

NIMBioS Short Term Visit – Stacy A Krueger-Hadfield
Public information

Population genetic and genomic markers are powerful tools with which to investigate evolutionary and ecological processes. However, designing an appropriate sampling methodology and deciding on the number of sampled individuals is a major statistical challenge. Often, *ad hoc* sampling or the methodology employed by a previous study is utilized. These choices can result in under- or over-sampling and may provide ambiguous results. Discerning patterns of genetic structure and reproductive systems is, particularly, a problem for haploid-diploid organisms, in which both ploidies need to be sampled. We identified three main goals in a study of haploid-diploid population dynamics: haploid diploid ratios, allele frequencies and paternity analyses. Then, we used stochastic sampling and individual based models to develop broad guidelines that should aid in population genetic sampling designs for haploid-diploid species in general. More specifically, with co-PIs Erik Sotka, Allan Stand and Courtney Murren (CofC) in which we are exploring shifts associated with biological invasions in a widespread, non-native, haploid-diploid red seaweed (NSF BIO OCE- 1357386). The guidelines we have outlined will be used in designing sampling strategies for a massive sampling effort this summer to explore shifts in reproductive mode, mating system and genetic structure. Finally, Sean and I are currently finishing a manuscript to be submitted for peer review in which our guidelines will be available for designing population genetic studies of haploid-diploid organisms.

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