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Contributed Abstracts

C1. Preliminary Results from a Baraminological Analysis of the Mole Salamanders (Caudata: Ambystomatidae)

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The mole salamander family (Caudata: Ambystomatidae) consists of 32 extant species in the single genus *Ambystoma* and is widely distributed throughout most of North America (Petranka, 1998; Frost et al., 2006; Pauly et al., 2007). We analyzed a published morphological dataset (Kraus, 1988) using baraminic distance correlation (BDC) and classical multidimensional scaling (MDS) on uncorrected distance matrices. The dataset consists of 32 characters from 14 extant ambystomatids (U.S. bisexual species) and nine extant outgroup taxa (genera from the Dicamptodontidae, Rhyacotritonidae, Plethodontidae, and Salamandridae) but excludes the ambystomatid species from the Mexican radiation (Shaffer, 1984; Reilly and Brandon, 1994; Shaffer and McKnight, 1996). We analyzed the following subsets of data: 1) BDC and MDS on complete dataset (character relevance = 0.85; 21 characters; 3D stress = 0.16); 2) BDC on dataset minus four *Ambystoma* species from the subgenus *Linguaelapsus* (character relevance = 0.85; 19 characters); 3) BDC and MDS on dataset including all *Ambystoma* species, but with *Dicamptodon* and *Rhyacotriton* (the most closely related outgroups according to conventional taxonomy; Tihen, 1958; Sever, 1992; Good and Wake, 1992; Petranka, 1998) as the only outgroups (character relevance = 0.95; 29 characters; 3D stress = 0.09); 4) BDC on dataset minus four *Ambystoma* species from the subgenus *Linguaelapsus*, but with *Dicamptodon* and *Rhyacotriton* as the only outgroups (character relevance = 0.95; 30 characters). A consistent pattern emerges from these various analyses. First, most of the subgenus *Linguaelapsus* displays both internal continuity and discontinuity with other groups in BDC, and forms distinct and well separated clusters in 3D-MDS. Second, most of the remaining *Ambystoma* (all but *A. gracile*) display internal continuity but lack discontinuity with all outgroups in BDC, and form only poorly separated clusters in 3D-MDS. Finally, *A. gracile* is continuous with *Dicamptodon* and *Rhyacotriton* in both BDC and 3D-MDS. An analysis of hybridization within this family reveals 33 unique interspecific crosses. Ten of these confirm the internal continuity of the second *Ambystoma* group in this study and four connect it with the subgenus *Linguaelapsus*. Based on the results of BDC, MDS, and hybridization, we conclude that all *Ambystoma* in this study (with the possible exception of *A. gracile*) represent one monobaramin. Additionally, seven interspecific crosses establish the internal continuity of the Mexican ambystomatids, two connect the subgenus *Linguaelapsus* to the Mexican ambystomatids, and ten connect the Mexican ambystomatids with the second *Ambystoma* group from this study. Based on these hybridization results and the fact that the entire Mexican ambystomatid radiation is thought to be a monophyletic assemblage related to *A. tigrinum* (Shaffer, 1984; Shaffer and McKnight, 1996), we conclude that the entire family Ambystomatidae represents a single monobaramin. The presence of discontinuity below the genus level in this study (between the subgenus *Linguaelapsus* and the other groups) may be due to the nature of the characters selected for analysis. One of the purposes of Kraus' (1988) paper, after all, was to elucidate relationships within the genus *Ambystoma*. This apparent discontinuity may also be due, however, to insufficient numbers of characters in the analyses and/or the potentially close relationship between *Ambystoma* and the outgroup taxa (particularly *Dicamptodon* and *Rhyacotriton*). Future analyses will utilize a dataset containing 115 characters for the same group of taxa, and the potential for different groupings of outgroup taxa (Kraus, 1987).

