



ABSTRACTS

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Congress Abstracts

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2011-12-09 17:15 Necessity spawns plasticity: Siberian Cranes abandon specialist foraging behaviors after an extreme flood event and implications for conservation

James Burnham*, *University of Wisconsin-Madison*;

It is unusual for specialist foragers to abandon their preferred food items. Since 1983, scientists have known that Siberian Cranes utilize the shallow-water wetlands of China's Poyang Lake during the winter months where they typically specialize on the tubers of the submerged aquatic macrophyte, *Vallisneria*. Following an extreme flood event during the summer of 2010, surveys for *Vallisneria* found minimal evidence of the plant, or its tubers. In January 2011, researchers documented Siberian Cranes at Poyang foraging on two plant species in upland sedge/forb communities for the first time. In addition, researchers observed multiple instances of Siberian Cranes exhibiting novel aggressive behaviors towards co-foraging White-naped and Eurasian Cranes. These observations provide evidence that under extreme circumstances the requirements of the species are not as rigid as previously suggested and lead to two propositions: 1) the extreme flood event of 2010 provides a tangible boundary for ecosystem function within the Poyang basin, and 2) novel habitat selection patterns and foraging behaviors by species at Poyang give insights into how future extreme events may impact the system's users. More generalized habitat uses by Siberian Cranes could lead to dramatic changes in management and conservation efforts as well as engagement with local policy makers who have committed to conserving the species.

2011-12-09 14:00 Quantitative and qualitative effects of loss of large frugivores on seed dispersal patterns: a New Zealand example

Jana, RC*, *School of Biological Sciences, University of Canterbury*; **Kelly, D**, *School of Biological Sciences, University of Canterbury*; **Richardson, SJ**, *Landcare Research, Lincoln*; **Garcia, D**, *Universidad de Oviedo, Spain*; **Ladley, J**, *School of Biological Sciences, University of Canterbury*; **Clout, MN**, *School of Environment, University of Auckland*; **Karl, BJ**, *Landcare Research, Lincoln*; **Tilley, J**, *School of Environment, University of Auckland*

There is no certainty whether the loss or decline of large frugivores will affect plant regeneration. Discussion has often focused on qualitative effects, i.e. when large-seeded plants are left with no competent dispersers. Here we test for quantitative effects, i.e. changes in the spatial pattern of seed movement when large frugivores decline relative to small frugivores. In New Zealand the last remaining large native frugivore is the New Zealand pigeon (*Hemiphaga novaeseelandiae*). Using a 12-year dataset on seed trapping under six tree species with different fruit sizes (3.5–15.5 mm fruit width), we tested for differences in seed-rain composition between species, and evaluated if fruit size and disperser assemblages explain these differences. The small fruit were consumed by both small and large birds, but the largest fruit only by NZ pigeons. We found that there was a gradient in the proportion of heterospecific seeds found under the canopy, from one species having 1% (*Elaeocarpus dentatus*) to other with 99% heterospecific seeds (*Dacrydium cupressinum*). In addition, the deposition patterns of large-fruit species were skewed towards under the canopy of other large-fruited species. This creates spatial heterogeneity in the composition of the seed rain under large- and small-fruited canopies, due to interactions between fruit and crop size, fruit attractiveness, and disperser composition and behaviour. Thus, a relative reduction in large frugivores can alter seed dispersal both qualitatively and quantitatively.

2011-12-08 10:30 Herbivory Interactions Cause Phylogenetic Changes in Pinyon-Associated Communities

Jarvis, KJ*, *Northern Arizona University*; **Craig, AJ**, *Northern Arizona University*; **Allan, GJ**, *Northern Arizona University*; **Whitham, TG**, *Northern Arizona University*; **Beresic-Perrins, RK**, *Northern Arizona University*; **Stone, AC**, *Northern Arizona University*; **Gehring, CA**, *Northern Arizona University*;

