epiphytic mosses. At Surumoni, humus accumulations are virtually absent and pure bark is the most common epiphyte substrate, followed by ant gardens. Adaptations to the scarcity of nutrients predominate in Tiptutini among both epiphytic individuals and species, while adaptations to water deficiencies are more important in Surumoni. We consider the uneven distribution of precipitation throughout the year to be the major reason for the low epiphyte diversity and abundance at Surumoni. On the other hand, the high and evenly distributed annual precipitation at Tiptutini and the proximity to the Andes cause the higher number of species with a predominantly montane distribution and thus exceptionally high epiphyte diversity in the lowlands. Besides, the influence of paleoclimate, soil fertility, topography, and forest structure is discussed.

22**THE IMPORTANCE OF TROPHIC STATUS FOR TESTING COMMUNITY SATURATION PATTERNS ACROSS MULTIPLE LOCAL AND REGIONAL SCALES**

Russell R & S Wood

Plots of local species richness versus regional species richness have provided a foundation for attempts at understanding the influence of regional-scale processes on local species richness. Here, we present an analysis of local species richness of rocky intertidal communities on the west coast of the U. S. A., emphasizing the relationship between local species richness and niche theory. The concept of saturation of ecological communities – an upper limit to species richness imposed by local ecological interactions – theoretically should be most evident by analysis of local richness of functionally similar species across a range of regional species pool richnesses. Our analysis of an enormous empirical dataset, encompassing various trophic levels and functional types, indicates that saturation is not a common feature of all intertidal communities. Nonetheless, there are certain situations where saturation is evident. For example, even subdividing intertidal communities into such broad groups as 'algae' and 'invertebrates' uncovers saturation patterns, especially in the high intertidal. Likewise, dividing vertebrates into broadly defined feeding-guilds leads to more wide-spread saturation patterns encompassing larger local scales. These results challenge the evidently growing consensus that saturation is not a common feature of biological communities, and caution against the application of such tests to data that are a) not grouped in ecologically relevant ways, and b) are not taken at appropriate scales for the ecological interactions of interest.

23**BIOGEOGRAPHY OF ANTS (HYMENOPTERA: *FORMICA*) AND OTHER INVERTEBRATES IN RIPARIAN AND UPLAND HABITATS ON THE COLORADO PLATEAU**

Williams W & TB Graham

Riparian areas located on the Colorado Plateau are separated from one another by relatively vast upland habitats of a different environment. These riparian ecosystems in a semi-arid environment are recognized as having a high biodiversity relative to the surrounding landscape; perhaps up to 90% of organisms in an area are found in or at least use riparian areas. In this regard they may be considered islands of biodiversity among the upland mesas and plateaus. We have collected invertebrate samples from several hundred pitfall traps at both riparian and upland sites scattered on the northern Colorado Plateau. Sorting the samples to order has shown that more orders are represented in riparian areas. Also, more individuals are caught per sample in riparian areas. It is theorized that these biodiversity 'hotspots' act as source areas for the expansion and establishment of species into less hospitable environments such as upland habitats. We test this theory by observing the abundance of seven genera of ants at riparian, upland, and bench (an alluvial deposit located in riparian corridor; contains both riparian and upland vegetation) habitats on the Colorado Plateau. All seven genera were found at each site in some numbers. The cold climate specialists and opportunists, *Formica* and *Dorymyrmex* were more abundant in riparian habitats, while hot climate species *Pogonomyrmex*, *Pheidole*, *Monomorium*, *Camponotus*, and *Myrmecocystus* were more abundant in bench and/or upland habitats. The hot climate species have become established in upland areas because of their ability to withstand high temperature stress.

24**CRYPTOBIOTIC CRUSTS AND THEIR FAUNAL ASSOCIATIONS IN ARID LANDSCAPES: A MODEL FOR EXAMINING PATTERN AND PROCESS IN INSULAR SYSTEMS?**

Shepherd UL & SL Brantley

A recent issue of the Journal of Biogeography (2002) called for a new paradigm of insular biology. In this study, we assign the conceptual framework suggested by Watson (2002) to our study of cryptobiotic crust patches in two pinyon-juniper sites in Central New Mexico. We asked whether these designations shed new light on the patterns of microarthropod species richness we discovered or whether additional factors were needed to account for these patterns. Initially, we examined species patterns for the faunas observed in three types of crust patch: mossy, lichen, and mixed. These were composed primarily of mites and springtails, but other small invertebrates were also collected. We asked whether patch type, area of the patch, number of different habitat types within a patch, or distance to the next patch accounted for any differences seen in species number or composition. ANOVA results showed that significantly fewer species occurred on lichen than on the other two types (mixed 29, mossy 26, lichen 21, $p = 0.02$). No clear relationship emerged between area, distance, or habitat diversity and species richness or abundance, except among lichen crusts (numsp = lgpsize, $p = 0.0085$, $r^2 = 0.1687$ at site 1; $p = 0.0069$, $r^2 = 0.1860$ at site 2). Here we ask whether these patches, which operate on a different spatio-temporal scale from patches considered by Watson, are islands or fragments, old or young, and of high or low contrast. We believe this system is of particular interest because it represents an island type that Watson demonstrates is understudied, and hence offers special opportunities for considering the factors that contribute to species patterns in those systems.

25**EFFECTS OF SCALE AND RANGE STRUCTURE ON PATTERNS OF SPECIES RICHNESS AND COMPOSITION**

Rowe R

Placing local studies in their regional context enhances our understanding of the processes shaping biodiversity. Because these processes have spatial properties, models accounting for local patterns cannot simply be 'scaled up' to explain phenomena at larger spatial scales. This study integrates local and regional approaches in examining meta-community composition and species richness patterns of non-flying small mammals (e.g. shrews, chipmunks, & mice) along a series of elevational transects within the Uinta-Wasatch front, Utah (37° - 42°N, 109° - 113°W; North America). Elevational gradients offer a unique method of placing local patterns in a regional context (i.e. along an entire mountain range) while accounting for range expansion in 3-dimensional space. This study primarily addresses the following question: can the factors shaping the local composition of ecological communities and their species richness patterns be deduced from an examination of species regional spatial distributions? Intraspecific geographic variation in elevational distribution is quantified and examined with reference to competitive release, as well as geographic range structure and range position. I will present preliminary results on the relationships between the extent of a species' geographic and elevational range and outline additional hypotheses that will be investigated during this study.

26**THE LIMITATION OF LATITUDINAL GRADIENT ANALYSES - A REVIEW**

Jetz W

Over the past decades a primarily latitudinal perspective has dominated the quest for an understanding of large-scale variation in core ecological patterns, such as species richness and range size. The understanding in all these analyses has been that latitude may be a good surrogate for underlying deterministic variables such as temperature or productivity. However, the purely latitudinal perspective is not only crude, but also holds some severe biases and limitations. Here I analyze global environmental data at 0.5° resolution and both simulated and empirical distributions to visualize and evaluate the following: 1) The value of latitude as a surrogate varies markedly across continents, latitudes and climate variables; 2) Latitudinal bands differ in area; 3) Band sums are affected by underlying range size distributions 4) Limited degrees of freedom of latitudinal analyses inflate correlation coefficients and hamper analysis of collinear variables; 5) Spatial autocorrelation across latitudinal bands is particularly strong; 6) The degree of spatial autoreplication across latitudinal bands is especially high. These limitations together with increasing availability of high-quality distribution data and sophisticated geographic analysis tools support the use of a fully two-dimensional approach, if at all possible.

27**ISLANDS OF WATER, OCEANS OF LAND: ARE THE DIVERSITIES OF LARVAL DRAGONFLY COMMUNITIES CONSISTENT WITH ISLAND BIOGEOGRAPHY THEORY PREDICTIONS?**

Gaines KH

The middle tract of the Bitter Lake National Wildlife Refuge in southeastern New Mexico is an unusual ecological mosaic consisting of Chihuahuan Desert scrub and grassland interspersed with constructed wetlands, playa lakes, and dozens of saline water-filled sinkholes of varying sizes, geomorphologies, and water chemistries. Recent collections of over ninety-five species of adult dragonflies and damselflies (Order Odonata) suggest that this relatively small area supports the highest diversity of odonates in the state of New Mexico and perhaps the southwestern United States. Thousands of exuviae (final instar larval exoskeletons) were collected in the sinkhole complex in 2000 and 2001 in order to characterize the composition of each sinkhole's breeding assemblage, and data about water quality parameters and sinkhole surface area were analyzed to determine which ecological factors explain most of the observed variability in species diversity. While larger sinkholes did tend to support more diverse communities, the breeding success of many species appears to be limited more by larval stenotopy than by sinkhole surface area, as species with broader larval salinity tolerances successfully bred in most sinkholes visited by their adults, regardless of sinkhole size. Although the patterns observed at Bitter Lake are not entirely consistent with those predicted by the equilibrium theory of island biogeography and similar models, these theories may still offer some insight into the origin and maintenance of odonate diversity in this remarkable ecosystem.

28**GLOBAL PATTERNS OF MAMMAL SPECIES DIVERSITY, ENDEMISM, AND ENDANGERMENT: IMPLICATIONS FOR CONSERVATION**

Ceballos G

A major global environmental crisis caused by the explosive growth of human population is the loss of biological diversity. Extinction rates have steadily increased in the last two centuries, and hundreds of vertebrates have become extinct. In recent years there have been considerable efforts to develop methods to select priority areas for conservation in order to

select hotspots for conservation or to maximize the number of species represented in protected areas. Patterns of species distribution provide an underlying framework for determining priorities for conservation. Using a heuristic algorithm I analyzed the complementarity of 2 X 2 degree cells required to protect at least one population of the different groups of mammals; i.e. all species, endemic species, restricted species, and endangered species. Preliminary results indicate that relatively few areas dispersed across all continental land-masses are necessary to protect 70% of all species. However, more than 120 additional areas are needed to protect the additional species, which in general have very restricted geographic ranges.

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AN EXAMINATION OF SCALE IN RELATION TO TAXONOMIC RICHNESS PATTERNS

Field R, BA Hawkins & RJ Whittaker

If we are to progress further in understanding taxonomic richness patterns, we must examine how scale affects these patterns. To achieve this, we must first distinguish between different facets of what is commonly referred to as 'scale'. We must also be clear and explicit about the scales at which any given study is working. Here we develop a simple tabular framework, in which two key aspects of 'scale' are differentiated: grain size (or focus) and geographical extent. Using this framework, we examine how different hypotheses of the causes of richness patterns perform at different scales. To do this, we locate the results of a large number of published studies of diversity patterns within the scale framework. At macro-scales the overwhelming weight of evidence, across a broad range of taxa, supports the idea that contemporary climate exerts the primary control over richness patterns: in particular, the dynamic relationship between water and energy. At smaller scales, the story is more complex. We briefly consider some of the implications of these findings.

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LEAF EVOLUTION AND THE ASSEMBLY OF CALIFORNIA CHAPARRAL COMMUNITIES

Ackerly D

Do the functional characteristics of ecological communities reflect recent adaptive evolution or the sorting of 'preadapted' lineages from regional species pools? Answering this question is critical to determine the balance of ecological and evolutionary processes underlying the functional similarity of distantly related taxa occupying similar environments. Mediterranean-type ecosystems have played an important role in ancestral state reconstructions to test the hypothesis that leaf size and specific leaf area (the area to mass ratio, SLA) of California chaparral shrubs have undergone evolutionary reductions, accompanying the shift to a Mediterranean-type environment, relative to inferred trait values in non-chaparral ancestors. Eleven chaparral lineages were examined, using leaf trait data for over 450 taxa in three families (Ericaceae, Rhamnaceae, and Rosaceae), and recent molecular phylogenies. Ancestral states and transitions along selected phylogenetic branches were evaluated using maximum likelihood methods, incorporating phylogenetic uncertainty. Evidence of significant evolutionary reductions in leaf size and SLA were observed in only three of eleven lineages, one for leaf size and two for SLA. Furthermore, two of these lineages with significant evolutionary change are descended from North Temperate groups, while those with no change in leaf traits are descended from subtropical, Madrean ancestors. A preliminary survey of leaf and seed traits of the woody flora of coastal California also revealed that SLA is significantly lower and seed size significantly higher in Madrean-derived groups compared to North Temperate lineages. These results support the view that ecological sorting of lineages, combined with phylogenetic niche conservatism, has played a critical role in the assembly of the California chaparral, and the apparent convergence in functional traits of its species.

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PLEISTOCENE REFUGIA AND POST-GLACIAL EXPANSION OF THE SOUTHERN RED-BACKED VOLE (*CLETHRIONOMYS GAPPERI*) IN NORTH AMERICA

Runck AM & JA Cook

The mitochondrial cytochrome b gene was amplified from 97 individuals from 15 populations of the southern red-backed vole (*Clethrionomys gapperi*). Phylogeographic and coalescent analyses were employed to determine the evolutionary history of these populations across their North American distribution. The results revealed three major evolutionary lineages (uncorrected $p > 3.5\%$): an eastern (east of the Appalachians), western (west of the Cascades), and mid-western clade. The levels of sequence divergence among these clades suggest Pleistocene separation of refugial populations. These findings are consistent with the hypothesis that at least two southern refugia existed south of the major continental glaciers. The mid-western clade included a subclade that was restricted to higher latitudes in Canada and Alaska. These results suggest that post-glacial range expansion northward into Canada and Alaska occurred along a more interior route (east of the coastal ranges) rather than along a coastal route.

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PHYLOGEOGRAPHY OF ARCTIC HARES

Waltari E & JA Cook

The arctic and subarctic regions have been host to immense climate-driven changes in the Pleistocene and Holocene, due to the numerous glacial-interglacial cycles. Glaciations isolated populations and in some cases led to evolutionary divergence. Lower sea levels allowed the exchange of Asian and American biota across the crossroads known as Beringia, an immense high latitude refugium supporting many endemic species. These climate-driven events have led to intricate phylogeographic patterns in Beringian mammals. Arctic hares (*Lepus timidus*, *L. arcticus*, & *L. othus*) have a Holarctic and trans-Beringian distribution, and have been hypothesized to be closely related. To assess the phylogenetic and geographic structuring of these taxa, we sequenced or retrieved from Genbank a portion of the mitochondrial control region (673 base pairs) from 202 arctic hares. We also estimated historical population sizes and coalescence times, and looked for evidence of population expansion. The hypothesis that these three species are closely related is further supported. Historical demographic estimates indicate that coalescence times between arctic hare populations are greater than previously suggested, and that population sizes estimates vary, with non-Alaskan populations larger and more stable than Alaskan populations.

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GENETIC FOOTPRINTS OF DEMOGRAPHIC EXPANSION IN NORTH AMERICA, BUT NOT AMAZONIA, DURING THE LATE QUATERNARY

Lessa EP, JA Cook & JL Patton

The biotic consequences of climate change have attracted considerable attention. In particular, “the refugial debate” centers on the possible retraction of habitats to limited areas that may have served as refuges for many associated species, especially during glaciations of the Quaternary. One prediction of such scenarios is that populations must have experienced substantial growth accompanying climatic amelioration and the occupation of newly expanded habitats. We used coalescence theory to examine the genetic evidence – or lack thereof – for late Pleistocene refugia of boreal North American and tropical Amazonian mammals. We found substantial and concordant evidence of demographic expansion in North American mammals, particularly at higher latitudes. In contrast, small mammals from western Amazonia appear to have experienced limited or no demographic expansion following the Late Pleistocene. Thus, demographic responses to climate change can be tracked genetically and appear to vary substantially across the latitudinal gradient of biotic diversity.