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C2. A Systems Biology Paradigm for Cellular Pathways and Organismic Populations: Insights from Principles of Systems Engineering

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Biology and its theoretical apparatus are largely guided by the axiom of materialistic reductionism (Autumn 2002; Auyang 1998; Robert *et al*. 2001); understanding complex systems achieved by breaking them down into smaller objects/components, whose individual explanation lead to the system explanation. The reductionist paradigm now hinders the development of both systems and cellular biology (Autumn 2002; Robert *et al*. 2001; Srere 2000). Reductionist over simplifications is seriously hampering understanding of diversification of biological populations and dynamics of ecosystems (Auyang 1998, Autumn 2002). Aristotle (Dwyer 1999; Lee 2003; Lennox 2000; Srere 2000) put forth the idea of synergy (Corning 1995, 1996, 1998, 2003, 2005; Dwyer 1999; Robert *et al*. 2001) as a paradigm to make sense of the world.

Synergy provides a framework for defining systems biology and for understanding of biological phenomena. Within systems engineering (Fink 1996) and cybernetics (Ashby 1957), a system may be thought of as a synergistic, complex, coadapted, codependent arrangement of objects/components (also subsystems), where the final effect/function/performance greatly exceeds the sum of the parts. System level behaviors result from the information flows (form, fit, and function) and synergistic interactions between corresponding functional components (Fink 1996).

Analogies with engineered software/hardware systems (Auyang 1998; Fink 1996) provide insight into biological systems and a framework for systems biology research; spanning biology from cellular systems, to biological populations, onto entire ecosystems. Problems in control, locomotion, signal transduction and signal processing have similarities to those encountered in hardware, like robotic systems. Systems biology provides a better framework for understanding natural history than atomic level, mechanistic explanations taken in isolation (Autumn 2002). System engineering principles provide tools to investigate the adaptive, feedback control and maintenance of complex systems operating in a robust, dynamic equilibrium within changing environments, accomplished through flows of system signals/information.

Hybrid computing systems are digital (discrete)/analog (variable) in nature. Regulating interlocking cellular metabolite processing control systems and signal transduction pathways represent hybrid computing/control. Metabolites' concentrations are analogous to voltages, and metabolite flow rates through enzymatic processing systems are analogous to current flow. Regulatory control of enzymes may be modeled with analog elements such as transistors, where gain is analogous to enzyme turn over rates, and comparators, where voltage thresholds are comparable to enzyme substrate dissociation constants (50% up progress curve, Lehinger 2004).

Cellular control systems using "random number generation" (thermal noise) for Monte-Carlo combinatorial optimization algorithms (simulated annealing, Cavanaugh 1988) are exemplified by copying errors producing the hyper-variable regions of antibodies through a sloppy DNA polymerase (1:100 to 1:1000, Lehinger 2004). A self directed, constrained DNA hyper-mutation in response to environmental stress or abundance might cause significant variation within basic kinds. Evidence of diversification trajectories have appeared in baraminological studies, providing evidence of ahistorical, perhaps adaptive (epigenetic? Jablonka 2005) morphogenetic systems. Such patterns could be explained by a neo-Lamarckian/systems theory (Lindberg 1998) diversification paradigm, resulting in a successful framework for understanding natural history and relationships among organisms within ecosystems.

Lamarckian vitalism may be understood as the synergistic interaction of interlocking molecular sub-systems maintaining a robust, dynamical equilibrium (Srere 2000). Lamarckian orthogenesis may be understood as behavioral or structural adaptation to ecological environments/niches by self sorting through learned behaviors, imprinting or organismic preferences (Corning 1995; Robert *et al*. 2001) derived from genetic/epigenetic variation, with reproductive isolation from historical contingency/canalization. Orthogenetic variation could arise from environmental feedback (environmental stress or opportunity) stimulating individual morphogenetic systems within biological populations to go to a state of self directed, hyper-mutation of germ line genetic information, resulting in correlated suites of characters achieving either trajectories or "orbits" about Chaotic strange attractors in morphospace.

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