We examined the hypothesis that pinyon host trees that are structurally altered by scale insect attack will support arthropod and mycorrhizal fungal communities with differing phylogenetic patterns. We collected community composition and abundance data on pinyon hosts susceptible and resistant to scale insects. We then assessed these data in relation to phylogenetic relationships among community members in the two community types. We found three major patterns: 1) arthropod

communities are phylogenetically clustered, especially communities on scale resistant hosts. This indicates that these arthropod communities are composed of species more closely related to each other than would be expected due to chance. 2) Mycorrhizal fungal communities exhibited low to no levels of clustering; 3) Phylogenetic Beta Diversity analyses indicated high levels of phylogenetic diversity from one host tree to the next in both arthropod and mycorrhizal fungal communities. These results suggest that the lineages that compose both community types can vary widely, but that the arthropod communities that are present are relatively closely related. This indicates that a single ecological interaction with potential genetic basis, such as scale herbivory, can have wide ranging effects on associated communities, and that restoration efforts focusing on single genotypes may not support the community diversity that multiple genotypes would.

2011-12-08 14:16 Invasive blackberry (*Rubus fruticosus* aggregate) retains the diversity of small terrestrial mammals in degraded landscapes
Jasmin Packer*, *University of Adelaide*; **Sue Carthew**, *University of Adelaide*; **David Paull**, *University of New South Wales*;

Invasive weeds are well recognised as a major threat to biodiversity worldwide. Yet surprisingly little is known of their contrasting role as habitat for fauna, nor of their effect on populations. Blackberry is a highly invasive Weed of National Significance and is considered a major threat to biodiversity in the Mount Lofty Ranges of South Australia, one of 15 National Biodiversity Hotspots. It is therefore being cleared extensively from sites, including where it is known to provide habitat for the endangered Southern brown bandicoot (*Isodon obesulus*) and other native fauna. Our research is investigating the effect of blackberry (*Rubus fruticosus* aggregate) as habitat for small terrestrial mammals. We surveyed 9 sites in the Mount Lofty Ranges during March-April 2010. The sites represented three habitat treatments: 1. control (dense native vegetation with no blackberry) 2. blackberry within dense native vegetation and 3. blackberry within sparse native vegetation. Paired trapping grids were set up 100m apart in the blackberry and native vegetation. Species richness was comparable across all sites. However, the species richness and abundance of small mammals was significantly higher in the blackberry than 100m away in native vegetation, regardless of whether the native vegetation was dense or sparse. The findings indicate that blackberry may be providing critical habitat for the persistence of small native mammals where the surrounding vegetation is sparse. This study is part of PhD research investigating the quality of habitat provided by blackberry for the endangered Southern brown bandicoot, and whether it is critical for their persistence. The research findings are informing conservation strategies for this threatened species in the Mt Lofty Ranges of South Australia.

2011-12-09 11:26 Community surveys increase the awareness and habitat restoration for the endangered Southern brown bandicoot (*Isodon obesulus*) by landholders

Jasmin Packer*, *University of Adelaide*;

The Sturt Upper Reaches Landcare Group Inc. has been training and supporting local landholders to monitor the endangered Southern brown bandicoot (*Isodon obesulus*) on their property since 2003. Each year landholders conduct hair funnel and vegetation surveys to detect bandicoot presence on their property. The findings indicate that landholders are able to reliably survey for bandicoot presence and conduct basic vegetation surveys, that bandicoot populations have been stable in the region during 2003-2010 and that the threshold for maximum distance from dense habitat for bandicoot presence is 20 metres. In early 2011 an evaluation of the program was conducted, including surveying landholders to assess their perception of the effect of the program on their knowledge of bandicoot conservation needs, and on their planning and action to restore habitat on their property. The majority of landholders indicated that their involvement in the program has increased their knowledge of bandicoots and their conservation needs, and that it has improved both their planning and action to restore native vegetation as habitat on their property.

