Microorganisms form complex ecosystems that perform many of the basic ecosystem processes of larger systems. Because bacteria form a large portion of these assemblages, their communities make good models for study of many of these processes. One such community is the intestinal microbiome in mammals. In this series of studies, 16S rRNA was used to determine the bacterial community of the lower mouse intestinal microbiome and determine the biogeography of that community. The biogeography of the lower intestine potentially influences how ecosystem developments, such as invasion, take place in the gut. *Clostridium difficile* was used to demonstrate how an invasive organism might take advantage of disturbance in the intestinal microbiome to colonize the intestine. Our current research on the fish mucosal microbiome is focused on similar processes that may occur during colonization of *Flavobacteria* in coldwater disease in Lake Trout (*Salvelinus namaycush*).