Questions for Sam/Tyler:

1. How intensive is field protocol? Can we collect fecal matter and place it in ethanol for a few days until we get back to Florida?
2. How much do we need to worry about degradation? Is collecting fecal matter that ended up in the trap overnight sufficient or does it need to be collected directly from the animal?
3. Which sequence should we use? We’ve read papers that have used both trnL and matK. Pros and cons of each?
4. How do you go about creating a reference library? If we can find sequences for some plants on BOLD but not others, what are the steps for getting sequences for the other plants? For example:
   1. How much plant tissue is required?
   2. How intensive is field collection protocol?
   3. What is the time frame for the library development?
   4. How much is it going to cost to make a reference library of, say, 50 plants?
5. A basic question, but what happens after you’ve collected your fecal samples? Do they get sent off and sequenced somewhere else? How expensive is that? Can the ICBR at UF run them for us?