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PHYLOGEOGRAPHY OF THE SOUTHEAST ASIAN STONE OAKS (*LITHOCARPUS*)

CH Cannon & PS Manos

We sampled three populations in Indochina: i) Yunnan province, China; ii) Pyin Oo Lwin area, Myanmar; iii) Northwestern Vietnam; two in western Borneo: i) Southwestern Sarawak; ii) West Kalimantan, Indonesia; two in central Borneo: i) North coastal Sarawak; ii) Northeastern Sarawak, Malaysia; and two in northern Borneo: i) Central Sabah; and ii) Northern Sabah, Malaysia. A phylogenetic reconstruction of chloroplast DNA sequence variation from numerous individuals of multiple species was used to determine geographic distribution of genetic diversity. A resampling scheme was used to determine the significance of these patterns at different hierarchical levels of the phylogeny. Results were compared to a previously published set of nuclear DNA sequence data. A high level of chloroplast sequence variation was found, which was divided equally between two major clades separated by four nonhomoplasious changes. One clade was confined to the island of Borneo, while the other was widespread. Strong geographic structure was observed in the chloroplast sequence variation. The Indochinese populations were much more closely related than expected, comparable to the highly endemic and isolated population on the western coast of Borneo. Conversely, individuals from the Kelabit Highlands were found to be more distantly related than expected. The highest levels of genetic endemism were observed in western Borneo. More geographic structure was observed in the Bornean clade than in the widespread clade, due to limited genetic diversity in the Widespread clade. Relatively weak geographic structure was found in the nuclear sequence variation: only populations in southern China and central Sabah were significantly related. The high levels of chloroplast genetic diversity and the persistence of an ancestral haplotype that is a single step away from a haplotype found in *Castanopsis* indicates the continuous presence of tropical rainforest in Southeast Asia throughout the evolutionary history of the genus (approx. 40 my). This conclusion is supported by the high frequency of numerous endemic types observed in every population and the relatively few number of “missing” haplotypes. This situation suggests both limited migration and limited extinction. In contrast, the nuclear genetic diversity contained less geographic structure, indicating that our taxonomic sampling among populations was unbiased and that gene flow mediated through both pollen and seed is less geographically restricted and contains less geographic structure than purely seed-mediated (chloroplast) gene flow. The most likely scenario suggested by the evidence involves four major patterns: 1) the widespread presence of an ancestral haplotype; 2) the large degree of separation (four nonhomoplasious base pairs) between the types found in the two major clades; 3) the concentration of derived types from both major clades found in central and northern Borneo; and 4) the molecular endemism found in each location. These patterns suggest four primary things about the population dynamics of *Lithocarpus* since the late Eocene; 1)

populations have either spanned the entire region throughout much of the genus' evolutionary history or substantial populations have persisted in both Indochina and Borneo with limited migration between them; 2) significant fragmentation has occurred subsequently between the Asian mainland and the Melasian island archipelago, leading to independent genetic diversification in both regions; 3) several locations possess significant independent histories, have experienced little migration and have never gone completely extinct; and 4) that the central highlands of Borneo have been reinvaded from the north and the west. The timing of these events is difficult to ascertain but probably predate the Quaternary Period, suggesting that although the recent ice ages might have affected the overall distribution of rainforest in Southeast Asia, it managed to persist in most regions even through the most dramatic drying events.

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THE PHYLOGEOGRAPHY OF THE MOUNTAIN WHITEFISH (*PROSOPIUM WILLIAMSONI*) AND PHYLETIC RELATIONSHIPS WITH THE ENDEMIC BEAR LAKE WHITEFISHES.

Miller BA, DK Shiozawa & RP Evans

Seventeen populations of whitefish were collected from the upper Missouri River, lower Columbia River, Colorado River, upper and lower Snake River, and Bonneville basins. The cytochrome B mitochondrial gene was sequenced, and phylogenies were generated assuming parsimony and maximum likelihood. Two distinct clades for whitefish were identified. Whitefish from the Colorado River, Snake River, and Bonneville basins comprise one clade and those from the Missouri River and Columbia River basins the second. Within these two clades, individual populations mainly clustered by drainage basin. The endemic Bear Lake whitefish complex, consisting of three recognized species, forms a separate clade, interior to the Colorado River, upper Snake River, and Bonneville Basin whitefish. Our data suggest that the mountain whitefish (*Prosopium williamsoni*) is comprised of four separate species. They also indicate that the mountain whitefish complex originated in the Upper Missouri system and separated into the two lineages early in the species' evolutionary history.

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A COMPARISON OF THE RANGE SHIFTS FOR MAMMALIAN ORDERS IN THE PLEISTOCENE

Lyons SK

Much attention has been focused on the response of species to the climate change associated with the last deglaciation during the Pleistocene. Generally, species respond in an individualistic manner to climate change and expand and contract their ranges independently; consequently, community composition is variable over time. I quantitatively assessed taxonomic trends in the ranges shift of Pleistocene mammals. Data on Pleistocene mammal assemblages from the FAUNMAP database were divided into four time periods (preglacial, glacial, holocene and modern). Range shifts were characterized by the change in the median position of the range from one time period to another, change in range size, and direction of the shift. Comparison of range shift parameters by taxonomic affinity yielded some interesting patterns. In all transitions, there were significant differences in the distances that mammalian orders shifted their ranges. There is a weak correlation with body size; larger bodied groups move longer distances in general than smaller bodied groups. During the Glacial to Holocene transition, there were significant differences in the degree to which species within different mammalian orders changed their range size. Change in range size was weakly correlated with body size; larger bodied groups had smaller changes in range size than smaller bodied groups. During the other transitions, there were few differences in the change in range size of different orders. There was little difference in the direction in which different orders shifted their ranges in all transitions. In general, mammalian orders differed mainly in the distance that their members shifted their range.

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CHANGES IN THE SOUTHERN ENDPOINTS OF DISTRIBUTION OF ROCKY INTERTIDAL SPECIES IN THE SOUTH EASTERN PACIFIC

Rivadeneira MM, M Fernández & PA Marquet

The current global warming scenario may generate substantial modification of species range sizes. The prediction that species geographic ranges should move poleward is largely supported by evidence from the northern hemisphere. To date, there is no information available for the southern hemisphere, so the generality of this pattern is unwarranted. Furthermore, while evidence for marine species is scarce, the data available suggest a pattern similar to that reported for terrestrial species, indicating an increase in the northern range of distribution of rocky intertidal species. However, the real magnitude of change has not been assessed, since geographical shifts were inferred from inter-decadal changes in species abundance. Thus, it remains unclear if the scale of the shifts in geographical boundaries in rocky intertidal species during last the century is within the 10's to 100's of kilometers observed in for terrestrial species. In this work we assess temporal (inter-decadal) changes in the southern endpoints of distribution of ten rocky intertidal mollusk species of the South Eastern Pacific, encompassing 24 ° of latitude (18°20'S to 42°35'S). Past and current southern endpoints of distribution of ten mollusk species were obtained from a literature review and field sampling, respectively. Changes in the position of southern endpoints were analyzed individually for each species as well as for the whole assemblage of intertidal species included in

the analysis. From ten species analyzed, nine presented significant changes in the southern endpoint of their distribution. Seven showed a reduction in their southern endpoint, while only two increased their southern endpoint of distribution. An estimate of the overall retraction of southern endpoints of distribution of more than 2° of latitude was made. Results indicate that changes have occurred at an average rate of 0.5° of latitude * 10 years⁻¹, regardless of past geographical position. Although most southern limits clustered around 33°S and 42°S, past southern range was poorly associated with the rate of change in southern endpoints. The overall retraction of southern endpoints of distribution of species contrasts clearly with previous findings reported for the northern hemisphere and contradicts predictions made under a global warming scenario. We discussed two non-mutually exclusive hypothesis in order to explain our results. This study suggests that the direction of global changes in the species' range distributions cannot be easily generalized. Further work in other taxa and systems are needed in order to provide a more comprehensive picture of the real effects of global climatic changes on species' geographical ranges.

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THE BIOGEOGRAPHY OF LOWER CENTRAL AMERICAN FRESHWATER FISHES

Smith SA & E Bermingham

The recent Pliocene development of the Lower Central American landscape (herein referred to as LCA) provides a useful setting to study the effects of regional and historical processes on the assembly and maintenance of biological communities. This is particularly true for primary freshwater fishes, whose dispersal is thought to be entirely dependent on direct connections between drainage basins. We described biogeographical provinces using the known distributions of the LCA primary and secondary freshwater fishes, and analyzed faunal relationships in light of the climatic and geological history of the LCA landscape. The biological turnover among biogeographical provinces was quantified in order to determine the relative permeability of barriers to dispersal, and our results indicate that the filtering effect of barriers changes in space (distance from source populations) and over time. The historical assessment facilitated understanding of landscape changes having positive or negative impact on the probability of fish dispersal and thus, on the evolution of the LCA freshwater fish fauna. Our study permits the inference that regional processes such as immigration and speciation probably play an ongoing role in the maintenance of LCA freshwater communities, and that the species composition of these communities is not simply a consequence of ecological interactions among community members.

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MOLECULAR PHYLOGEOGRAPHY OF THE ENDEMIC HAWAIIAN SUCCINEIDAE (GASTROPODA: PULMONATA)

Rundell RJ, BS Holland & RH Cowie

The endemic Hawaiian Succineidae represent an important component of the exceptionally diverse land snail fauna of the Hawaiian Islands, yet they remain largely unstudied. We employed 663-bp fragments of the cytochrome oxidase I (COI) mitochondrial gene to investigate the evolution and biogeography of 13 Hawaiian succineid land snail species, six succineid species from other Pacific islands and Japan, and various outgroup taxa. Results suggest that: 1) species from the Island of Hawaii are paraphyletic with species from Tahiti and Japan, and this clade may have had a Japanese (or eastern Asian) origin; 2) species from five of the main Hawaiian islands form a monophyletic group, roughly following the progression rule, which states that species from older islands are basal to those from younger islands; no geographic origin could be inferred for this clade; 3) succineids from Samoa are basal to all other succineids sampled; 4) the genera *Succinea* and *Catinella* are polyphyletic.

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COMPLEX BIOGEOGRAPHICAL PATTERNS IN THE NORTHERN HEMISPHERE MOUNTAIN PLANTS OF ANDROSACE (PRIMULACEAE)

Schneeweiss GM, P Schöenswetter, S Kelso & H Niklfeld

Androsace, the second-largest genus within Primulaceae, is distributed mainly in northern hemisphere mountain ranges from S. W. Europe to W. North America. Based on species-richness and the occurrence of the most primitive group within Androsace, sect. *Pseudoprimula*, East Asia is thought to be the centre of origin, from where Androsace spread east- and westwards. Recent molecular phylogenetic analyses, however, reveal a more complex biogeographical pattern in the evolution of Androsace. A phylogenetically well-defined group (informally called the Aretia-group) comprises the amphiberingian sect. *Douglasia* (often separated as its own genus *Douglasia*), the exclusively European sect. *Aretia* and sect. *Vitaliana* and the high-arctic Siberian *A. triflora* of sect. *Chamaejasme*. Although formally the distribution area of this group can be termed as arctic-alpine, there are some significant distribution gaps: The Aretia-group is absent in the European arctic as well as in the Asian mountain ranges from Caucasus to Himalaya. We propose the following biogeographical model: The Aretia-group has evolved in Europe (from Tertiary woodland species?) with the ancestors probably in East Asia. From there, it reached the amphiberingian region either via a northern Asian connection latter disrupted by the Pleistocene ice-shields or via long-distance dispersal and subsequent east- and westward migration. This model of a northern Asian connection outside the Asian mountain ranges disrupted during the Pleistocene ice-ages might be applicable to similarly disjunct distribution patterns seen in some groups of *Primula* (Primulaceae) or in *Ranunculus glacialis* s. l. (Ranunculaceae).

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BIOGEOGRAPHY OF THE FLORA OF ARMENIA. THE OLD WORLD CASE.

Saghatelyan A

Investigation of some rich and diverse floristic complexes of subtropical mountainous regions of the Old World is of a special interest since the genesis of the contemporary plant cover of the Temperate Euro-Asia is highly associated with such Tertiary refugia. In North-Subtropical floras we find some relic species which have survived Pleistocene Ice Ages and again have inhabited vast Euro-Siberian territories, released from ice sheets in Holocene. Many of those species became the sources for new speciation and adaptive radiation. Caucasian mountainous junction along with some Mediterranean, West, Central and especially East Asian regions is one of such essential objects for study of the history of the biota of Palearctic. Another great paleo-geographical event – digression of the Tethys Ocean and the Frontal – Middle Asian land masses emergence, establishes their floristical connections with some deserts of the Southern Gondwanaland, through low mountain land belts of the mountains of Eastern Africa (examples – floristical connections of the West-Central Asian Chenopodiaceae, many bulb Lilioideae, Iridaceae, Zygophyllaceae). And the third important consequence of the previous events – the development of the Ancient Mediterranean flora, or “Flora Ephedra” according to M. G. Popov. This flora is characterized with the large scope of endemic genera (sections in Apiaceae, Brassicaceae, Asteraceae, Fabaceae, Limoniaceae), rich of peculiar examples of xeromorphogenesis, different, but as amazing, as those in great deserts of the US South-West. To reveal all this threads coming from different directions and different periods is a wonderful task for a biogeographer. At the same time, biogeographical method is an important test for systematics: “good” species have “good” areas. On the basis of data obtained during previous decade of investigation of biodiversity of Armenia I developed a check-list of the vascular species of Armenian flora. It contains 3320 species and their area-diagnoses, and is an attempt to provide a substantial view of the distribution throughout the area of the vascular plants known to grow in Armenia. Publication of many recent South-West Asian and European “floras” and systematic monographs, gave me an opportunity to study species distribution, generalize and analyze out knowledge on the fitostroma of the Republic. Every “Flora” is a space-time section in the continuous process of the origin and transformation of natural floras and communities. This process of evolution of firostroma always goes along with and by means of speciation. Armenia is situated in the Minor Caucasus, which constitutes the volcanic Armenian Highland, at an altitude ranging from 1400 to 13419 ft. The boundary between two floristic Subkingdoms of the Holarctic Kingdom – the Boreal and the Ancient Mediterranean passes through this territory. Northern minor part of the Republic belongs to the Caucasian Province of the Boreal Subkingdom. Here passes the Southern edge of the distribution of many of the Eucaucasian endemics (*Pseudovesicaria digitata*, *Muscari pallens*), as well as many of the Euro-Siberian (*Daphne mezereum*, *Padus racemosa*) and Arcto-Mountainous (*Poa alpina*) species. All the floristic districts of Armenia to the South of V. Achurjan, Lori, Ijevan, belong to the Armeno – Atropateno – Zagrossian Province (Saghatelyan 1997) of the Frontal Asian Subregion. On the volcanic Mt. Aragatz and other high elevation to the North of it, Armenian endemics prevail (*Scilla rosenii*), while Altropatenean (*Acantholimon sahendicum*, *Tulipa florinskii*) and Atropateno-Zagrossian (*Fritillaria kurdica*) species are largely represented on the southern mountain ranges. A huge number of endemics are typical for the larger Armeno-Atropatenean part of the Republic. Most of them belong to young Tehyan genera with mighty sources of xerophilous speciation in the Middle East, such as *Astragalus* (112 sp. In Armenia), *Centaurea* (43 sp.), *Verbascum* (29 sp.); Iran-Middle Asia: *Cousinia* (19 sp.), *Allium* (36 sp.), *Tragopogon* (18 sp.). But the largest one is the list of Atropatenean xerophytes: *Gaillonia szovitsii*, *Acantholimon fedorovii*, *Veronica microcarpa* – altogether 204 endemics. Being situated near mesophilous refugia of the Euxinian and the Hyrcanian Provinces, the flora of Armenia also contains 99 mesic relicts which have survived on specific ecotopes (*Allium paradoxa*, *Zelkova carpinifolia*). The florogenetical correlation of species of the 3 Subdominions of the Holarctic Kingdom in the flora of Armenia is as follows: Circumboreal – 643 species, Submediterranean – 892 species, Ancient Mediterranean – 1519 species.