2011-12-07 11:00 Lost islands? Biodiversity conservation weaknesses, challenges and opportunities in French Pacific islands

Jean-Yves Meyer*, *Délégation à la Recherche, French Polynesia*; **Atoloto Malau**, *Service de l'Environnement, Wallis and Futuna*;

The overseas territories of French Polynesia (FP) and Wallis and Futuna



(WF) are two French overseas territories located in the South Pacific, similarly surrounded by English-speaking island countries. FP includes 120 islands with a high number of endemic plants and animals, and a wide diversity of natural habitats. The comparatively small WF is composed of three islands located between Samoa, Tonga and Fiji, with a low number of endemics and few remaining native forests under high anthropogenic pressure. Whereas FP has a network of protected areas and has launched conservation programs on endangered species, WF has no legally protected area or species. The ability of France to support biodiversity conservation is limited because protection falls under the jurisdiction of local governments. Large conservation organizations are absent and only a few local nature protection groups are active. Furthermore, conflicts of interest with local communities (e.g. marine turtles) and different perceptions of species and habitats value (agrosystems vs natural ecosystems) increase the constraints facing conservation. We advocate for the reconciliation between modern and traditional conceptions of nature, the integration of local knowledge, and for more collaboration between FP and WF and their neighbouring island states and territories which were historically separated by colonialism.

2011-12-08 11:45 Climate change and freshwater ecosystems in Oceania: an assessment of vulnerability and adaptation opportunities
Jenkins, KM*, *University of NSW*; **Kingsford, RT**, *University of NSW*; **Closs, GP**, *University of Otago*; **Wolfendenac, BJ**, *New South Wales Office of Water*; **Matthaei, C**, *University of Otago*; **Hay, S**, *University of NSW*;

Human-forced climate change significantly threatens the world's freshwater ecosystems, through projected changes to rainfall, temperature and sea level. We examined the threats and adaptation opportunities to climate change in a diverse selection of rivers and wetlands from Oceania (Australia, New Zealand and Pacific Islands). We found common themes, but also important regional differences. In regulated floodplain rivers in dry regions (i.e. Australia), reduced flooding projected with climate change is a veneer on current losses, but impacts ramp up by 2070. Increasing drought threatens biota as the time between floods extends. Current measures addressing water allocations and dam management can be extended to adapt to climate change, with water buy-back and environmental flows critical. Freshwater wetlands along coastal Oceania are threatened by elevated salinity as sea level rises, potentially mitigated by levee banks. In mountainous regions of New Zealand, the biodiversity of largely pristine glacial and snow melt rivers is threatened by temperature increases, particularly endemic species. Australian snow melt rivers face similar problems, compounding impacts of hydro-electric schemes. Translocation of species and control of invasive species are the main adaptations. Changes to flow regime and rising water temperatures and sea levels are the main threats of climate change on freshwater ecosystems. Besides lowering emissions, reducing impacts of water consumption and protecting or restoring connectivity and refugia are key adaptations for conservation of freshwater ecosystems. Despite these clear imperatives, policy and management has been slow to respond, even in developed regions with significant resources to tackle such complex issues.

2011-12-06 16:30 Patterns of bushmeat consumption in eastern Madagascar

Jenkins, R K B, *Bangor University, UK & Madagasikara Voakajy, Madagascar*; **Keane, A M***, *University College London & Institute of Zoology, UK*; **Rakotoarivelo, A A**, *Madagasikara Voakajy, Madagascar*; **Rakotomboavonjy, V**, *Madagasikara Voakajy, Madagascar*; **Randrianandrianina, F H**, *Madagasikara Voakajy, Madagascar*; **Razafimanahaka, H J**, *Madagasikara Voakajy, Madagascar*; **Ralaarimalala, S R**, *Madagasikara Voakajy, Madagascar*; **Jones, J P G**, *Bangor University, UK*

