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distributed larval habitats.

(693) (NB52C-02) Phylogenetic Relationships of *Cottus beldingi* in the Basin and Range and Colorado Plateau of Western North America.

Crystal N. Smith[1], Jared M. Crowley[1], Dennis K. Shiozawa[1], and R. Paul Evans[2]. [1]Brigham Young University, Department of Integrative Biology, Provo, UT, USA, [2]Brigham Young University, Department of Molecular and Microbiology, Provo, UT, USA
buggirl225@aol.com

Cottus beldingi (Paiute sculpin) is found in scattered populations across the Western United States. Their distribution should be related to ancient river connections. To investigate these relationships, *C. beldingi* were collected from 14 locations in Nevada, Utah, Idaho, Colorado, and Wyoming. Three regions of mitochondrial DNA were sequenced including a 363 bp segment of ND4-L/ND4 gene, the cyt b gene, and the d-loop. Phylogenies were constructed using Maximum Parsimony (PAUP), Maximum Likelihood (PAML), and Bayesian analysis (MrBayes). Preliminary analyses of the ND4 gene show Lahonta Basin (Nevada) *C. beldingi* have the most basal relationship in phylogenies based on Maximum Parsimony and Maximum Likelihood. *C. beldingi* in the Lost River system of Idaho, Eagle River of Colorado, and the Provo and Weber Rivers of the Bonneville Basin form a clade. Populations from the Upper Snake River of Idaho and Wyoming, and the Logan River drainage form a separate clade. The latter clade may reflect the capture of the Bear River and subsequent Bonneville flood 18,000 to 30,000 years ago. The former clade is likely a result of older drainage connections.

(694) (NB52C-03) Distribution and Feeding Preferences of Newfoundland larval Hydropsychidae.

Cherie-Lee Fietsch and Murray Colbo. Memorial University of Newfoundland, Biology Department, St. John's, NL, CAN
w02clf@mun.ca

Caddisflies of the family Hydropsychidae (Trichoptera) are widely distributed across North America (145 species), however the large scale distribution of the impoverished Newfoundland fauna (8 species) is unknown. Low species diversity and irregular stream profiles on the island provide a template for community distribution. Sampling a variety of rivers at lake outlets and downstream in forested and barren habitats revealed the influence of landscape on Hydropsychidae distribution and abundance. Forested and barren streams supported the same species of hydropsychids but barren streams generally had much lower densities. Community composition changed on a longitudinal gradient. Extensive measurements of nutrient quantity (phytoplankton, zooplankton, periphyton) did not strongly correlate with community composition or landscape effects. The literature suggests that nutrient quality may have a stronger influence due to premised resource partitioning. One method of investigation is lipid analysis, where nutrient composition is determined via free fatty acid biomarkers. Preliminary results indicate that the fauna are general opportunists, feeding over a range of trophic levels, with outlet community feeding habits being distinctive from downstream. Current trophic categorizations of hydropsychids are questioned.

(695) (NB52C-04) How to Compare Biomass and Drift of the River Benthos?
Victor Vsevolodovich Bogatov. Institute of Biology and Soil Science, Far Eastern Branch,

Russian Academy of Sciences, 159, pr-kt 100 letia Vladivostoka, Vladivostok, RUS
bogatov@ibss.dvo.ru

Drift flux per unit bottom area (D_b) of different river reaches can be expediently estimated as biomass of transported organisms at a particular collection time through the cross sectional area of water flow for width of 1 m and height equals to the depth of river part (H, m) at the time of sampling (D_b, mg/m^2/day). In this case, independent of river depth, water velocity and discharge D_b for 24 h will be defined as simple multiplication of two parameters: $D_b = L(m) \times M_b$ (mg/m^3/day), where L is distance of drift and M_b is daily migratory activity of the aquatic organisms equals biomass of organisms lifted during 24 h from 1 m^2 of the river bottom into the water column with volume 1 m$^2 \times$ H. This method allows one to calculate specific drift rate (D_{cb}), which takes into account benthic density on the river bottom and is estimated with units of inverse time, i.e., the fraction of benthic biomass that enters the drift in 24 hours. So $D_b = D_b/B$, where B is biomass of benthos, mg/1 m^2 The specific drift rate calculated for various groups of invertebrates surprisingly showed a negative correlation between D_{cb} and benthic biomass. Thus, our results contradict the generally accepted hypothesis describing drift as competition among aquatic organisms for food and substratum.

(696) **(NB52C-05) Taxonomic Resolution as a Conceptual Problem for Understanding Ecological Science.**

Toben Lafrancois. University of Minnesota, Department of Philosophy 831 Heller Hall 271 19th Ave South, Minneapolis, MN, USA
lafr0026@umn.edu

The results of ecological analyses can vary with the taxonomic resolution(s) used to sort and quantify the organisms studied. It seems intuitive that the finest unit of taxonomy results in the finest discrimination of ecological processes, and this is certainly true in many cases (e.g. Hawkins 2000, Attayde 2001). However, other important work suggests that some ecological processes (e.g. Bowman 1997) or concepts (e.g. Schoener 1986, Olsgard 1998) are only supported by analysis at supra-specific taxonomic resolution. In fact, taxonomic levels above species are often necessary for detecting certain ecological relationships, such as key measurements of food webs (Vanderklift 1998) or stability of ecological communities over time (Bowman 1997). If some levels of organization result in different ecological outcomes, two questions are immediately raised. First, why do these levels lead to different outcomes, and second, what is the basis of choosing one resolution over another? I will address the first question by outlining four aspects of the problematic relationship between taxonomy and ecology: taxonomic variance, taxonomic heterogeneity, and taxonomic ambiguity both within and between groups. I aim to show that these interactions suggest a dependence relationship of ecological outcomes on taxonomic concepts.

(697) **(NB52C-06) Molecular phylogeny of the Drusinae (Trichoptera: Limnephilidae): preliminary results.**

Steffen Pauls[1], Thorsten Lumbsch[2], and Peter Haase[1]. [1]Department of Conservation and Limnology, Research Institute Senckenberg, Lochmuehle 2, Biebergemuend-Bieber, HE, DEU, [2]Department of Botany, The Field Museum, 1400 S. Lake Shore Drive, Chicago, IL, USA
steffen.pauls@senckenberg.de