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THE PHYLOGEOGRAPHIC SIGNATURE OF PERIODIC RANGE FRAGMENTATION AND DISPERSAL: MOSAIC-LIKE GENETIC STRUCTURE IN A SOUTH-EAST ASIAN FRESHWATER COMPLEX OF CATFISH, *HEMIBAGRUS* SP. (SILUROIDEA: BAGRIDAE)

Dodson J, F Lecomte, F Colombani & PKL Ng

The geographical history of South-east Asia has created the potential for extensive admixture during low sea levels of genetic groups of an obligate freshwater fish (the river catfish, *Hemibagrus* sp) isolated during periods of high sea levels. During Pleistocene glacial maxima, the sea level was lower than at present and the islands of the Sunda shelf (Sumatra, Borneo and Java) and the Asian mainland were connected by lowlands traversed by rivers. We sequenced part of the mitochondrial DNA cytochrome *b* gene of 370 fish collected from 25 rivers associated with the 3 major drainage systems purported to have existed during Pleistocene low sea levels; the Siam River collected tributaries from the present-day Gulf of Thailand to the southern tip of Peninsular Malaysia, the North Sunda River collected tributaries from present day southeast Sumatra and west Borneo. Phylogenetic reconstruction based on mitochondrial haplotypes revealed 2 major clades with highly distinct genetic structures; a phylogeographically well-structured clade composed of several species whose geographic distributions are constrained to the headwaters of specific contemporary drainage systems and a second clade composed of nested hierarchies of monophyletic groups of lowland catfish that are far less geographically constrained. Very few of these subclades are associated uniquely with contemporary rivers. Rather, their distribution exhibits a strong regional

component reflecting dispersal within and between historical drainage basins, with the more divergent and hence older subclades showing the most extensive distributions. Considerable geographical overlap occurs among these subclades. This second major clade thus exhibits a unique mosaic-like genetic structure whereby genetically divergent groups of lowland catfish occur in sympatry with widely separated locations on the present-day landscape. Low sea levels apparently aided the repeated dispersion and mingling of distinct genetic groups of lowland catfish on various occasions as opposed to the isolation, divergence and geographically distinct distribution of highland catfish. This process has led to the periodic accumulation of genetically distinct catfish groups within present-day rivers and may well be responsible for generating the astounding biodiversity of the region's contemporary freshwater fish fauna.

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LATE QUATERNARY BIOGEOGRAPHY OF THE ATACAMA DESERT AND PACIFIC SLOPE OF CENTRAL ANDES

Betancourt JL, J Quade, C Latorre, J Rech, KA Rylander, C Holmgren, C Placzek, & A Maldonado

The hyperarid Atacama Desert extends along the Pacific Andean slope from the southern border of Peru (18°S) to Copiapó, Chile (27°S). There has been considerable speculation about biodiversity gradients with latitude and elevation, patterns of endemism, and the relative influences of tectonic and climatic events on the biogeography of the Atacama Desert. The region's hyperaridity is due to the extreme rainshadow of the high Andes, which blocks the advection of tropical/subtropical moisture from the southern Amazon Basin; the blocking influence of the semi-permanent South Pacific Anticyclone, which limits the influence of winter storm tracks from the south; and the generation of temperature inversion at ~1000 m by the cold and north-flowing Humboldt Current, which limits inland (upslope) penetration of Pacific moisture. The South Pacific Anticyclone has been anchored against the westward bend in the South American continent throughout the Neogene, the Andean orogeny doubled the average elevation of the central Andes during the past 10 million year, and the Humboldt Current reached its present intensity by early Pliocene. Throughout the Quaternary, the most pervasive influence on Atacama biogeography has been millennial-scale changes in the frequency and seasonality of the scant rainfall, and associated shifts in plant and animal distribution with latitude and elevation. Today, and throughout the Quaternary, precipitation variability in both summer and winter is modulated by Pacific SST gradients and associated upper-air circulation anomalies. These anomalies promote either greater spillover of summer moisture from the Amazon and Altiplano to the east, or conversely, greater penetration of winter storm track from the southwest. During the past five years, we have mapped modern vegetation gradients developed a number of paleoenvironmental records, including vegetation histories from fossil rodent middens, ground-water levels from wetland (spring) deposits, and lake levels from shoreline evidence, along a 1600-km transect (16-26°S) in the Atacama Desert. A strength of this paleoclimate transect has been the ability to apply the same methodologies across broad elevational, latitudinal, climatic, vegetation and hydrological gradients. This paleoclimatic transect is being used to reconstruct the histories of the South American tropical and extratropical rainfall belts, precisely at those elevations where average annual rainfall wanes to zero. The focus has been on the transition from sparse, prepuna vegetation into 'absolute desert', an expansive waterless terrain that extends from just above the coastal fog zone (800 m) to more than 3000 m in the most arid sectors. The current margins of 'absolute desert' represent one of the few places on Earth where life and water episodically overran lifeless habitat, and our ongoing research can pinpoint these places and times with great accuracy. Our paleoecological data have matured and can now be used to test theories and empirical models about the influence of present and past climate on both physical and biological systems in the Atacama.

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THE FATE OF CLADES IN A WORLD OF RECURRENT CLIMATIC CHANGE – MILANKIVITCH OSCILLATIONS AND EVOLUTION

Dynesius M & R Jansson

Variations in the Earth's orbit with periods of 10-100 thousand years (kyr) (Milankovitch oscillations) have led to recurrent and rapid climatic shifts throughout Earth's history. The climatic shifts cause changes in the geographical distributions of clades, which we term orbitally-forced range dynamics (OFD). The magnitude of ORD varies geographically. For example, ORD is higher at high latitudes and lower in areas with steep slopes. Climatic shifts cause extinction, splitting, and merging of gene pools and clades. They select among individuals and clades for traits enhancing the ability to survive the shifts in situ and to establish new populations. There is also non-adaptive sorting caused by the large geographical variation in ORD, as only gene pools that are in the right place when climate shifts survive. Clades that have survived climatic shifts during at least one entire period (100 kyr) of the longest significant Milankovitch oscillation we name β -clades. The products of more recent cladogenesis (<100 kyr ago) are α -clades, which are always nested with a β -clade. We conclude that ORD may promote α -clade formation, but curb rates of β -clade formation. In areas with little ORD where gene pools persist longer (without going extinct or merging), clade splits and divergence may accumulate leading to high rates of β -clade formation and β -anagenesis (evolutionary change persisting >100kyr). We suggest ORD to be a fundamental factor in evolution and that geographically and temporally varying levels of ORD cause a number of patterns. High ORD should lead to (1) low numbers of β -clades, β -clades with (2) large ranges, (3) low levels of genetic divergence and (4) little within-clade geographical subdivision, organisms with (5) high vagility and (6) low specialization, (7) high proportions of β -clades formed by polyploidization, and (8) little β -anagenesis. High ORD should also make biotas less vulnerable to many human activities.

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STABLE ISOTOPE, BIOGEOGRAPHIC, AND GROWTH RATE EVIDENCE FOR PLEISTOCENE TEMPERATURE CHANGE IN THE GULF OF CALIFORNIA: ANALYSIS OF LAST INTERGLACIAL *PORITES* COLONIES, BAJA CALIFORNIA SUR, MEXICO

Fenberg PB, DH Goodwin & KW Flessa

The biogeographic distributions of coral reefs are largely restricted to the warmer tropical regions of the ocean. Temperature and, to a lesser extent, light intensity appear to be the most important environmental conditions governing reef development. Therefore, the presence of fossilized coral reefs can give an indication of past oceanographic conditions. It has generally been confirmed that sea-surface temperatures during the last interglacial were slightly warmer than today. Given these conditions, it becomes apparent that climate change since the last interglacial could have had an impact on the geographic range distributions of coral reefs due to altered growth rates. This is especially true for corals growing at or near the water temperature threshold for reef development. How did late Pleistocene climate change affect the growth of the zooxanthellate coral *Porites californica* in the Gulf of California? Today, the northernmost reefs in the Gulf of California occur south of La Paz at Cabo Pulmo (~23N). During the last interglacial (Marine isotope substage 5e, ~125,000 ybp), however, *P. californica* reefs developed approximately 400 km farther north near Loreto at Punta Bajo (~26N). Previous studies suggest that winter temperature is the controlling factor limiting the growth of *Porites* spp. The modern winter isotherm at Cabo Pulmo is ~20C, while the modern winter isotherm at Loreto is ~17C. This difference suggests that during the last interglacial, winter temperatures at Loreto were ~3C warmer than today. To evaluate this idea, we determined annual oxygen isotope profiles from last interglacial specimens of *P. californica* from Punta Bajo and estimated their annual growth rates. Specimens of *P. californica* from Punta Bajo were cut parallel to the axis of maximum growth and sampled for annual oxygen isotope (d18O) variation. The average maximum (winter) d18O value is -2.58 per mil. After correcting for changes in the d18O composition of the water during the last interglacial, the minimum sea surface temperature (SST) was 19.6C; 2.1C warmer than the modern winter isotherm at Loreto (17.5C). Average annual growth rates of last interglacial corals from Punta Bajo were 12.4mm/yr, whereas the annual growth rate of modern corals from the Loreto area today is 6.5mm/yr. These data suggest that warmer winter temperatures in the southern Gulf of California during the last interglacial enhanced growth rates at Loreto, thus allowing the development of massive *P. californica* colonies.

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GLOBAL PATTERNS IN ENDEMISM EXPLAINED BY PAST CLIMATIC CHANGE

Jansson R

I hypothesized that global patterns in numbers of range-restricted, endemic species are caused by variation in the amplitude of climatic change occurring on time-scales of 10-100 thousand years (Milankovitch oscillations). The smaller the climatic shifts, the more likely that paleoendemism survive, and that diverging gene pools persist without going extinct or merging, favoring the evolution of neoendemism. Using the change in mean annual temperature since the last glacial maximum estimated from global circulation models, I show that the higher the temperature change in an area, the fewer endemic species of mammals, birds, reptiles, amphibians, and vascular plants it harbors. This relationship was robust to variation in area (for areas >10,000 km²), latitudinal position, extent of former glaciation, and whether or not areas are oceanic islands. Past climatic change was a better predictor of endemism than annual temperature range in all phyla except amphibians, suggesting that Rapoport's rule (i.e., species range-sizes increasing with latitude) is best explained by the increase in the amplitude of climatic oscillations towards the poles. Globally, endemic-rich areas are predicted to warm less due to greenhouse-gas emissions, but have denser human populations and are more rapidly deforested than endemic-poor ones, suggesting that conservation actions are urgent.

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RECONCILING HOST-ASSOCIATION WITH PHYLOGEOGRAPHY: PATTERNS OF GENETIC VARIATION IN THE TROPICAL NUDIBRANCH GENUS *PHESTILLA*

Fauci A, BS Holland, & MG Hadfield

Substrate-specificity is common among marine invertebrates and is often related to settlement-cues. Nudibranchs of the genus *Phestilla* occur throughout the tropical Pacific and include seven species, all of which feed and reproduce on specific scleractinian corals. The planktonic larvae of *Phestilla* spp. require a host-specific chemical cue to metamorphose and settle onto their species-specific host coral. *Phestilla sibogae*, *P. lugubris*, *P. minor*, and *Phestilla* sp. 1 occur on species of the genus *Porites*, the dominant reef building coral in Hawaii; *Phestilla* sp. 2 on *Goniopora* spp.; and *P. melanobranchia* on the ahermatypic corals *Tubastrea* spp. A 654-base-pair fragment of the mitochondrial cytochrome c oxidase I (COI) gene and a 404-base-pair fragment of the ribosomal 16S gene were sequenced for six species of *Phestilla* from Guam, five species from Palau and three species from Hawaii. Neighbor-joining, maximum-likelihood, and maximum-parsimony trees were produced. Morphological species of *Phestilla* were usually separable based on COI and 16S sequences, but the inferred phylogeographic pattern was complex and highly structured. *Phestilla minor* and *Phestilla* sp. 1 appear to comprise a cryptic species complex, and cluster according to host-corals and geographic locations. Although species of *Phestilla* do not form monophyletic clades according to host corals, there is an apparent relationship between the mtDNA phylogeny and

substrate-specificity. The inferred molecular phylogenies suggest that host-associated speciation may have played an important role in the evolution of this genus.

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NEW PERSPECTIVES ON THE ORIGIN AND DIVERSIFICATION OF HAWAIIAN TREE SNAILS (ACHATINELLIDAE: ACHATINELLINAE) BASED ON MOLECULAR EVIDENCE

Holland BS & MG Hadfield

Tree snails of the endemic subfamily Achatinellinae represent an important component of the diverse land snail fauna of the Hawaiian Islands. In an effort to address long-standing, fundamental questions regarding the biogeography and evolutionary relationships within the Achatinellinae, we used 675 base-pair fragments of the cytochrome c oxidase 1 (CO1) gene to reconstruct the phylogenetic relationships among the extant representatives of the subfamily spanning its range from five Hawaiian Islands. Outgroups included terrestrial pulmonates from eleven families from Polynesia, Micronesia, New Zealand, Asia, Africa, N. American and Europe. The phylogeographic pattern inferred for Hawaiian tree snails does not agree with the traditional biogeographic theory of a Maui origin of the Achatinellinae, and a revised mtDNA substitution rate, age of the lineage, and novel pattern of island colonization are proposed. Morphological species were genetically distinct, and the phylogeographic pattern inferred for the subfamily generally followed an island-progression pattern with several instances of back-colonization and generic polyphyly.

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THE INFLUENCE OF LATE QUATERNARY CLIMATE CHANGE ON THE ECOLOGY AND THE EVOLUTIONARY DYNAMICS OF SMALL MAMMALIAN HERBIVORES.

Smith FA

Animals respond to climatic change by adapting or by altering distributional patterns. How an animal responds is influenced by where it is positioned within its geographic range; the probability of extirpation is increased near range boundaries. Our objective is to characterize the relationship between the magnitude and rapidity of temperature shifts, the position in the geographic range, and the type of elucidated response. By examining different species at different locations within their range over the late Quaternary, and estimating the thermal thresholds at which various responses occurred, we may be able to better predict the impacts of anthropogenic climate change on mammalian populations. Here, we examine the impact of Holocene climatic fluctuations on a small mammalian herbivore, the bushy-tailed woodrat (*Neotoma cinerea*), at a variety of locations within the western United States. This is a topographically complex region, with climatic variability responding to the behavior of the large-scale features of the global climate system. It is also a region rich in paleoclimatic data, much of it from fossil packrat (=woodrat) middens. We measure the radiocarbon-dated fossilized pellets contained in abundance within middens, and from them estimate body size (a technique validated in earlier work). Overall, we find that woodrats adapted to the frequent temperature fluctuations of the late Quaternary by altering body size; they were larger during the glacial and smaller during the warm conditions of the middle Holocene. Yet morphological change is only one potential response of mammals to climate change. Local extirpations may be likely at the periphery of the range where animals exist at the edges of their thermal and ecological thresholds. Animals might also evolve novel innovations, that is, radical life history, physiological or ecological solutions to particularly rapid or drastic climate change. We identify several time periods when changes in environmental temperature exceeded the adaptive flexibility of *N. cinerea*. A smaller-bodied species, the desert woodrat (*N. lepida*) apparently invaded lower elevation sites in Idaho and Utah during the mid-Holocene, despite being behaviorally and physically subordinate to *N. cinerea*. Analysis of contemporary patterns of body size and thermal tolerances for both woodrat species suggests this was because of the greater heat tolerance of *N. lepida*.

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PHYLOGENETIC RELATIONSHIPS OF THE GENUS *PTYCHOCEILUS* (TELEOSTEI: CYPRINIDAE) AND CLOSELY RELATED TAXA AND THE BIOGEOGRAPHIC IMPLICATIONS

Houston DD, DK Shiozawa & MF Whiting

There are four extant species of pikeminnows in the genus *Ptychocheilus*. Two competing hypotheses show relationships that differ only in their polarity. We used molecular data from the cytochrome *b* gene along with morphological characters to infer relationships within this genus using parsimony analysis. The results show that the genus as it currently stands is paraphyletic and should include *Mylopharodon conocephalus*. We also hypothesize about possible dispersal routes that would allow for the current distributions of these species.

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PHYLOGEOGRAPHY OF SPECKLED DACE, RHINICHTHYS OSCULUS, IN THE INTERMOUNTAIN REGION, U.S.A., BASED ON MITOCHONDRIAL DNA SEQUENCES

McKell MD, DK Shiozawa & RP Evans

Speckled dace (Pisces: Cyprinidae) were collected from 51 populations in the Colorado and Snake river systems and the Bonneville and Lahontan drainage basins. The mitochondrial DNA (mtDNA) gene, cytochrome b, was amplified and sequenced, and parsimony and likelihood methods were used to generate phylogenies. The haplotypes grouped into one of three clades, each representing major mitochondrial lineages. One clade consists of populations in the Lahontan and western Bonneville basins. A second clade includes populations of the Snake River and northern Bonneville basins, including some Bear Lake haplotypes. Within this clade haplotypes are widely shared. The third clade indicates a close relationship between populations in the Sevier River of the southern Bonneville Basin and populations in the Colorado River system. Two haplotype sets are basal to this clade. One is from the Virgin River of the lower Colorado, and the other is from Bear Lake of the Bonneville Basin. These Bear Lake haplotypes are distinct from the Bear Lake haplotypes in the second clade. Phylogenetic placement of these Bear Lake haplotypes indicates ancient gene flow between Bear Lake and the Virgin River of the Colorado, suggesting a former drainage connection between these systems.

