

## **Exploring bryophyte relationships in the age of high-throughput phylogenetics**

**Norm Wickett** (Chicago Botanic Garden, Chicago, IL)

As is the case for many lineages that are rich in species but lack multiple well-developed model systems, the study of bryophyte systematics had benefitted enormously from advances in DNA sequencing. Bryophytes (mosses, liverworts, and hornworts) are a relatively ancient group of land plants (embryophytes) that, unsurprisingly given their long history, have undergone many instances of rapid radiations, including recently. Therefore, understanding relationships within the bryophyte lineages requires the application of data and analysis that accommodates their long and varied history. While many areas of the bryophyte Tree of Life remain unresolved, I will focus here on two: (1) the relationships of the three bryophyte lineages (Are bryophytes monophyletic?), and (2) the rapid radiation of pleurocarpous mosses. To reconstruct both gene and species histories that address these questions, we have applied both transcriptome and target enrichment data. The combination of these approaches allows us to infer a species tree that takes into account discordance among gene histories (for example, incomplete lineage sorting) and allows us to evaluate levels of support that may be more appropriate than traditional methods. With transcriptome data, in particular, we can use gene trees to infer, at least in part, the history of the genome in addition to the relationships of extant species. In this talk, I will discuss our application of these kinds of data, the development and application of new methods, and the implications for our understanding of bryophyte relationships.