

reported as the proximal cause of mortality events in declining amphibian populations of Panama and Queensland, Australia in 1998. Since then, a great deal of research into its pathology, etiology, ecology and impact on host populations has been conducted by researchers in the USA, Australia and other countries. Here, we report some significant recent findings. These include hypotheses on the origin of chytridiomycosis and the causes of its recent emergence in some populations. Recent findings show that some populations of susceptible species can persist in the presence of the disease and that in others, the pathogen continues to cause severe, rapid depopulation. Other work has examined how this disease causes death in amphibians, and how immunological defenses and behavior act to fight primary infection. Finally, these data, information on the biological characteristics of the pathogen and on the life history and behavioral traits of host species allow us to deduce why some species decline and others persist as this disease moves through populations.

Molecular DNA variation and mitochondrial sequence analysis of *Triturus v. vittatus* (Urodela) at different breeding place altitudes at its southern distribution limit

Degani G³, Pearlson O^{1,2}, Blaustein L², Goldberg D¹

¹MIGAL - Galilee Technology Center, P.O. Box 831, Kiryat Shmona 10200, Israel

School of Science and Technology, Tel-Hai Academic College, Galilee, Israel

²Institute of Evolution, Faculty of Sciences and Science Education, Haifa University, Israel

³Faculty of Civil and Environmental Engineering, Technion - Israel Institute of Technology, Israel
oren@migl.org.il

Molecular DNA variations in sub-species *Triturus vittatus vittatus* larvae at different breeding places in northern and central Israel, its southern distribution limit, were studied. Altitudes ranged from 740 meters above sea level (ASL) to sea level. Genetic variations were studied using RAPD-PCR and sequencing of conserved and variable mitochondria DNA genes, the cytochrome b fragment and the most variable part of the mitochondrial genome, the control region (D-loop). The cDNA sequence of cytochrome b fragment (413 bp long clone) was determined and differed in only four base pairs, starting at nucleotide position 32 (Nahalit pond, altitude of 665 m ASL), 237 (Amiad, 212 m ASL), 250 (Dovev, 740 m ASL), and ending at 355 (Nahalit). Dovev, the highest altitude pond examined in this study, was the most variable. The cDNA sequence control region fragment was determined from a 569 bp long clone and differed in seven base pairs, starting at nucleotide position 7 (Afeka pond, 15 m ASL), 102 (Amiad), 103 (Afeka), 294 (Afeka), 390 (Dovev), and ending at 565 (Amiad) and 567 (Nahalit). Afeka, the lowest altitude pond and farthest away from the others, was the most variable followed by Dovev at the highest

altitude. The control region was found to be more variable in the lowest and highest altitude ponds, possibly being affected by differences in ecological conditions.

Are cannibalistic morphs of the tiger salamander obligatory cannibals?

Denoël M^{1,2}, Whiteman HH^{2,3} and Wissinger SA^{2,4}

¹Chargé de Recherches FNRS, Behavioural Biology Unit, Department of Environmental Sciences, University of Liège, 4020 Liège, Belgium

²Rocky Mountain Biological Laboratory, Crested Butte, CO 81224, USA;

³Department of Biological Sciences, Murray State University, Murray, KY 42071, USA;

⁴Biology Department, Allegheny College, Meadville, PA 16335, USA

Mathieu.Denoel@ulg.ac.be

Tiger salamanders exhibit alternative trophic morphologies, with cannibals developing a larger head and longer teeth than typical larvae. Resource partitioning is known between morphs, with cannibal morphs usually foraging on conspecifics and rarely on small organisms. Our aim was to determine whether the cannibal and typical morphs shift their diets across time and particularly whether conspecifics are necessarily the main prey of cannibals and plankton the primary prey of typicals. We found that only the cannibal morph foraged on conspecifics, but not all the time. Cannibalism typically occurred only early after the ontogenetic divergence between morphs. Cannibals shifted their diet later in the summer to plankton, and this ontogenetic shift led to dietary overlap with the typical morph. In contrast to other studies, our findings suggest that the cannibal morphology actually allows the consumption of a larger variety of prey, rather than specialization on specific resources (i.e., conspecifics). The outcomes of the cannibalistic ontogenetic pathway include a higher biomass intake from food and a larger size than typicals. From a foraging perspective, the cannibalism pathway is clearly advantageous over the typical morphology. However, the increased diet breadth of cannibal morphs found in this study suggests that the maintenance of the polyphenism is more complex than has previously been suggested.

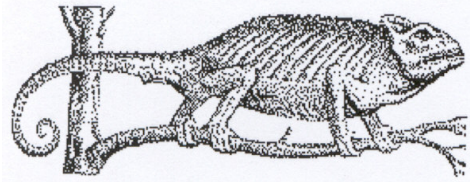
Structure of the herpetofauna of two wildlife management areas in Ouachita Parish, Louisiana, USA

Dixson M and Carr JL

The University of Louisiana at Monroe, Department of Biology, Monroe, LA 71209-0520, USA

Madixson23@yahoo.com

Ouachita (OWMA) and Russell Sage Wildlife Management Areas (RSWMA) are state-owned and managed public lands in Ouachita Parish, northeast Louisiana. Both are comprised of bottomland hardwood forest within the Bayou Lafourche floodplain, although OWMA also has extensive areas of reforested



**FIFTH
WORLD CONGRESS
OF
HERPETOLOGY**

STELLENBOSCH

June 2005

ABSTRACTS AND PROGRAMME

5th World Congress of Herpetology General Business Meeting

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**Tuesday 21 June 17:30 at Jannasch
Hall, Conservatory of Music,
Stellenbosch University**

1. Opening of the meeting
2. Minutes of the last meeting
3. Report of the Secretary-General
4. Report of the Secretary-Elect: Next venue for the World Congress of Herpetology
5. Report of the Treasurer
6. Report of the Auditors
7. Report of the Congress Director
8. Elections:
 - 8.1 Executive Committee
 - 8.2 International Herpetological Committee
9. Future role of the International Herpetological Committee
10. Any other business

Note: All congress participants have the right to take part and vote in the meeting. A list of eligible candidates for the Committees will be distributed with this programme. Additional items for the agenda can be presented to the Secretary General until 24 hours before the business meeting.