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A POPULATION GENETIC PERSPECTIVE ON THE EVOLUTION OF MONTANE GRASSHOPPERS

Thompson DB

The diversification of montane species of grasshoppers in Western North America, particularly in the genus *Melanoplus* (Orthoptera: Acrididae), and the general pattern of evolution of reduced flight capability in montane grasshoppers are biogeographic patterns that can be explored from the perspective of microevolution and population divergence. To elucidate the evolutionary processes that may be involved in clinal or allopatric speciation of montane grasshoppers, I quantify phenotypic plasticity and morphological and quantitative genetic divergence within a wide ranging species (*Melanoplus sanguinipes*) that occupies low elevation habitats and montane meadows throughout Western North America. Using field and lab measurements of six populations, I have studied flight capability, local adaptation, and phenotypic plasticity in response to temperature and diet, all of which are factors that are hypothesized to affect speciation and patterns of diversification in the face of environmental change.

Phenotypic plasticity or norms of reaction may enhance or retard the evolution of morphological and life history adaptations to cool, short season environments in mountaintop populations relative to populations occupying warm, long season environments. In sampling replicated high and low elevation populations of *M. sanguinipes*, I have found extensive genetic divergence in all traits measured including body size, relative wing size, relative femur size, development rate, and maturation time. Although all of these traits also exhibit phenotypic plasticity in response to rearing temperature and diet, there is no evidence of generalized adaptive norms of reaction across all populations. Rather, there is genetic divergence in norms of reaction between montane and low elevation populations indicating that extensive phenotypic plasticity has not precluded evolutionary divergence of populations separated by distances of 50 to 90 km. Mountaintop populations are genetically divergent in body size and allometry, having smaller adult size and smaller wings and legs, adjusted for body size, in comparison to nearby low elevation populations. Montane orthopteran species typically have reduced flight capability (I have measured flight time) and in many cases have evolved wingless forms. I have measured natural selection (through female fecundity) of relative wing size in montane environments and found no evidence of a trade-off between investment in wing or leg size and female egg-laying. Instead, there was natural selection of larger relative wing size in females. Overall, I have uncovered substantial genetic divergence in morphology, allometry, and developmental norms of reaction across a relatively small geographic scale indicating the potential for rapid divergence among grasshopper populations for suites of traits that affect locomotion and life history. Surprisingly, many of these patterns do not match widely held hypotheses about local adaptation and selection of reduced flight capability. This and other evidence indicates that genetic correlations among traits and genetic/developmental constraints contribute to the patterns of population divergence hypothesized to contribute to speciation in grasshopper taxa.

53PHYLOGEOGRAPHY OF *DIPDOMYS MERRIAMI*, INCLUDING A NESTED CLADE ANALYSIS OF POPULATION HISTORIES.

Alexander LF, BR Riddle & DJ Hafner

Alternative phylogeographic hypotheses that explain the current population structure of the Merriam's kangaroo rat (*Dipodomys merriami*) are evaluated by analyzing combined sequence data from a relatively slowly-evolving mtDNA gene, CO III (699 bp), as well as a portion of the control region (491 bp) from 96 individuals collected throughout the distribution. The separation of a southern Baja lineage of *D. merriami* occurs at the earliest node with approximately 6% sequence

divergence. Previous comparative phylogeographic studies have suggested that the separation of northern and southern forms of several species of mammals from the Peninsular Desert of Baja California can be placed within a middle Pleistocene timeframe congruent with the hypothesized mid-peninsular seaway of about 1 MYA. Using the mid-peninsular signal as a rough calibration point for the same geographic separation in *D. merriami* allows us to postulate that all remaining phylogeographic structure within *D. merriami*, which includes 4 additional clades (northern Baja peninsula, western continental, northern Chihuahua and southern Chihuahua) has developed within the last million years. Nested clade analysis is a statistical tool that uses an intraspecific cladogram estimation procedure to help distinguish between the effects of population history, such as past fragmentation, and the effects of recurrent evolutionary forces. A minimum-spanning haplotype network of the COIII sequence data set for 93 *D. merriami* individuals was constructed and the null hypothesis of a random geographical distribution of all clades within a nested clade was tested. Four clades had significant values that resulted in a statistical inference (2 of past fragmentation, 1 of restricted gene flow with isolation by distance, and 1 of range expansion with long distance colonization). Of these, the most interesting is the Chihuahuan subclade, which demonstrated statistical evidence of past fragmentation, consistent with isolation in the vicinity of the Nazas River in Durango, Mexico and the east-west extension of the Eastern Sierra Madre in Durango and Coahuila, Mexico.

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FROM A TREELESS PRAIRIE TO AN URBAN FOREST: THE TRANSFORMATION OF THE BIOGEOGRAPHY OF NORMAN, OK, 1820-2002

Fagin T & M Brown

Within the past two centuries, grassland ecosystems across the globe have faced rapid destruction as 10,000 years of ecology has succumbed to the plow and urban sprawl. The Great Plains of North America stands at the forefront of this transformation, where in the span of little more than half a century, an estimated 30 million North American bison (*Bison bison*) and 50 million pronghorns (*Antilocapra americana*) were slaughtered, and countless other prairie species, such as the Great Plains wolf (*Canis lupus nubilus*), black-tailed prairie dog (*Cynomys ludovicianus*), and lesser prairie chicken (*Tympanuchus pallidicinctus*), have been extirpated from all but a handful of locales. Currently, there are 55 threatened or endangered species in the United States, and an additional 728 species of concern. Prior to European settlement, the North American prairie covered more than 350 million ha in the Central Lowlands. Today, mere remnants of this once vast biome remain, as more than 90% of the tallgrass prairie, once the largest contiguous ecosystem in North America, now the most endangered, has been converted to intensive agriculture. The mixed and shortgrass prairies, also devastated by the effects of land conversion for agriculture, have fared slightly better, with some 20% of these native grasslands remaining. In this poster, we document the rapid transformation of a tiny facet of the North American prairie through the analysis of various historical documents. Surrounded by a matrix of monoculture agriculture, remnant grasslands, and post oak-black jack oak (*Quercus stellata*-*Q. marilandica*) woodlands of the prairie and an extreme example of environmental transformation linked to settlers perceptions of an ideal environment. We show that in a period less than two centuries, the entire biogeography of Norman has changed as an aggressive and belligerent campaign of faunal extirpation coupled with a seemingly innocuous policy of tree planting and fire suppression has irreversibly altered the landscape of one of the last vestiges of the prairie frontier.

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THE FRAGILE WEB: ANNET, ISLES OF SCILLY, UK

Randall RE

Annet is a low, small, uninhabited granitic island in the Isles of Scilly archipelago (Fig. 1). The island rises are overtopped by waves during most severe winter storms. It is known that in the early nineteenth century Annet was used for grazing sheep and cattle (Woodley 1822) and bracken was cut for fuel. In the 1970s, the most abundant plant species was thrift, which formed a hummocky turf over most of the island (Fig. 2). There were also large patches of bracken on deeper soils that cover larger areas every year as a result of changing land-use. Around seabird nests, Yorkshire Fog was plentiful. Only 53 species of higher plants have been recorded on Annet. A significant date in the biogeographic history of Annet was 1887 when the steamer Castleford, laden with 450 head of cattle bound for London from Montreal, went aground (Fig. 3) near Annet on May 27th (Bowley 1990). The crew was saved and they offered £2 per head of cattle rescued alive. Many cattle were buoyed up with timbers and swam to Annet. Hay from Cornwall rich in Yorkshire Fog was imported to feed the cattle until they could be shipped to the mainland. As a result of severe overgrazing and a plentiful supply of seeds hay, Yorkshire Fog invaded the spaces between thrift tussocks and has continued to spread at the expense of native plants unchecked by the light grazing of local domesticates. Bracken has also ceased to be cut for fuel and is also spreading where soil is deep enough. As thrift tussocks senesce, they blow out in strong winds and some of the friable substrate is lost before being recolonised (Fig. 4). On deeper soils *P. bracken* invades as described by Watt (1947, Fig. 5). During the last 30 years, the area dominated by thrift has declined by around 30%, and bracken has increased, covering 10% of the original *Armeria* areas. It now seems to be limited in expansion by soil depth. The other 20% has been taken over by Yorkshire Fog. The knock-on effects of vegetation changes are faunal and human. The substrate in which Puffins nest is disappearing; other seabird nest-sites are also declining and environmental tourism is becoming less rewarding year-on-year. Some blame at least can be laid on the changing environment of Annet and the Castleford disaster of 1887.

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NATURAL VS. MAN-MADE EPHEMERAL POOLS: PRELIMINARY ANALYSIS OF USE BY TWO CONGENERIC PAIRS OF FAIRY SHRIMP ON THE COLORADO PLATEAU (AND A LITTLE BEYOND)

Graham TB

Ephemeral pool habitat on the Colorado Plateau consists primarily of two types: natural pools in exposed sandstone, and small floodwater catch basins constructed by damming small drainages. These ephemeral aquatic habitats contain a number of branchiopod crustaceans, including at least five species of fairy shrimp. I've found *Streptocephalus dorotheae* only in constructed stock pond and catch basins: *S. texanus* has been found only in rock pool (pothole) habitats. *Branchinecta packardii* has also been found only in rock pools in southeastern Utah, while *B. lindahli* occurs primarily in constructed pools in southeastern Utah, but has been found in both man-made and natural habitats in southwestern Utah. These differences may be due to different dispersal abilities, water chemistry affinities, or stochastic events.

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LAND IMPRINTING SPECIFICATIONS FOR RESTORING THE BIOGEOGRAPHY OF DEGRADED TERRAIN

Dixon RM & AB Carr

The no-till method for seeding of plants called land imprinting has been under development in Tucson, Arizona since 1976. Through ecological weed control, land imprinting has restored perennial grasses to 20,000 hectares of degraded rangeland in southern Arizona since 1980. Imprinting accelerates the secondary succession of plant types past the weed stage through superior control of rainwater at the soil surface. Early imprinters were massive machines with large diameter rollers that were designed to operate on the rocky, brushy terrain of southwestern deserts. Newly designed imprinters have smaller diameter rollers and are easier to transport. Some can work on 2:1 slopes and even steeper. Simple seeders, directly driven from the imprinting roller, deliver complex mixes of native seeds to the roller top where they are carried forward, dropped on the soil surface and then imbedded in the imprint surfaces. V-shaped imprints funnel resources downward where they can work in concert to germinate seeds and establish seedlings. Based on more than 2 decades of field experience, land imprinting specifications have been developed for ecological restoration and sustainable agriculture. These include general imprinter and seeder design specifications that will help to insure success of revegetation projects. Also, experienced fabricators can use these specifications as a guide for constructing state-of-the-art seeding imprinters. Beyond the arid regions of Arizona and California, the theory and practice of land imprinting are almost terra incognita, even though these advancements in science and technology have great potential for restoring the biogeography of severely degraded terrain, globally.

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GEOGRAPHIC RANGE CONTRACTION OF DECLINING SPECIES: EXAMINING THE INFLUENCE OF CROPLANDS AND HUMAN POPULATION DENSITIES.

Channell R

Previous studies on range contraction of declining species have suggested that the geographical distribution and the spatial dynamics of the extinction generating forces are the primary factors in shaping the remnant distributions that we currently observe. Large-extent anthropogenic changes of the environment have been tentatively identified as the source of these extinction generating forces. In this research, I examine whether the regions in which species persisted (remnant range) had less anthropogenic disturbance than other regions in which the species had once existed (historical range). I used percent of landscape converted to croplands and human population density as measures of human disturbance. I examined the distributions of 127 species (32 African species, 36 Australian species, 57 Eurasian species, and 40 North American species). 91 of the 165 examined species persisted in regions with lower rates of conversion to cropland ($p = 0.080$, binomial test). 96 of the 165 examined species persisted in regions with lower human population densities ($p = 0.007$). However, if we look within the individual regions a different pattern emerges. Species from North America (25 of 40 species persisting in regions with lower agricultural disturbance, $p = 0.040$, binomial test; 28 of 40 species persisting in regions with lower human population densities, $p = 0.005$, binomial test) and Eurasia (34 of 57 species persisting in regions with lower agricultural disturbance, $p = 0.055$, binomial test; 35 of 57 species persisting in regions with lower human population densities, $p = 0.024$, binomial test) demonstrated significantly greater persistence in regions with lower agricultural disturbance and lower human population densities. African (15 of 32 species persisting in regions with lower agricultural disturbance, $p = 0.430$, binomial test; 14 of 32 species persisting in regions with lower human population densities, $p = 0.188$, binomial test) and Australian (17 of 36 species persisting in regions with lower agricultural disturbance, $p = 0.566$, binomial test; 19 of 36 species persisting in regions with lower human population densities, $p = 0.434$, binomial test) species showed no significant tendency to persist in regions of lower agricultural disturbance or lower human population density. These results suggest that the species in the different regions are reacting differently to similar environmental stresses. This difference in species response maybe the dependent on the environments and populations on which the environmental stresses are imposed.

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PHYLOGEOGRAPHY OF AN INVASION: WHITE AND RIO GRANDE SUCKERS IN THE UPPER RIO GRANDE, NEW MEXICO.

McPhee MV

White sucker (*Catostomus commersoni*) was introduced into the upper Rio Grande in the 1930s and has been expanding its range within the basin ever since. Concurrently, the native Rio Grande sucker (*C. plebeius*) has been displaced from mainstem habitats and is now limited to isolated headwater populations. I hypothesize that both a consequence of and a factor contributing to the white sucker's success in the Rio Grande is its ability to maintain large, connected populations. Conversely, I hypothesize that the Rio Grande sucker's small body size and preference for smaller streams has resulted in smaller, more isolated populations, contributing to its susceptibility to extirpation in the Rio Grande. Accordingly, mtDNA sequence variation was used to compare phylogeographic structure of the two species across their ranges in New Mexico. Genetic diversity of Rio Grande sucker showed considerable geographic structure and low connectivity between populations, as expected for a small stream-dwelling fish. Consistent with both a history of introduction and higher dispersal capacity, white sucker genetic diversity showed very little geographic structure. However, white suckers in the Rio Grande basin contained considerable genetic diversity for an introduced population, with the presence of two distinct clades suggesting multiple source populations. These genetic data are one part of a larger study investigating how interspecific differences in geographic history and ecological traits are facilitating displacement of the Rio Grande sucker by the white sucker.

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THE DEVELOPMENT AND VALIDITY OF USING SIMPLE SEQUENCE REPEATS (MICROSATELLITES) TO ASSESS THE GENETIC VARIATION AND THE GENOTYPIC DISTRIBUTION OF *MONTASTRAEA FAVEOLATA*

McNutt CA, GM Wellington, & T Snell

We report on the development and potential application of short tandem repeat motifs (microsatellites) to evaluate the genetic variation and genotypic distribution of the scleractinian coral *Montastraea faveolata* along Florida Keys National Marine Sanctuary (FKNMS). Genomes of most eukaryotic organisms have thousands of loci that contain short nucleotide repeat motifs. Microsatellite markers offer increased resolution of population differences due to their random nature and high frequency of mutation over more conservative techniques such as allozymes. Once developed, this type of marker can be easily used to test for genetic variation between spatially separated populations at both small and large scales. Currently, we have approximately 200 microsatellite inserts that were isolated from a library screen using a (GA)₁₂ and (CA)₁₂ fluorescently labeled probe. To date we have isolated 30 inserts and three of these have yielded consistent polymorphic markers in *M. faveolata*. We anticipate developing at least four to five additional loci, which will be used to assess the degree of genetic variation from three spatially separated reefs along the FKNMS. The possibility that population substructure exists along the Florida Keys has not been explicitly tested for many of the major reef-building corals, including *M. faveolata*. Population structure may be an important process affecting coral populations. Understanding the dynamics of this structure may be vital for helping managers make decisions about the placement of marine reserves, the type of marine reserve employed, or even the feasibility of current marine reserves along the Florida Keys National Marine Sanctuary. In addition to assessing genetic variation between reefs, the relationship between spatial and environmental variables and how they interact with the genotypic distribution of *M. faveolata* will also be evaluated. Differences in environment and spatial features (e.g. currents and geographic barriers) have the potential to influence populations through several processes, including natural selection or differences in gene flow. The genotypic distribution will be evaluated using the "assignment test", which assigns individual genotypes to particular source populations based on where the genotype has the highest probability of occurrence. To test for the influence of environmental and spatial variable on the genotypic distribution of *M. faveolata* both variables will be analyzed simultaneously using multivariate analysis to determine their combined influence on the occurrence of genotypes across the FKNMS.

