**Molecular Biogeography of the amphipod genus *Hyalella* in North America**

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Once thought to be one of the most broadly distributed North American freshwater invertebrates, the amphipod *Hyalella azteca* has since been characterized as a morphologically cryptic complex of over ninety species. Two primary ecotypes (a large and small-bodied morph) have been identified and their evolution is thought to have been mediated by size-biased fish predation. The present day distributions of these species have been shaped by their own unique evolutionary pasts in conjunction with the demographic consequences of the Pleistocene glaciations. Specifically, current patterns of variation result from the interplay of vicariance events caused by the advancing glaciers and the subsequent dispersal of hyalellids to post-glacial habitats. These processes had a profound effect on genomic markers, and through the application of phylogenetic and population genetics methodology, we can discern the biogeographic history of the *Hyalella azteca* species complex. To this aim, the diversity of the mitochondrial cytochrome c oxidase subunit I was analyzed, as well as structural and sequential variation within the first internal transcribed spacer (a component of the nuclear rRNA multigene family).   
  
This presentation will compare the post-Pleistocene migration of hyalellid species. It will focus on those members of the *Hyalella azteca* species complex that have successfully recolonized glaciated regions and draw a line of comparison between dispersal patterns of large and small-bodied ecomorphs.