

HerbVar Species Selection Plan

In an attempt to efficiently plan our sampling efforts, the Herbivory Variability Network (HerbVar) will focus on three broad sampling goals: 1) taxonomic breadth, 2) focal families, and 3) focal species. Each emphasis has the ability to explore unique biological questions, which are fleshed out in more detail below. This stratified sampling approach will also help us avoid potential biases in geographic and/or taxonomic coverage.

- 1) Taxonomic breadth: Here we will focus on sampling from as many plant families as possible. The more species the better, but we seek broad taxonomic and geographic coverage. We will provide guidance so that we can avoid potential biases, such as oversampling woody species in the tropics and herbaceous plants in temperate systems. Some repeat surveys of the same species may be helpful as pseudo-controls, but ultimately this objective prioritizes new species in new families over repeat sampling.
 - a) Some questions we can explore with these data are:
 - i) Is there a macroevolutionary, phylogenetic signal to variability and skew in the distribution of herbivory?
 - ii) Are certain functional groups more prone to more variable and skewed distributions (forbs vs. shrubs, etc.)?
- 2) Focal family sampling: Here, we aim to robustly sample many species within five selected focal families: Apocyanaceae, Asteraceae, Fabaceae, Rubiaceae, and Solanaceae. We chose these families due to their global distributions, variation in growth forms, and history of past plant-herbivore studies involving these families. As these families are large, we aim to sample across the phylogeny of each family so that a diversity of subfamilies, tribes, and genera are represented. We also aim to sample across the geographic distributions of these families. The most valuable surveys for the focal family sampling will be of species from subfamilies/tribes we have not yet sampled, as well as species occurring in unique environments or bioclimatic regions. As above, some repeat surveys of the same species may be helpful as pseudo-controls, but ultimately the objective is to sample as many genera and species from each family as possible.
 - a) Some questions we can explore with these data are:
 - i) Do abiotic factors predict herbivory or skewness? Working within a single plant family will allow some phylogenetic control.
 - ii) Do families mainly attacked by specialists vs. generalists result in certain distributions of herbivory (more or less skewed)? We can address this by comparing among the five families.
- 3) Focal species: In addition to inter-specific comparisons, we also aim to robustly sample two globally distributed species (*Taraxacum officinale*, *Plantago major*). This provides a more tightly controlled (intraspecific) way to answer questions about spatial and

temporal variation in herbivory distributions. This approach will be particularly powerful when combined with future common garden experiments in phase two of HerbVar.

a) Some questions we can explore with these data are:

- i) How do herbivory distributions vary geographically, and with abiotic or biotic conditions?

Finally, we would like to emphasize that this plan is the first phase of the Herbivory Variability Network. This phase is largely focused on pattern documentation. Observing and quantifying patterns in the natural world is an essential step in the scientific process, one that yields foundational knowledge, reveals surprising relationships and connections, and inspires and informs mechanistic hypotheses. We are tackling mechanistic hypotheses generated by our initial observational dataset in a second phase of the Herbivory Variability Network using globally-distributed experiments.