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COMPARATIVE PHYLOGEOGRAPHY OF THE ENDEMIC PHILIPPINE FRUIT BATS *PTENOCHIRUS JAGORI* AND *PTENOCHIRUS MINOR*

Roberts TE

The fruit bat genus *Ptenochirus* (Pteropodidae) contains only two species, *P. jagori* and *P. minor*. *Ptenochirus jagori*, the larger of the two, is endemic to the Philippines and widespread in the archipelago, while *P. minor* is endemic to the islands of the Greater Mindanao faunal region within the Philippines. I sequenced fragments of the mitochondrial genes ND2 (700 bp) and cytb (800 bp) in 75 individuals of *P. jagori* and 39 individuals of *P. minor* and constructed statistical parsimony networks to determine the relationships among sequenced haplotypes. Sampling locations cover eleven different islands, including two sites on Mindanao. In *Ptenochirus minor*, there is a substantial break between two subnetworks, one formed by individuals from Biliran and Leyte and one from the two sites on Mindanao; within these subnetworks there is no geographic structure. *P. jagori* is largely unstructured through the whole archipelago, with relatively high levels of gene flow. Mitochondrial mismatch analysis suggests that this species has undergone exponential population growth in the past; this is weakly supported by nested clade analysis, which suggests contiguous range expansion in parts of the *P. jagori* haplotype

network. Geographic structure in *P. jagori* is comparable to that shown for the non-endemic bat *Cynopterus brachyotis* in the Philippines; both *P. jagori* and *P. minor* are less strongly structured than another Philippine endemic, *Haplonycteris fischeri*.

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PHYLOGEOGRAPHY OF NIGHTSNAKES (*HYPSIGLENA TORQUATA*): WITH IMPLICATIONS CONCERNING BIOGEOGRAPHY OF WESTERN NORTH AMERICA

Mulcahy DG

Currently, there are approximately 17 subspecies recognized within the species *Hypsiglena torquata*, many concordant with major biogeographic regions of western North America; the rest endemic to islands off the coast of Baja California. As part of my doctoral research—comparative phylogeography of several western North American squamates—I am studying the phylogeography and systematics of this species complex using molecular markers. I currently have tissue samples for approximately 161 Nightsnakes, have sequenced an approximately 850 base pair section of the mitochondrial (mtDNA) gene ND4 for over 80 individuals, encompassing all mainland and three island subspecies, with additional sequences of *Eridiphas*, and other *Leptodeirins* as outgroup taxa. Preliminary phylogenetic analyses of these sequences suggest five major clades exist within *Hypsiglena torquata*. The most basal split supports *H. t. janii*, the Texas Nightsnake, as sister to all other *Hypsiglena*. Within the rest of *Hypsiglena*, my data indicate four additional clades. One, referred to as the “Coast clade,” is comprised of samples from the Cape of Baja to the Bay Area of California. The second, referred to as the “Desert clade,” includes all desert samples from the Sonora, Mojave, Great Basin deserts and the Colorado and Columbia plateaus. The remaining two clades consist of: 1) samples from Sinaloa, Mexico (*H. t. torquata*) and 2) unique haplotypes from San Bernardino Valley, in Cochise County, Arizona. Here, I focus on the relationships among these major clades, with emphasis on how they correspond with the major biogeographic regions of western North America.

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COMPARATIVE PHYLOGEOGRAPHY OF THREE CALIFORNIA REPTILES

Feldman CR & GS Spicer

The center of California is characterized by a large expanse of prairie and marsh (now agricultural plots) entirely enclosed by mountains. Because valley habitat is unsuitable for much of the region's mesophilic fauna, a number of species display a ring-like distribution, restricted to the surrounding hills and mountains. This ring-like distribution has long interested biologists, and several vertebrate taxa have been examined via the phylogeographic approach. We use mitochondrial DNA sequence data from the ND4 gene and three linked tRNAs to reconstruct the population histories for three, syntopic, circum-valley reptiles: *Contia tenuis* (sharp-tailed snake), *Diadophis punctatus* (ringneck snake), and *Elgaria multicarinata* (southern alligator lizard). We compare our phylogeographies to each other and to patterns seen in other co-distributed California vertebrates. In addition, we employ a molecular clock hypothesis to roughly correlate the timing and geographic location of cladogenic episodes with known historical events.

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LATITUDINAL VARIATION IN GENETIC DIVERSITY IN PACIFIC SARDINE (*SARDINOPS SAGAX*) AND NORTHERN ANCHOVY (*ENGRAULIS MORDAX*): INTERPLAY OF DEMOGRAPHY AND ENVIRONMENT IN SHAPING GENETIC ARCHITECTURE

Lecomte F, WS Grant, R Rodriguez-Sanchez & BW Bowen

Understanding how environmental variability influences genetic diversity is key to understanding speciation. Environmentally induced events, such as population bottlenecks, founder events, crash-and-flush cycles, and extinctions and recolonizations, can alter the pace of genetic divergence among populations. Molecular genetic techniques can be used to infer the nature of historical events that lead to observed patterns of population divergence. In addition to vicariance and dispersal events, influences in population demographics can be equally important in shaping genetic architecture. Coastal marine species, such as sardines and anchovies, are noted for strong fluctuations in population abundance that are related to variations in productivity. Previous molecular studies of sardines and anchovies have typically revealed shallow gene genealogies, but high haplotype diversities. The present study investigates how periodic changes in geographical range following population crashes and flushes influence genetic architecture. Since environmental variation is more likely to affect peripheral than central populations, we would expect to observe lower diversities in marginal populations, if gene flow between populations is not significant. For both anchovies ($n = 197$; 539 bp) and sardines ($n = 107$; 427 bp) along the west coast of North America, haplotype diversities (h ; mtDNA cytochrome *b*) were larger in centrally located populations that have persisted during periods of low species abundance. In anchovies, F_{st} indicated that northern populations were differentiated from the southernmost site, corroborating the results of tagging studies, which show migration rates insufficient to genetically homogenize populations. Increases in the number of haplotypes for anchovies in northern areas rapidly level off for increasing sample size (94.1% of haplotypes shared between sites, $n = 17$). However, in southern areas, the number of haplotypes continued to increase with increasing sample size (only 48.7% of haplotypes shared between sites, $n = 39$). For both species, haplotype diversities were high in central populations but lower in peripheral populations. Since abundances of these species are closely related to the strength of upwelling, sites close to areas of high primary productivity should be

more resilient during population crashes. Small body size, high fecundity, and a short life cycle contribute to local extinctions following down turns in productivity, but to population flushes during times of high productivity. The resulting cycles of geographic contractions and expansions may hinder local adaptation and prevent speciation on scales of even thousands of kilometers within an upwelling zone.

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SEARCHING FOR GLACIAL REFUGIA IN THE EASTERN ALPS: EVIDENCE FROM COMPARATIVE PHYLOGEOGRAPHY AND PATTERNS OF ENDEMISM

Schönswetter P, A Tribsch & H Niklfeld

The fate of the flora of the European Alps during Pleistocene glaciations has been of great interest for a long time. Recently, the raise of molecular techniques and the increasing knowledge about paleoclimatology and Quaternary geology have given a new impetus to the debate. As in most other mountain systems, in the European Alps there is a great difference between the floristic composition of plant communities growing on limestone and on siliceous bedrock. Due to the geological situation in the Eastern Alps with a central siliceous core flanked by peripheral limestone ranges over long distances, the possibility for peripheral glacial survival for plants confined to limestone or to silicate are different. While large limestone areas remained free of ice, there are only few well circumscribed areas providing siliceous bedrock which was unglaciated or at least situated below the Pleistocene snowline and, consequently, have presumably acted as refugia. Thus, silicicolous plants are very useful models to test hypotheses on glacial survival in the Alps. Our approach was to test these presumed refugia defined by geological and palaeoclimatological data with distribution patterns of 40 endemic silicicolous plants and with phylogeographic patterns of several vascular plant taxa inferred from amplified fragment length polymorphism (AFLP) fingerprinting. Our sampling covers at least their entire distributional areas in the Alps. The pattern of endemism is strongly reflecting Pleistocene glaciation, with most endemics confined to unglaciated or weakly glaciated areas. The genetic data confirm this pattern. Although the phylogeographic patterns of the investigated taxa are not congruent, they are all relateable to the presumed peripheral Pleistocene refugia. There are no hints for glacial survival in the formerly most extensively glaciated areas in the highest and most central parts of the Alps, i.e. nunatak regions defined by classical biogeographers early in this century.

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ANCIENT GENE-FLOW OF THE LONG-TAILED VOLE: POST-GLACIAL COLONIZATION OF YELLOWSTONE NATIONAL PARK, WYOMING, USA.

Spaeth PA, Y Chan & EA Hadly

Several factors contribute to the unique biogeographic history of the greater Yellowstone ecosystem. During the last glacial maximum, Yellowstone was the site of a continental ice cap. Consequently, the park was one of the last regions in North America to deglaciate and thus constitutes a relatively young (~12 ka) ecosystem. Additionally, Yellowstone is located at the intersection of three major biogeographic provinces (Rocky Mountain, Great Plains, and Great Basin) that differ in their floral and faunal species composition, geologic histories, and climate. The deglaciation of this region provides an opportunity to study the assembly of an ecosystem by contributions from neighboring provinces. This problem can be tackled from a biogeographic perspective: source populations for different species can be predicted based on proximity of populations across the modern landscape. The same question can also be addressed from a phylogenetic point of view, determining the genetic affinities of populations within species and assessing their connectivity through space. A previous phylogeographic study has revealed three major clades of *Microtus longicaudus*, the long-tailed vole to provide a temporal perspective on the assembly of this community by assessing the relative contributions of the geographically distinct source populations through the last 3,000 years, using fossils excavated from within the park. We propose to use this type of phylochronologic data to predict the highways of colonization of the Yellowstone National Park ecosystem, one of the last remaining intact temperate ecosystems of the world.

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ANALYSIS OF LANDSCAPE CHANGE BETWEEN THE YEARS 1871 AND 1897, ARBUCKLE MOUNTAINS, SOUTH-CENTRAL OKLAHOMA.

Hoagland BW, B Watkins & T Fagin

Landscape fragmentation often alters many ecosystem parameters, including species composition, biogeochemical interactions, exotic species introduction, and extinction. Much research has focused on fragmentation of modern landscapes, but what about historical changes? In this study, we examine changes in landscape composition and structure between two survey years in the Arbuckle Mountain region. Biogeographically, the Arbuckles are situated on the boundary of the eastern deciduous forest and western grasslands. This region was chosen for study because of the dynamic interaction between woodland and grassland and the occurrence of numerous state rare species. We analyzed change in this region by first digitizing 1871 and 1897 General Land Office survey plat maps using ArcInfo GIS. Coverages were generated for vegetation, agriculture, settlements, hydrology and roads. Landscape structure was analyzed using

FRAGSTATS. In addition, vegetation composition and woody plant densities were calculated from distance data extracted from surveyor notes. The most significant factor in landscape change was a marked increase in size and number of agricultural patches between 1871 and 1897. The affect was a loss of grassland and woody vegetation and an increase in landscape patchiness. Trees greatest tree densities were recorded for *Quercus* species, particularly *Quercus stellata*. Density and size classes varied as well between 1871 and 1897. Therefore, significant landscape change predates modern landuse activities.

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IMPLICATIONS OF PLANT FOSSIL IDENTIFICATION IN RECONSTRUCTING PAST CLIMATES

Arundel ST, KL Cole, JA Cannella & T Andrews

Although changes in plant distributions have been used to reconstruct past climates for over a century, precise climatic limiters of most terrestrial species are unknown. General relations between plant species and climatic factors, like a dependence on growing season precipitation and range truncation due to freezing temperatures are often relied upon to estimate past environments. However, it is widely accepted that each species responds differently to varying stressors. Hence a need for clear, precise, and reliable identification of plant fossils is mandatory for assessing more specific climatic changes. In this paper we analyze pinyon macrofossils from packrat middens to present some dangers in relying on generalities in both plant identification and climate-plant interactions.

Based on anatomical differences in modern needles, four pinyon types in the western United States were carefully delineated: *Pinus edulis* (two needles/fascicle), *fallax*-type (one needle/fascicle, less than 20 stomatal lines, 2 resin canals), *P. monophylla* (one needle/fascicle, less than 8 resin canals, and more than 18 stomatal lines), and *californiarum*-type (one needle/fascicle, 8 or more resin canals and less than 23 stomatal lines). Modern distribution maps for the four types were created in a Geographic Information System (GIS) using published data. The ranges of *P. edulis* and *P. monophylla* were compiled from various published maps and the *fallax* and *californiarum* types were created from field data. The ranges were analyzed spatially using CLIMLIM, a GIS utility that extracts and quantifies statistically important climatic limiters based on historical climate data and the digital distribution map. CLIMLIM also indicates places the species may migrate if limits were removed. Twenty climate variables were used during five seasons, including monsoon. Analyzing pleistocene midden records of pinyon species in conjunction with their climatic limiters, we present differing climatic scenarios depending on alternate fossil identifications. Preliminary results indicate that while three of the distributions are statistically ($p < .05$) limited by excessive fall precipitation, one (*californiarum*-type) is not. *Fallax*-type and *P. monophylla* are only limited by excessive precipitation amounts, whereas *californiarum*-type and *P. edulis* are each restricted to its range by insufficient rainfall during two seasons: fall and monsoon, and spring and monsoon, respectively. Temperatures were only statistically restrictive at the 95% confidence interval in the case of *fallax*-type, by cold temperatures during fall. Low winter temperatures limited one distribution (*P. monophylla*) at the 75% confidence range. The preliminary climate interpolations, which were based on a lower resolution elevation dataset (10 km) for speed, probably smoothed some temperature affects since they depend so heavily on elevation variances. It is likely that the final results will find additional temperature variables limiting. Differing climate interpretations based on these limiters are best demonstrated using fossils with possible alternate identifications. For example, fossil records of pinyons occurring in Cedar Canyon, northern Arizona, during the late Wisconsin were identified as *Pinus edulis*. If this is the case, it tells us nothing about the twenty climatic variables in the past because the potential distribution includes the macrofossil location. If the needles are interpreted as *Pinus monophylla*, only a reduction in excessive monsoon precipitation is required to explain its past occurrence there, i.e. values were below the limiting amount in the past. If the macrofossils were identified as *fallax*-type, however, it would indicate merely that there was more fall precipitation in the past, while *californiarum*-type tells us that not one of the variables examined explains its previous location there; more than one of the climate variables studied was probably quite different. The results exemplify the importance in both high taxonomic resolution and accurate identification of plant fossil data in reconstructing climates.

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HABITAT DIFFERENCES IN BODY SIZE STRUCTURE AND ENERGY FLOW IN SMALL MAMMAL COMMUNITIES

Ernest SKM

A major theme in ecology is the influence of energy on community and ecosystem properties. While this research traditionally focused on the relationship between energy and species richness, current research increasingly focuses on the relationship between body size and energy flow. One of these recent studies is Holling's Textural-Discontinuity Hypothesis which claims that species clump in body size space, reflecting underlying discontinuities in resource availability. Holling's hypothesis makes two specific predictions: 1) that energy flow should be body size specific and closely correspond with lumps of species in body size space and 2) that the way resources are available to a local community should vary across habitats, resulting in different patterns of lumps of species in body size space. I examined these predictions using detailed community data for nine small mammal communities from eight different habitats: arid grassland, creosote shrubland, juniper woodland, pinyon-juniper woodland, mixed shrub-grassland, a dune grassland, alpine tundra, and temperate coniferous forest. Most of these sites occur within the Chihuahuan Desert allowing me to assess the importance of habitat type and shared species pool on body size structure and energy flow in individual communities. Individual body size was used to estimate the energy use for each individual using the allometric equation for basal metabolic rate. For all communities the relationship between the body size distribution and energy flow was highly multimodal, indicating that energy availability

across a wide range of habitats does appear to be discontinuous with respect to body size. Furthermore, habitats differed in the pattern of energy flow through body size categories, even when only Chihuahuan Desert sites were considered. However, the body size structure was highly conserved across habitats, indicating that different habitats were very similar in the way species clumped on a body size axis. These results appear to support the one of the Textural-Discontinuity Hypothesis' predictions that energy is available in a discontinuous manner with respect to body size, but does not appear to support the claim that there is a relationship between energy flow and body size lumps. In summary, these results suggest that in small mammal communities the body size composition of a community may be very similar across habitats but that the actual species composition and habitat structure of a site results in large differences in energy flow patterns across geographic space.