Wild meat consumption from tropical forests is a major threat to biodiversity and a potential pathway for transmission of emerging diseases. Understanding patterns of bushmeat consumption is important for designing mitigation measures. Madagascar is one of the world's 'hottest' biodiversity hotspots, but the issue of hunting as a threat to biodiversity on the island is only now being fully recognised. Using interviews with 1154 households in 12 communes in eastern Madagascar and local monitoring data we investigated the importance of socio-economic variables, taste preference and traditional taboos on consumption of 50 wild and domestic species. Most meals contain no animal protein, but 95% of respondents have eaten at least one

protected species during their lifetime (and nearly 45% have eaten >10). The rural/urban divide and wealth are shown to be important predictors of bushmeat consumption, but their effects vary between species. Bushmeat species are generally less preferred than fish or domestic animals, suggesting that projects which increase the availability of domestic protein may have success at reducing demand. In the past taboos have provided protection to certain species, particularly the Endangered Indri, but our data suggest that this protection is rapidly eroding. Urgent action is required to ensure that heavily hunted species are adequately protected.

2011-12-08 18:30 The genetic status of threatened Manchurian trout (*Brachymystax lenok* Pallas; Salmoninae, Salmonidae) in Korea, inferred from mitochondrial DNA sequences

Jeong-Nam Yu*, *National Institute of Biological Resources*; **Young-Woon Lim**, *Seoul National University*; **Soonok Kim**, *National Institute of Biological Resources*; **Myounghai Kwak**, *National Institute of Biological Resources*;

The genetic status of Manchurian trout (*Brachymystax lenok*) in two distinct Rivers, Han River and Nakdong River, in Korea was investigated. Since this area is the southern limit line of Manchurian trout, the distribution of this species was brought to the attention of scientist as well as the public. According to the records, Manchurian trout in Nakdong River has been extinct and artificial seedlings from Han River were introduced into Nakdong River in 1980's. The mitochondrial control region (CR) of 68 individuals from two rivers was characterized into 9 haplotypes with 18 variable sites. Among two haplotypes from Nakdong River, one (H1) was dominantly found in Han River but the other (H5) was only found in Nakdong River. Moreover, populations in Nakdong River showed high haplotype diversity but low nucleotide diversity, suggesting rapid population growth from a small ancestral population. Thus, we suspected that H5 haplotype might be a private Nakdong genotype, suggesting that Manchurian trout in Nakdong River had not been extinct. The two genotypes can be explained that the very small number Nakdong endemic survivors (H1) and introduced Han River founders (H5). The alternative hypothesis is that H1 genotype was very rare genotype in Han River but it might be introduced into Nakdong River. Our genetic analysis about Manchurian trout shows that the declaration of extinct in Nakdong River might have been impatient and introduction of individuals should be determined after genetic analysis, even though it is from geographically very close distance.

2011-12-08 18:30 The genetic variation of Korean water deer (*Hydropotes inermis argyropus*; Cervidae, Hydropotinae) inferred from mitochondrial and nuclear microsatellite markers

Jeong-Nam Yu, *National Institute of Biological Resources*; **Jumin Jun***, *National Institute of Biological Resources*; **Changman Won**, *National Institute of Biological Resources*; **Byoung-Yoon Lee**, *National Institute of Biological Resources*; **Myounghai Kwak**, *National Institute of Biological Resources*;

The vulnerable water deer (*Hydropotes inermis argyropus*) was investigated for extent of genetic variation using mitochondrial control region and 82 nuclear microsatellite markers. Firstly, the complete mitogenome of Korean water deer (*H. i. argyropus*) was obtained and compared to previously reported Chinese water deer mitogenome (*H. i. inermis*). Overall characteristics of two mitogenomes were identical and 98-100% nucleotide sequence similarities exist between them. Using next generation sequencing (NGS), we developed water deer specific microsatellite markers. We chose 400 microsatellites with higher copy numbers from di-repeat motifs for PCR amplification and assessment of polymorphism. Of these, the 79 markers were polymorphic with 2 to 11 alleles (total 334 alleles). We compared genetic variation between two Korean and Chinese subspecies using 3 microsatellite markers and it showed clear genetic differentiation between them. Moreover, Korean water deer showed lower value of H_e and H_o compared to Chinese population, even though Korean water deer has hundred-fold bigger and stable population size than Chinese. This implies limited gene flow between the Korean water deer populations, caused by habitat fragmentation or extreme bottleneck phenomenon in Korea, recently.