Points to discuss:

1. It seems (A DNA barcode for land plants, 2009) that the choice of the CBoL workgroup was to pursue a two-locus barcode using rbcL and matK. However, another option was discussed, extracting for 3 loci (including the intergenic spacer trnH-psbA) and further testing for performance both in PCR success and discriminatory power as there is some question about the PCR success for matK and the variability of length in the spacer that might affect the ability for "bidirectional unambiguous sequences".

*Question*: Would it be viable to undertake a 3-locus project of a regional flora (not just angiosperms). This would provide large-scale testing as well as some insurance should the barcode standard change in the future.

Note from the 2009 statement: As stated in the 2009 PNAS paper by the Plant Working Group, "In the short term, where further resolution and universality are required, we envisage that the core rbcL-matK barcode will be augmented in individual projects from a flexible short-list of supplementary loci including the noncoding plastid regions examined here (trnH-psbA, atpF-atpH, and psbK-psbI), and the trnL intron which has been advocated for situations involving highly degraded tissue (19). The rapidly evolving internal transcribed spacers of nuclear ribosomal DNA also represent a useful supplementary barcode in taxonomic groups in which direct sequencing of this locus is possible." For this reason, CBOL's Executive Committee encourages the community to collect data on trnH-psbA and other non-coding regions as a back-up to matK and to enhance protocols for the use of non-coding regions for DNA barcoding.

2. Collaboration: This seems a particularly opportune time to pursue inter-institutional and international collaboration. There is not only the CBoL working group