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THE ECOLOGICAL IMPLICATIONS OF A RANGE EXPANSION: NORTH AMERICAN RED SQUIRRELS IN THE CENTRAL HARDWOODS REGION OF THE UNITED STATES

Goheen JR, RK Swihart & JH Robins

Species with expanding ranges provide unique opportunities to examine environmentally induced adaptations in ecological characteristics and behaviors. Since the late 1800s, the North American red squirrel (*Tamiasciurus hudsonicus*) has expanded its range into the central hardwoods of the United States in conjunction with increasing agricultural fragmentation. We conducted two experiments with regard to this range expansion. In the first experiment, we investigated the dispersal behaviors of red, gray (*Sciurus carolinensis*), and fox (*S. niger*) squirrels in west-central Indiana using a series of experimental releases. We hypothesized that all species would display increased willingness to disperse in the pre-harvest season and with decreasing distance to forest patches. We hypothesized further that gray squirrels would be inferior dispersers relative to red squirrels, given the recent range expansion of red squirrels. All three hypotheses were supported. In the second experiment, we examined whether red squirrels from the central hardwoods displayed differences in foraging behaviors and morphology relative to red squirrels from conifer-dominated environments, a biome in which red squirrels evolved, in the upper peninsula of Michigan. Red squirrels from Indiana and Michigan differed significantly in the efficiency with which they used food items, with individuals from each region more efficiently using those items to which they previously had been exposed. The enhanced efficiency of southern red squirrels feeding on black walnuts (*Juglans nigra*) presumably was due to differences in cranial morphology; skulls of southern squirrels were larger, with longer jaws and higher metrics associated with greater mandibular force than northern squirrels. Contrary to our expectations, red squirrels from Indiana and Michigan did not differ qualitatively in preferences for food items, suggesting that diet choice is constrained by perishability of food items.

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COLD BIOGEOGRAPHIC FILTERS AND WOOD FUNCTIONAL EVOLUTION IN THE FLOWERING PLANT FAMILY WINTERACEAE

Feild TS

The Winteraceae are traditionally regarded as the least-specialized descendants of the first flowering plants, based largely on their lack of xylem vessels. Since vessels have been viewed as a key innovation for angiosperm diversification, Winteraceae have been portrayed as declining relicts, limited to wet forest habitats where their tracheid-based wood does not impose a significant hydraulic constraints. In contrast, phylogenetic analyses place Winteraceae among angiosperm clades with vessels, indicating that their vesselless wood is derived rather than primitive, while extension of the Winteraceae fossil record in to the Early Cretaceous suggests a more complex ecological history than has been deduced from their current distribution. However, the selective regime and ecological events underlying the possible loss of vessels in Winteraceae have remained enigmatic. Here we examine the hypothesis that vessels were lost as an adaptation to freezing-prone environments in Winteraceae by measuring the responses of xylem water transport to freezing for a diverse group of Winteraceae taxa as compared to *Canella winterana* (Canellaceae, a close relative with vessels) and sympatric conifer taxa. We found that mean percent loss of xylem water transport capacity following freeze-thaw varied from 0 to 6% for Winteraceae species from freezing-prone temperate climates and approximately 20% in those taxa from tropical (nonfreezing) climates. In contrast, water transport in *Canella* stems is nearly 85% blocked by freeze-thaw. By integrating Winteraceae's phylogenetic relationships and fossil history with physiological and ecological observations, we suggest that, as ancestors of modern Winteraceae passed through temperate conditions present in Southern Gondwana during early Cretaceous, they were exposed to selective pressures against vessel-possession and returned to a vascular system relying on tracheids. These results suggest that the vesselless condition is advantageous in freezing-prone areas, which is supported by the strong bias in the ecological abundance of Winteraceae to wet temperate and tropical alpine habitats, rather than a retained feature from the first putatively vesselless angiosperms. We believe that vesselless wood plays an important role in the ecological abundance of Winteraceae in Southern Hemisphere temperate environments by enabling the retention of leaves and photosynthesis in the face of frequent freeze-thaw events.

72**USING BIOGEOGRAPHY TO HELP SET PRIORITIES IN MARINE CONSERVATION**

Lourie SA & ACJ Vincent

In response to urgent needs, marine conservation is becoming more systematic. It is moving away from its historical link with fisheries management and towards a representative ecosystem focus. For representative conservation planning we require an understanding of 1) the spatial distribution of biodiversity, 2) the processes that determine it, and 3) the scale at which these processes operate. Unfortunately marine biogeography still lags far behind that on land. Here we examine some of the physical, biological and human differences between the sea and the land, and the implications that these have for marine biogeography and conservation. We review marine classifications at various spatial scales and show how these can/have been used in marine conservation at global, regional, national, and local levels. We give examples of conservation approaches that explicitly take biogeography into account (e.g. Great Barrier Reef Marine Park Authority's representative areas programme) and those that do not (e.g. Conservation International's hotspots). Recommendations for future work include a review of currently protected areas within an ecological framework encompassing a greater number of habitat types than presently assessed so that we can identify gaps in our representation of different habitats. We also need to extend terrestrial concepts of biogeography and conservation planning in order to adequately represent the dynamic, interconnected, three-dimensional nature of the marine realm and its links with land. The urgency of the situation however, means that we should put flexible conservation plans into action now, while continuing with biogeographic research and applying new knowledge to regular reviews of these plans.

73**HERPETOFAUNA DISTRIBUTION PATTERNS AND CONSERVATION IN WESTERN MEXICO**

Garcia A

The determination of distribution patterns of species has been proved to be an important tool to set priority areas for conservation. High conservation priority is given to those areas with high diversity and/or endemism. Priority areas for conservation of Mexican biodiversity have been proposed in western Mexico, but do they include most of the herpetofauna species richness and endemism? This area forms a latitudinal strip of 15 degrees dominated by seasonally tropical dry forest. It contains the second highest plant and animal diversity in Mexico but deforestation rates are among the highest too. A database of the herpetofauna from western Mexico, was created by georeferencing 15,000 records from Mexican and US museums, and published dot maps. Latitudinal bands of 1 degree were used to plot distribution patterns. On one hand, both species richness and endemism followed a latitudinal gradient, especially marked in amphibians. On the other hand, percentage of endemism along the area was uniformly high in both amphibians and the reptiles (>45% and 35%), suggesting high conservation priority must be given to multiple areas. Priority areas previously proposed included most of the herpetofauna species richness and endemism.

74**GEOGRAPHIC VARIATION IN ABUNDANCE AND DISTRIBUTION OF PARROTFISHES**

Jiménez JM & FA Zapata

We examined variation in parrotfish abundance by comparing new data from Gorgona Island, Colombia (Playa Blanca reef and La Azufrada reef) with published data from 13 localities in the Caribbean and the Indopacific. In general, the maximum densities and maximum lengths found at Gorgona Island, for two *Scarus* species, were higher than those reported in other studies for congeneric and non congeneric species from the Caribbean and the Indopacific. One possible explanation for these patterns is that because of nutrient rich waters along the Pacific Coast of Colombia the seaweeds eaten by parrotfishes are more abundant than in other regions with low nutrient concentrations.

75**ASSESSING RAPOPORT'S RULE IN SOUTH EASTERN PACIFIC TELEOSTEI: PATTERNS IN LATITUDE AND BATHYMETRY.**

Hernández CE, F Labra, P Marquet & FP Ojeda

Rapoport's rule has been proposed as a general biogeographical principle. This rule was originally stated as a correlation between the latitudinal extent of species' geographical range sizes and latitude. Subsequently it has been suggested that this rule also holds over elevational and bathymetric gradients. Research on the latitudinal extent of several North American taxa has supported this relationship, and both latitudinal and bathymetric Rapoport effects have been documented in northeastern Pacific fish taxa. However, the generality of the latitudinal pattern has been questioned by studies of Indo-Pacific and Atlantic teleost fish. In this study we assess the generality of Rapoport's rule in teleost fish. To this end we analysed the latitudinal and bathymetric ranges of southeastern Pacific fish taxa. We also evaluated the effect of controlling for phylogenetic dependence in the assessment of the rule, analysing two fish groups for which genetic sequences are available: the genus *Sebastes* and the family *Nototheniidae*. Results for latitudinal range of southeastern Pacific fish do not

support Rapoport's rule, while the data for bathymetric ranges do support the rule. Both latitudinal and bathymetric Rapoport effects were observed for *Sebastes*, while only bathymetric effect was seen for *Nototheniidae*. Controlling for phylogenetic dependence did not alter these results. Our results support the view that latitudinal Rapoport effects are a local phenomenon, occurring only for marine fish in the northeastern Pacific. On the other hand, the bathymetric effect seems to be a general pattern for teleost fish. The phylogenetic independence of the latter suggests that the mechanisms that give rise to this pattern do not depend on the past history of diversification in the groups we studied.

76**ENDEMISM ON LATITUDINAL AND ALTITUDINAL GRADIENT IN TROPICAL FORESTS: A TEST OF THE CLIMATIC VARIABILITY HYPOTHESIS**

Boyle B, BJ Enquist & MD Weiser

The Climatic Variability Hypothesis (CVH; Stevens 1989, 1992) predicts that species' latitudinal ranges should decrease with decreasing latitude (Rapoport's Rule) and that the increased proximity of range boundaries should lead to higher local species richness at low latitudes (the latitudinal diversity gradient). Although most tests of the CVH have focused on temperate zone and temperate-tropical comparisons, the relationship between latitude and seasonality implies that the predictions of the CVH should apply within the tropics as well. In this study, we tested two predictions of the CVH for tropical forest communities: 1) species richness should be positively correlated with the proportion of endemics (range-restricted species), and 2) percent endemic species should increase from high to low latitudes within equivalent environments. We compared species richness and percent endemic species in 0.1 ha samples of wet forest plant communities from four elevations and three localities spanning the latitudinal extent of the northern Neotropics. We determined range limits from herbarium specimen databases and taxonomic literature. Contrary to the first prediction, communities with high proportions of endemic species tended to be species-poor. The second prediction was supported for only one of the four elevations: percent endemism increased monotonically toward the equator in the lowlands, but peaked in Mexico and Costa Rica at higher elevations. Within regions, endemism was consistently lowest in the lowlands, but was highest at a different elevation in each of the three regions. Finally, relative rankings of endemism were sensitive to the spatial scale at which endemism was defined. This study thus failed to uphold the predictions of the CVH. Rather, the uniformly low levels of endemism observed for geographically-widespread tropical lowland forests, as well as the scale-dependence and regional specificity of endemism at higher elevations, support the conclusion that patterns of endemism—and range sizes in general—reflect the age, area, and historical isolation of particular environments within particular regions.

77**FROM SAMPLING STATIONS TO ARCHIPELAGOS: INVESTIGATING ASPECTS OF THE ASSEMBLAGE OF INSULAR BIOTAS**

Sfendourakis, Spyros

Species assemblages of insular biotas are one of the major foci in ecological biogeography during the last 40 years. Patterns of nestedness, of species co-occurrence, and of similarity among insular communities are still among the major themes in island biogeography, together with the related issues of the species-area relationship, immigration-extinction and species turnover. Most of these patterns and processes are influenced by the geographical scale of analysis. In this study we use detailed data on the distribution of terrestrial isopods on Aegean islands (Greece) in order to investigate the emergence of interesting biogeographical patterns as we move from within-island to between-islands species assemblages. We check the levels of nestedness in the communities of each island using sampling stations as the lower unit of analysis. We examine their relation to the patterns of nestedness between these same islands, as well as their relation to the Whittaker's index of beta-diversity, which uses the same kind of information. Nestedness among sampling stations is due to the interplay of widespread vs. locally occurring species and habitat heterogeneity among stations. An important question thus raised is: Are the same species responsible for deviations from perfect nestedness at both scales? We also examine the patterns of co-occurrence of species within and among islands and the possible effects of habitat diversity on the formation of these patterns, and we address the following questions: Are the species that usually occur together at the local scale the same with those occurring together at the archipelago scale? Are the species that are widespread within islands the same with those that are widespread at the archipelago level? Is it possible to extrapolate from the species diversity within an island to the species diversity among islands? We propose that this kind of 'scale ascending' studies may eventually lead to a unified theoretical framework encompassing nestedness, co-occurrence and species-area relations.

78**BIRDS, LANDSLIDES AND PASTURES: A BIOGEOGRAPHIC CONDUNDRUM**

Welford MR

Landslides, common in the Northern Andes as naturally-occurring, highly-disturbed narrow features in the landscape, have been little studied. This is particularly problematic given that landslides create a heterogeneous mix of cleared forest, linear strips of successional forest, and undisturbed primary forest that may possibly contribute to increased local biodiversity. The resulting mosaic of plant and food resources might explain why Antpittas, Tapaculos, and Tanagers reach their highest

diversity in the Northern Andes. Pastures and cropland, which surely reduce biodiversity, are usually broader and more permanent than landslide scars and are also common in the part of the Andes. Nevertheless, recently abandoned pastures and cropland near Quito, Ecuador seem to mimic vegetation succession dynamics observed in landslide scars. Moreover, both common and rare restricted-range bird species use these pastures shortly after abandonment just as they do recent landslides. The trajectory and spatial dynamics of plant succession in these abandoned pastures and croplands, and the resulting bird community, appears to be largely determined by both the presence of exotic grasses in these areas and the intensity of prior human use (e.g. regularly burnt pastures appear to suffer arrested succession). A series of models are presented, based on 6 years of data collected in Ecuador, that predict vegetation and bird community change within abandoned pastures and landslide chutes and depositional fans across a range of landscape segments (i.e. slopes, ridges, gorges).

79

THE INTERPLAY OF MIGRATION ABILITY AND GLOBAL BIOGEOGRAPHY IN RAPTORS (CLASS AVES, ORDER FALCONIFORMES)

Bildstein KL & J Zalles

We explore how migration ability affects the global biogeography of raptors (Class Aves, Order Falconiformes) by comparing global distributions and species richness in three genera of falconiforms, *Accipiter*, *Buteo*, and *Falco* that differ considerably in their migration abilities. Together, these three species-rich genera (*Accipiter*, 50 species; *Buteo*, 28; *Falco* 37) comprise 37% of all birds of prey, and 38% of all migratory raptors. Overall, the three genera differ considerably in wing structure and aerodynamics, and the three typically use different flight mechanics while migrating. These differences, in turn, are reflected in differences in both migration tendencies and behavior. Although more than 80% of all buteos and falcons are complete, partial, or irregular migrants, 60% of all accipiters are non-migratory, sedentary species. In addition, buteos and, in particular falcons, are more likely to be trans-equatorial, long-distance migrants than are accipiters. Accipiters tend to be more island-restricted, forest-dependent, range-restricted, and wholly tropical than are buteos and falcons. Island-restricted accipiters tend to occur on fringing archipelago islands more so than on truly isolated oceanic islands, whereas island-restricted buteos and falcons occur on both. Buteos probably occur on isolated oceanic islands because they tend to be wind drifted while migrating in flocks; falcons, probably because of their considerable overwater flight abilities. The hourglass configuration of continental landmasses and the north-south orientation of mountain ranges in the New World have enhanced long-distance *Buteo* migration and speciation there. The vast open habitats of sub-Saharan Africa have enhanced long-distance falcon migration and speciation there. The largely forested, fringing archipelagos of the South Pacific have enhanced long-distance accipiter migration and speciation there. We describe a mechanism called "migration dosing" that we believe contributes to the latter relationship. Migration ability and continental geography are important emergent factors in determining global patterns of biogeography and diversity within this group.

