Introduction:
The phylogeny of Ephemeroptera has undergone revision based on morphological work (Jacobus and McCafferty, 2004 & 2006; and Jacobus and Sartori, 2006) and has recently undergone molecular analysis on select species (Ogden et al., 2009a & 2009b). The research indicates that there are some incongruences between molecular and morphological trees. For example, the genera Attenella and its placement within the tree, being located either in the subfamily Timpanogoninae or the subfamily Ephemeroptera. The monophyly of certain genera (Ephemarella and Drunella) are unclear as well. We performed the largest DNA analysis of Ephemeroptera to date, a study consisting of over 20 genera, in order to further investigate the relationships within the Ephemeroptera.

Methods:
- PCR & sequencing of six genes: Cytochrome Oxidase 1; Histone; Mitochondrial 12S & 16S rDNA; Nuclear 18S & 28S rDNA
- Phylogenetic analyses were performed via MEGA (Tamura et al. 2007)
- Alignment in Muscle (Edgar 2004a, 2004b)
- Tree reconstruction was performed under Parsimony and Likelihood (GTR+Γ model).
- Bootstrap analyses consisted of 100 reps in ML and 1000 reps in MP.

Results:
- 6307 aligned sites; 1449 were parsimony informative
- 8 most parsimonious trees with length 7237
- Likelihood tree with -42194.93 Score
- 38% missing data

Conclusions:
- Drunella likely monophyletic
- Ephemarella non-monophyletic
- Timpanogoninae non-monophyletic

Acknowledgements:
Funding: UVU SAC Grants, GIF Grants, SCO grants
UVU Faculty and Staff: Dr. Catherine Stephen, Dr. Jim Harkin, Dr. Olga Kopp, Laura Kornsjo, Kelli Hancock, Ogden Lab members
Collaborator: Dr. Luke Jacobus

References: