

John Hopple Section 17

My interests are broadly defined in mycology but I consider my work to be systematic in nature. Fungal systematics involves everything from collecting and identifying species from the wild (taxonomy) to attempting to establish evolutionary relationships between taxa (phylogenetics). The basidiomycete group I am working is *Coprinus*. *Coprinus* is a cosmopolitan genus of several hundred species. A unique characteristic of the genus is the ability of individual mushrooms to digest themselves during maturation by releasing autolytic enzymes that break down its gills permitting an increased production of spores. This leads to the name Inky Caps as the fungi are often found after autolysis as white stalks with a gooey, drippy, black fluid hanging from the remnants of the mushroom cap. Species are often found in disturbed habitats such as lawns, gardens, pastures, and even within homes. *Coprinus* lends itself to systematic work in that individuals are easy to culture and work with in the laboratory. Many species will actually produce mushrooms following growth in a petri dish!

## Defining Species in Fungi

Species have traditionally been defined in fungi through a morphological species concept. In short, individuals that look similar are classified together and individuals that look different are classified into different species. In the latter half of the 20th century mycologists began applying a biological concept to species. If individual fungi could mate together and produce fertile offspring then they were considered to be the same species. Today we are exploring how species might be defined phylogenetically; by the derived characteristics that have evolved in different species that make them unique. My research is looking at a species complex in the genus *Coprinus* (the Inky Cap mushrooms) called the Lanatuli. The Lanatuli all superficially resemble each other so morphology alone is not useful in species demarcation. Individuals can be mated together to determine their biological species affinity. We are in the process of expanding the number of individuals in the project, determining which biological species they belong to, and then using DNA sequencing to assess their phylogenetic position relative to each other. This project involves species collection from the wild, microbiological work to get individuals in culture and to determine their biological species affinities, and molecular work designed to extract, purify, and sequence DNA from the nuclear genes coding for the large ribosomal subunit.