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STRENGTH OF PLANT-HERBIVORE INTERACTIONS VARIES ACROSS LATITUDE IN ATLANTIC COAST SALT MARSHES

Salgado CS, CK Ho, NB Dave & SC Pennings

Biogeographic theory predicts that plant-herbivore interactions are more intense, and plant defenses therefore better developed, at low versus high latitudes. Atlantic coast salt marshes provide an ideal system to examine these theories, because similar plant and animal communities occur across a wide range of latitude from central Florida through Maine. We tested two hypotheses: 1) herbivores are more abundant, and damage to plants more severe, at low versus high latitudes, and 2) plants from low latitudes are less palatable to herbivores than plants from high latitudes. To test these hypotheses, we used a combination of monitoring and experimental approaches. Monitoring: We studied the seaside goldenrod, *Solidago sempervirens*, at ten salt marsh sites in New England (ME, MA, RI, CT) and ten sites in the southeast (SC, GA, FL). We counted herbivores and measured leaf damage on plants at all sites monthly from June through September. As predicted by the first hypothesis, herbivores were consistently more abundant at southern sites than at northern sites. Similarly, damage to leaves by herbivores was greater in the south than in the north. Experimental: We collected plants from four sites in each region (total of 8 sites) and transplanted plants from each site to all 8 sites. After 1 month, we measured herbivore damage to marked leaves. Herbivore damage was greater for plants placed in southern sites, as predicted by the first hypothesis, and for plants originating from northern sites, as predicted by the second hypothesis. Moreover, as predicted by the second hypothesis, laboratory feeding experiments confirmed that leaves from northern plants were more palatable than leaves from southern plants. Future work will determine whether these results are unique to *Solidago* and its herbivores, or whether they also apply to interactions between other salt marsh plants and their herbivores.

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ECOLOGICAL SPECIATION IN TROPICAL SEAS

Rocha LA, DR Robertson & BW Bowen

Even after significant recent developments, processes that lead to the formation of new species are still some of the most debated topics in biology. Darwin proposed that natural selection was the main cause of speciation, however, studies developed as part of the Modern Synthesis concluded that isolation, not selection was the central mechanism. In a recent return to Darwinism, it was demonstrated that divergent natural selection promotes speciation even in the presence of gene flow, and this process is now being called ecological speciation. The marine environment is an especially challenging medium in which to test speciation models, mainly due to the presence of a widely dispersing pelagic larval stage in most marine organisms and the lack of evident geographical barriers. This has created a long debated paradox about the mechanisms that generate and maintain biodiversity in an apparently high gene flow medium. Based on the geographic distribution of genetic populations in five wrasse species and other common reef denizens, we challenge the widely accepted hypothesis of marine speciation driven by present or past vicariance and distance, and provide evidence for ecological speciation. In our study group genetic homogeneity was observed between widely separated (3000 - 4500km) locations, indicating that, despite growing evidence for local larval retention in reef fishes, at least sporadic long distance dispersal occurs. However, deep genetic divergences were observed between apparently connected, geographically close locations (96 - 360km). Ecology brings an additional variable that seems to balance the co-occurrence of long distance dispersal and genetic breaks over short geographical distances, deep divergences were found between ecologically different locations, whereas genetic homogeneity is consistently maintained among environmentally similar locations, regardless of geographical distance. The pattern observed in this study indicates that ecological partitions have a previously neglected role in tropical marine speciation, and a combination of geological history, early life history and benthic-stage ecological characteristics shape the phylogeography of reef fishes and other organisms.

82

A FIRE HISTORY OF AN OAK SAVANNA IN WISCONSIN.

Wolf J

Fire plays a significant role in the persistence of the oak savanna. This study documented the fire history from oak sections in southeastern Wisconsin. Using dendrochronology, fire occurrence was quantified prior to and since European settlement and calculated to reflect specific time periods. Fire frequency was 3.7 years before European settlement in 1840, 19.5 years during the early settlement years in 1841-1872, 4.77 years for the post settlement years in 1873-1979 and 6.7 years during increased industrial years of 1980 to the present. The majority of fires occurred during the dormant or early spring season. Fire events corresponded with six of the nine years of lowest precipitation. Although climate data suggest a correlation exists with marker years, it is more likely that recent fires were associated with human activity more than climate. Quantified fire history records are limited in Wisconsin. These data are essential in understanding oak dynamics and in developing management programs for restoration and preservation of remnant areas of oak savanna.

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DEMOGRAPHY OF SUGAR MAPLE (ACER SACCHARUM) SEEDLINGS AT THEIR NORTHERN LIMIT, ONTARIO, CANADA

Goldblum D & LS Rigg

Sugar maple reaches its northern limit along the eastern shore of Lake Superior (Ontario, Canada) in Lake Superior Provincial Park (LSPP). The park is dominated by east-west trending hills that provide favorable conditions for sugar maple on the uplands, with the intervening low-lying terrain dominated by boreal species. At the hillslope scale repeated ecotones occur between the hardwood uplands and the boreal lowlands. Previous studies have shown that sugar maple seedlings (but not saplings) are found downslope of adult maples suggesting that if global climate continues to ameliorate, sugar maple may be able to migrate downslope and eventually beyond its current latitudinal limit. During the summer of 2000 (a mast year for sugar maple) a series of 19 seedling plots were established in one of three topographic positions (ridge, north slope, and south slope). Approximately 750 seedlings within the small plots were permanently tagged. Seedling heights have been measured annually since plot establishment, and seedling ages were determined using leaf scars during summer 2001. This poster will describe the demographics (density, growth rates, and mortality rates) of sugar maple seedlings at the boreal forest /deciduous forest ecotone in LSPP. Significant differences in both growth rates and mortality rates exist between the relatively moist 2001 summer and the drier summer 2002. Additionally, differences in growth rates and mortality rates differ by topographic position during the drier summer of 2002, but not during 2001. Mortality rates from the 2000 mast cohort have been extremely high. The nearly complete lack of sugar maple seedlings on the north and south facing hillslope topographic positions suggest that ultimately sugar maple seedling mortality may be mediated by larger scale micro-climatic factors such as cold air drainage and /or winter desiccation.

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THE FATE OF PONDEROSA PINE FORESTS DECADES AFTER INTENSE CROWN FIRES

Mast JN & M Savage

The exclusion of low-intensity surface fire from Southwestern ponderosa pine forests has changed ecosystem structure and functions such that intense crown fires increasingly cause extensive mortality in burns. What is the trajectory of recover in these burns? This research explores the regenerational response of ponderosa pine and other woody species to crown fires that occurred from the 1950s to the early 1970s. We address two main questions: 1) what is the natural regenerational response of ponderosa pine and what is the survival rate of planted ponderosa pine seedlings, and 2) can these sites be "captured" or inhibited by other woody species. In the Southwest, sites of large crown fire burns are now increasingly extensive, and by themselves merit and inquiry into their restoration. Moreover, these burns offer an unusual opportunity to investigate whether crown fires in ponderosa pine forest are actually driving the ecosystem past a critical threshold into a new domain. By analyzing ten crown fires in Arizona, New Mexico and Colorado, we conclude that the resulting post-crown fire vegetation offer another justification for restoration of ponderosa pine forests of the Southwest, and answer critics who suggest that allowing crown fires to burn is an acceptable option.

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A LONG LIVED PIONEER: YELLOW BIRCH GROWTH RATES COMPARED TO COMPETING FOREST SPECIES AT THE DECIDUOUS/BOREAL FOREST ECOTONE, ONTARIO, CANADA

Rigg LS & D Goldblum

The boreal/deciduous ecotone in North America is marked by the gradual disappearance of hardwood species (e.g. *Acer saccharum* and *Betula alleghaniensis*) and increase of conifer species (e.g. *Abies balsamea* and *Picea glauca*). Both sugar maple and yellow birch reach their northern limit on the east shore of Lake Superior within Lake Superior Provincial Park (Ontario, Canada), with yellow birch having a slightly more northern distribution. At this ecotone hardwood species become restricted to ridge tops, while conifers generally dominate colder valley bottoms. It is hypothesized that deciduous species such as yellow birch and sugar maple become successively less vigorous as they reach their northern limit. This study compared growth rates of yellow birch to other species, both deciduous and coniferous, within the ecotone. Since yellow birch can be considered a long-lived pioneer we explored the ability of this species, over the past 250 years, to compete with more shade-tolerant species. Given anthropogenic increases in carbon dioxide and 20th century warming it is possible that the normal decline of growth rates with age, may be offset by warming conditions, perhaps affording yellow birch some competitive advantage with respect to conifer species. We collected increment cores from trees growing within this ecotone to examine relative growth rates between species. Results show for yellow birch individuals greater than 100 years of age, growth rates have not decreased to the extent expected. The ability of yellow birch to persist within this ecotone is assured given sufficient regeneration.

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THE MOJAVE DESERT – COLORADO PLATEAU INTERFACE: A SEMI-PERMEABLE BOUNDARY FOR XEROPHYTIC BEES

Griswold T & O Messinger

The Mojave Desert and the Colorado Plateau are home to two of the most diverse bee faunas in the world, supporting 75 and 58 genera, and at least 934 and 721 species, respectively. Xerophytes, species restricted to the deserts of the southwestern United States and northern Mexico, constitute 50% of the Mojave Desert fauna and 27% of Colorado Plateau. Both deserts have high levels of bee endemism among the xerophytes: 19% for the Mojave Desert, 41% for the Colorado Plateau. Less than 100 species of the xerophytic bees cross the boundary between the hot and cold desert. Fifteen xerophytic genera and 19 additional subgenera found in the Mojave Desert do not occur in the Colorado Plateau. Additional genera such as *Ancylandrena* are present only as rare disjuncts in the driest portions of the Plateau. A similar pattern occurs at the species level where many widespread Mojave Desert species do not cross into the Colorado Plateau or are rare and limited to one or two localities. There is no such pattern in the reverse direction. There are no genera restricted to the cold deserts; nor are there xerophytic species with disjunct distributions in the Mojave. Causes for the restriction to the hot deserts are not clear. Bees which are floral generalists are no more likely to cross the boundary than are floral specialists. Similarly, larger species with greater flight ranges are not better colonizers. Climatic factors may be the principal determinants of northern limits. The only low elevation pathway between the two deserts, the poorly studied Colorado River corridor, would be a fruitful area for investigation.

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INTERACTIONS BETWEEN LOGGING HISTORY AND TOPOGRAPHICALLY MEDIATED ENVIRONMENTAL CONDITIONS IN DETERMINING THE LOWER LIMIT OF THE SPRUCE/FIR COMMUNITY IN THE GREAT SMOKEY MOUNTAINS

Hayes M & A Moody

The highest elevations of the Great Smoky Mountains National Park (GSMNP) harbor the southernmost populations of *Picea rubens* and *Abies fraseri* in the United States, and the largest continuous expanse of old-growth spruce/fir in eastern North America. This community exhibits strong fidelity to cool, moist sites. This is most likely due to the necessity for abundant near-surface soil moisture during early growth stages for both *P. rubens* and *A. fraseri*, as well as to reduced competition from broad-leaved tree species at higher elevations. Much of the GSMNP, including spruce/fir forest, was logged prior to establishment of the park in 1934. While in some previously logged areas spruce/fir successfully regenerated, in other areas it did not. We used modeled surfaces of environmental conditions, historical logging data, and a satellite based map of the spruce/fir distribution, to test for interactions between site factors and disturbance history in determining the lower limit of the spruce/fir community in the GSMNP. Our results indicate a strong interaction between solar radiation and logging history in the elevation of the lower limit. Where potential solar radiation loads were low, spruce/fir did successfully regenerate following logging, even at lower elevations. However, where radiation loads were high, regeneration of spruce/fir was restricted to higher elevations, where lower temperatures and greater fog frequency prevail. We hypothesize that the extra evapotranspirative demand due to high solar radiation loads on freshly exposed, south-facing slopes, inhibited post-logging regeneration by reducing surface soil moisture below a critical threshold for seed germination and seedling survival of *P. rubens* and *A. fraseri*. This added draw on soil moisture stores is reduced at higher elevations due to lower temperatures and fog, and thus, even on exposed slopes, spruce/fir was able to regenerate. This research demonstrates the importance of historical disturbance in structuring current biotic distributions, and that potential interactions between disturbance and environmental conditions are potentially important components of vegetation models. In addition, these results may have implications for management of forest resources in a range of community types.

88

EXAMINING PATTERNS OF FISH ENDEMISM ON SEAMOUNTS USING THE ONLINE INFORMATION SYSTEM SEAMOUNTS ONLINE

Stocks KI

Seamounts (undersea peaks in the ocean's floor) support unique biological communities that are of interest both as natural laboratories for studying biodiversity in the oceans and as commercially-fished habitats requiring wise management. This project has two aims. The first is to compile existing information on the biota of seamounts globally and make it freely available through a web-based portal (<http://seamounts.sdsc.edu>). Over 8,000 species records from seamounts, mainly from published literature and data sets donated by researchers, currently can be accessed through the portal for use by researchers and managers, and the system is constantly growing. The second aim is to use the data holdings in SeamountsOnline to investigate patterns of community structure and endemism on seamounts. Here, data on demersal fish species of the Hawaiian and Emperor seamount chains are presented. Community similarity showed a strong spatial pattern, with nearby seamount communities sharing more species than distant ones. The total level of endemism (species recorded only from the seamounts and islands of the Hawaiian and Emperor chains) was ~21%. Two groups of endemics were separated: those found only on seamounts, and those found on both seamounts and islands. The two groups had opposite spatial patterns: the percent of seamount-only endemics increased with distance from Hawaii on seamounts <650m deep, while seamount-and-island endemics decreased away from Hawaii. Levels of endemism of both types were low on deeper seamounts.

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THE OCEAN BIOGEOGRAPHIC INFORMATION SYSTEM

Zhang PY & JF Grassle (Presented by: KI Stocks)

As data concerning living marine resource distribution and abundance accumulates, it has become clear that the multitude of independent databases harboring such information do not, individually, provide an adequate or easily-accessible medium for a global information system. The Ocean Biogeographic Information System (OBIS), a component of the Census of Marine Life (CoML), links a large number of geo-referenced taxonomic and regional databases in a format that allows simultaneous searches to map output onto a variety of oceanographic datasets, online, globally (www.iobis.org). At present, the OBIS portal provides access to over 500,000 georeferenced species distribution records from 10 distributed servers and has links to mapping and analysis tools. In the future, OBIS will expand to allow four-dimensional access to both biological and physical datasets with the possibility for online statistical analysis and modeling to compare species distributions with environmental conditions over time and space. The power of this system is growing steadily, and OBIS will become a useful tool for integrating global biological, physical and geochemical data and modeling coupled ocean processes. Membership in the OBIS federation is open to any interested individual, country, or organization committed to the long-term maintenance of an accessible, relevant biological or environmental database. In addition to compiling and displaying existing databases on

a global scale, OBIS will house the datasets created by all CoML projects. OBIS aims to become the definitive tool for ocean research, marine resource management, and public information, and is the principle marine component of the Global Biodiversity Information Facility (GBIF).

90**I SPY - IMAGE MANAGEMENT AND RECOGNITION TRAINING FOR BIOGEOGRAPHERS**

Pearson S, P Shimeld, F Hopf & L Gayler

An image collection is a teaching tool in many sub-disciplines of biogeography. Recognition of pattern, comparing material and being able to record phenomena is core to the training of biogeographers. We have developed a collection of pollen grains using the simplest image capture and presentation software available. It reduces the training time needed for research projects without substantial cost increases. Although this project report relates to a pollen collection, the principles and techniques used have universal application to people working with digital images. Sharing reference material is an important aspect of being part of the international scientific community. We have found our modest initiative has built links globally that we are keen to grow as technology and cooperative databasing develops. The system we are using is described in detail on the poster. The hardware configuration we have used is probably already antiquated and should encourage researchers without large budgets.

91**GEOGRAPHICAL PATTERNS OF THE SPECIES-TIME RELATIONSHIP**

White, EP

The species-time relationship (STR) describes the increase in species richness in biological communities with the length of time censused. I analyzed species-time relationships for 521 North American breeding bird communities. I used a probability based calculation of sampling effects to show that the increase in richness was not exclusively due to sampling in any of the communities. Species tend to be more clumped in time than expected on the basis of random sampling. On average, STRs were better fit by logarithmic functions than by power functions. Relationships generated by random sampling were more biased towards logarithmic functional fits than observed data, indicating that perhaps the sampling aspect of the curve caused the tendency towards logarithmic fits. The model chosen to characterize the relationship has important impacts for understanding observed patterns, because logarithmic functions are additive and power functions are multiplicative (with respect to doublings of time). The rate at which species accumulate in ecological systems may depend on a variety of physical and biological factors. Here I investigate geographical patterns of the STR and attempt to determine which variables influence its slope and intercept.

92**LATITUDINAL PATTERNS OF FOREST PRODUCTION AND THE COMPENSATORY EFFECTS PLANT STOICHIOMETRY**

Kerkhoff AJ, BJ Enquist, JJ Elser & W Fagan

The anthropogenic alteration of global biogeochemical cycles makes understanding ecosystem dynamics an imperative. Vegetation canopies, via primary production, are the energetic and material drivers of most terrestrial ecosystems. Here we explore latitudinal trends in forest productivity and develop a simple model integrating the effects of body size, temperature, and C:N:P stoichiometry on primary production, in order to better delineate the fundamental constraints on ecosystem structure and function. A global compilation of forest productivity indicates that there is not a pronounced latitudinal trend in forest productivity. This observation implies that at a given temperature, colder, high latitude forests are more productive than warmer, low latitude forests. We hypothesize that this counter gradient variation in productivity is accomplished primarily through compensatory changes in plant stoichiometry. In this context, our model makes two predictions. First, in accordance with the "growth rate hypothesis" of ecological stoichiometry, at a common temperature (latitude), productivity should be linearly related to phosphorous content of vegetation. Second, across latitude, plant nutrient content (C:N, C:P) should show an exponential (Boltzmann) relationship with temperature. Thus, stoichiometric ratios in vegetation should increase substantially from the poles to the tropics. Preliminary data for wetland and riverine forests of Florida and Puerto Rico support the first prediction. We lack sufficient data to test the second prediction directly, but an extensive compilation of leaf stoichiometry data shows substantial increases in C:P with decreasing latitude, in accordance with our model. These preliminary results indicate that allometry, biochemical kinetics, and ecological stoichiometry may provide the fundamental principles necessary for a macroecological theory of ecosystem function.

93**COMMUNITY STRUCTURE AND FUNCTIONAL DIVERSITY ALONG CLIMATIC GRADIENTS: A SPATIALLY EXPLICIT MODEL**

Schwiik DW & DD Ackerly

In heterogeneous environments, the distribution of plant species is the outcome of a series of biotic and abiotic filters: the community assembly process. Recent developments in neutral models emphasize the importance of incorporating non-equilibrial processes (e.g., ecological drift) in models of niche-structured community assembly. Here, we examine community diversity of sessile organisms in response to spatial variation in habitat. Our framework combines the potential for ecological drift with a non-neutral competition for space in a heterogeneous environments. We constructed a spatially explicit model to simulate the distribution of species in a one-dimensional spatial landscape with an underlying gradient in environmental conditions. Our objective is to examine the influence of niche breadth, dispersal distances, community size (total number of individuals) and the breadth of the environmental gradient on levels of species and functional trait diversity. In our model, organisms' response to environmental condition is described by a Gaussian fitness function and species vary in the location of their fitness mode along the gradient. As expected equilibrium diversity (species richness) decreased with increasing niche breadth. Increasing dispersal distances, however, increased diversity. Although increasing the breadth of environmental variation range increased diversity, community size had a more dramatic positive effect on diversity than did environmental variability. The importance of community size agrees with results from neutral theory, but preliminary results from our model suggest that the pattern of diversity with increasing community size may be dependent on the pattern of environmental heterogeneity.

94**SPECIES INVASIONS EXCEED EXTINCTIONS AT SUB-GLOBAL SCALES**

Sax DF, SD Gaines & JH Brown

Species richness is decreasing at a global scale. At sub-global scales, i.e. within any defined area less extensive than the globe, species richness will increase when the number of non-native species becoming naturalized is greater than the number of native species going extinct. On oceanic islands, we show that species richness has: 1) remained relatively unchanged for land birds, with the number of naturalizations being roughly equal to the number of extinctions; and 2) increased dramatically for vascular plants, with the number of naturalizations greatly exceeding the number of extinctions. In fact, for plants, the net number of species on islands has approximately doubled. On the continent of North America, we show that species richness of U.S. States has: 1) remained relatively unchanged for breeding birds; and 2) increased dramatically for vascular plants. These results suggest that species richness may be increasing at sub-global scales for many groups and that future research should address what consequences this may have on ecological processes.

95**SPATIAL PROCESSES FOR MACROECOLOGY**

McGill B

I present a theory that starts with three well-known and empirically well-documented patterns in variation in abundance between species and across ranges. I show through analytical and Monte Carlo models that these three patterns alone are sufficient mechanisms to generate four well-known and poorly explained macroecological patterns: species abundance distributions (SADs), species area relations (SPARs), decay of species similarity with space, and positive correlation between range size and abundance. In short, superimposing individual species ranges creates community patterns. I then test multiple predictions of the theory against empirical data. In particular, I will show that this theory enables a priori prediction of not just the shape but the parameters of the SAD and SPAR. I will also briefly discuss what makes for a strong and a weak test in macroecology and will apply this standard to existing theories in macroecology.

96**ANALYSIS OF DETERMINANTS OF MAMMALIAN SPECIES RICHNESS IN SOUTH AMERICA USING SPATIAL AUTOREGRESSIVE MODELS**

Tognelli MF & D Kelt

Classically, hypotheses concerning the distribution of species have been explored by evaluating the relationship between species richness and environmental variables using ordinary least squares (OLS) regression. However, in general, environmental and ecological data show spatial autocorrelation, thus violating the assumption of independently distributed errors. It is well known that ignoring spatial autocorrelation can lead to overestimating environmental effects on species richness. To overcome this problem, an alternative is to use autoregressive models that assume spatially autocorrelated errors. Two of the most well known autoregressive models are the Conditional and Simultaneous Autoregressive Regression (CAR and SAR, respectively) models. In this study, I examined the relationship between mammalian species richness in South America and environmental variables. More specifically, I evaluated the contribution of four competing

hypotheses (ambient energy, contemporary climate, habitat heterogeneity, and productivity) to mammalian species richness, using high-resolution digital data-bases, and compared the results of classical statistical tests and spatial autoregressive models. I found that residuals from an OLS model between species richness and environmental variables were strongly autocorrelated, therefore I fit spatial autoregressive models to account for the spatial structure in the data. Residuals from these latter models showed less spatial autocorrelation, particularly the SAR model, indicating the appropriateness of the model. Moreover, autoregressive models fit the data better than the OLS model, increasing the variance explained by 5% and 14% in the CAR and SAR models, respectively. The results also show a shift in the relative importance of the explanatory variables, as well as the alternative hypotheses when spatial autocorrelation is accounted for. These are examples of how the relative importance of environmental variables, or competing hypotheses can be misconstrued when there is no control for spatial autocorrelation.

97

STOCHASTIC IDENTIFICATION OF THE STRONGEST, GREATEST, HIGHEST EPISODE IN A PALEO RECORD

Biondi F, TJ Kozubowski & AK Panorska

Visual identification of particularly relevant episodes in a paleorecord is quite common and often useful practice in scientific research and literature. For instance, the plot of an environmental parameter (temperature, moisture, wildfire frequency, tree-ring indices, pollen percentages, etc.) over time is often used as a starting point to describe which historical periods were most remarkable (warmer, cooler, wetter, drier, with more fires, with less fires, etc.). Such classification of multi-annual events is usually subjective, and we have therefore developed a stochastic model to answer questions related to the probability of observing episodes of a given size and/or of one episode being 'more remarkable' than another. Although we study temporal processes, time series analysis methods do not provide solutions to our inquiries. Our methodology does not detect change in a time series, because the change is explicitly identified. We define regimes (or episodes) as time periods being continuously above or below a reference line. In other words, we consider the time series process as fluctuating around a constant level, and the covariance structure of the process is irrelevant to our model. We begin by quantifying multi-annual time series events in terms of three random variables. First, duration is the number of years the series remains continuously above (or below) its reference line. Second, magnitude is the sum of all series values for a given duration, hence it is equivalent to the area under (or above) the curve. Third, intensity is the ratio between magnitude and duration, therefore it is equal to the average magnitude. Computation of the three parameters for every multi-annual event is straightforward, and allows for objective ranking of the events themselves. While it is useful to quantify the relative importance of multi-annual events in a paleorecord, a stochastic framework is required to answer questions about the probability of occurrence and statistical significance of differences between regimes. In particular, our model provides answers to the questions (a) what is the probability of an episode being larger than a given amount? (b) is the difference between two episodes statistically significant? (c) do positive episodes behave differently from negative ones? Here we analyze a reconstructed time series of the Pacific Decadal Oscillation (PDO), explicitly describe the geometric, exponential, and Laplace probability distributions for regime duration and magnitude, and estimate parameters from the data obtaining a reasonably good fit. This stochastic approach to modeling duration and magnitude of multi-annual events enables the computation of statistical significance of climatic episodes, and provides a rigorous solution to deciding whether two regimes are significantly different from one another.

98

ARE CLADOGRAMS APPROPRIATE REPRESENTATIONS OF BIOGEOGRAPHIC HISTORY?

Hovenkamp P, PC van Welzen & MC Roos

No, they are not. It is not possible to delimit biogeographic entities that comply with the two basic requirements that validate cladistic analysis: - a strictly divergent history, - the possession of both mutable and heritable characters. When areas are used as basic units, the first requirement does not hold unless investigations are restricted to strictly limited periods of geological history during which accretion or coalescence of terranes did not occur. The second requirement is invalidated in all cases where contraction or expansion of species ranges has occurred. Curiously, although the adoption of a cladistic representation has never been convincingly argued, it is still widely seen as the only alternative to the adoption of narrative scenarios. Given the nature of the most commonly used cladistic algorithms, their use will result in cladograms even if informative data are virtually absent. Thus, this strategy is likely to lead to spurious and/or artifactual results. This will be demonstrated with an example involving the Malay Archipelago, based on the meta-analysis of Turner, Hovenkamp & Van Welzen (2001).

99

"BIODIVERSITY WAVE MECHANICS": GOALS, CONCEPTUAL BACKGROUND AND RELATION TO OTHER THEORIES

Hashmi D

A number of approaches exist to study the distribution of individuals of different species in space and time. Biodiversity wave mechanics is an attempt to construct truly physical (energetic and mechanistic) theories of living systems at the organismic scale in conceptual analogy to atomistic wave mechanics. The time-independent Schroedinger equation applies basic physical axioms to determine which equilibria of interacting atomic nuclei and electrons match the assumption of energy conservation. Biodiversity wave mechanics applies measurable axioms related to living systems to determine equilibrium states of interacting lineages of information under the assumption of energy flux conservation. The only realistic situation which is amenable to analytical treatments by atomistic wave mechanics is the H-atom as a two body problem. Numerical methods allow to compute solutions for up to about 10 particles, since the calculation time increases exponentially with the number of particles involved. As regards biodiversity wave mechanics, no realistic situation is simple enough to be analytically tractable, but cellular automata (self-reproducing computer worlds which are discrete in space and time) allow to approximate reality in accordance with the philosophy of evolutionary epistemology. The theory yields transscalar patterns of basic macroevolutionary variables that can be calculated on the basis of spatial coordinates, cladistic identities (i.e. positions in phylogenetic trees), body masses, metabolic rates and niche characteristics of coexisting lineages. Contrary to earlier approaches to study biodiversity, the present theory initially ignores all demographic processes happening in evolutionary time scales. To enter biological complexity from the perspective of purely evolutionary reasoning allows to apply Lotka's maximum power law so that the assumption of energy flux conservation becomes realistic at least for larger spatial scales. Whereas the axioms applied by atomistic wave mechanics are related to basic physical constants, the present theory is based on variables, which have to be measured in the biosphere to which it is applied. Hence biodiversity wave mechanics is not a theory allowing precise prediction. It is primarily an energetic and mechanistic null model allowing to study causality, while demographic rationales, processes or phenomena happening in ecological time scales (like ecological neutrality or deterministic oscillations of population sizes or densities) may be among the reasons which may allow to explain differences between purely evolutionary virtual equilibria and demographic reality. Biodiversity wave mechanics is a conceptually narrowly defined approach which pursues a so far neglected strategy. It is certainly only one of several interesting and useful ways to examine biogeographical patterns.

100

LATE QUATERNARY SAVANNA HISTORY OF THE COLOMBIAN LLANOS ORIENTALES: A TRANSECT SYNTHESIS

Berrio JC, H Hooghiemstra, H Behling, P Botero & K van der Borg

Comparison of pollen records from 8 savanna lakes from the Llanos Orientales of Colombia, located along a 400-km transect, showed the dynamic history of this ecosystem since 18,000 BP (the Last Glacial; Maximum). Present vegetation is consisting of a mosaic of open grass-dominated savanna, savanna shrubland, and wet evergreen forest along the drainage system (galley forest). Vegetation change in lakes El Pinal, Angel, Sardinias, Carimagua, Carimagua-Bosque, Chenevo, Loma Linda and Margaritas is indicative of migrating biomes following changing climatic conditions. Although there are no indications that the present-day floral composition is different from that of the last glacial and early Holocene, the biogeographical distribution of palms (*Mauritia*, *Mauritiella*) changed markedly around 4000 BP, showing that the present-day vegetational aspect of the Colombian savannas is of recent age, stressing vegetation communities may reflect ephemeral categories in time. (2001)

101

POLLEN-BASED BIOME RECONSTRUCTIONS FOR THE MID TO LATE HOLOCENE FROM COLOMBIA: A REGIONAL RECORD OF ENVIRONMENTAL CHANGE

Marchant R, H Behling, JC Berrio, A Cleef, J Duivenvoorden, B van Geel, T van der Hammen, L Herrera, H Hooghiemstra, P Kuhry, A Melief, G van Reenen & M Wille

The geographical location of biomes (ecosystems) in Latin America has been reconstructed as part of the BIOME 6000 project. 'Biomising' pollen data combine spatial and temporal perspectives and determine migration of biomes and vegetation dynamics. In this poster we focussed on changes in biogeographical distribution of Colombian biomes for having extensive pollen data available. Results from specific sites are presented as change in colour code dots. A visual comparison of the modern reconstruction to a map of modern potential modern vegetation shows for the majority of the sites the biomes predicted from modern core-top pollen data reflect the potential vegetation. This confirms the robustness of 'biomisation' to Colombian pollen data. The 6000 BP reconstruction shows a range of biomes reflective of a higher temperatures relative to today. A mid-Holocene period of vegetation change in response to a wetter environment occurred between 4000 BP and 3000 BP time windows. Between 1000 BP and modern reconstructions a transition to more xeric biomes is apparent. Changes in biogeographical distribution of biomes resulted from a factor complex that includes changes in temperature, precipitation, seasonality, ecological dynamics and human impact. (2002)

102

POLLEN-BASED BIOME RECONSTRUCTIONS FROM LATIN AMERICA AT 0, 6000 AND 18000 YEARS AGO

Marchant R, et al (Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam & Max-Planck Institute for Biogeochemistry)

The geographical location of biomes (ecosystems) in Latin America has been reconstructed as part of the BIOME 6000 project. 'Biomising' pollen data combine spatial and temporal perspectives and determine migration of biomes and vegetation dynamics. Modern biome reconstructions for the area between Mexico and Patagonia (based on the Latin American Pollen Database) accurately reflects the modern distribution of biomes and confirm the robustness of the application of the biomisation method. The time slice of 6000 BP show a shift to more xeric biomes: tropical dry forest was more abundant in SE Brasil and more *Nothofagus*-rich steppe in southern South America. At equatorial latitudes there is no significant shift relative to modern vegetation distribution. In the northern Andes forest reached highest altitudes. The Yucatan Peninsula shows a transition to more mesic biomes: xerophytic woods/scrub and warm mixed forest was replaced by tropical dry forest and tropical seasonal forest. The time slice of 18000 BP has insufficient data points but nevertheless trends in geographical distribution of biomes are significant. SE Brazil showed more xeric conditions with much 'cool grassland/shrubs'. Cool mixed forest expanded throughout the Andes. The Central Mexican Highlands showed more mesic biomes and climate seems moister than recorded further south.

Frontiers of Biogeography

Symposia Abstracts

Program Additions & Changes

*International Biogeography Society
Inaugural Meeting
4 ~ 8 January 2003
Oasis Resort, Mesquite, NV*

**The Following is the
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