Hi Pam,

It was great meeting yesterday!! Thank you guys for the great discussion and insightful directions pointing out!

I just want to refresh myself, and it will be helpful for guiding me what I'm going to in future. Please forgive me if I did not remember it clear.

1. Target Enrichment data

# Miao will reconstruct phylogeny for all the samples together for each gene; then using all gene trees with all samples from all groups building a summary coalescent tree using ASTRAL.

WE DISCUSSED THIS A BIT.  IT WAS NEVER THE INTENT TO HAVE A SINGLE TREE, BUT IT MIGHT BE AN INTERESTING WAY TO TEST THE COINCIDENCE OF THE DISJUNCTION ACROSS ALL OF THE GENERA.  I THINK THIS IS A LOWER PRIORITY THAN BUILDING THE INDIVIDUAL GENUS-LEVEL TREES AND DATING THEM.

# Do we need to do this for each individual genus and each individual gene? (sorry my memory is blurred at this part.)

YES, THE KEY PART IS THAT WILL NEED A TREE FOR EACH GENUS:  this means:

1. Build a RAxML tree for each gene for each genus
2. Use ASTRAL to build a species tree for each genus
3. Each genus tree will need to be dated (this is where we will need help from the separate labs to provide calibrations). One of the goals will be to infer the timing of the disjunction(s) in each genus so that we can see how they vary.

# We don't need to do a global tree that combined all genes and all samples (like supermatrix style).

CORRECT, WE WILL NOT HAVE A CONCATENATED TREE, EITHER OVERALL OR FOR EACH GENUS.

# If there was missing data for some genes, Miao will try his best to complete it from GenBank and 1kp data

YES, GOOD!

# Miao will do the dating using treePL after all groups providing their fossil information.

YES, GOOD!

# Miao will finish his tutorial writing for how to assemble target enrichment on UF PHC using Hybpiper and build phylogeny

GREAT, THANKS!  THIS WAY, WE WILL HAVE INFO FOR THE PAPERS THAT WILL RESULT.

2. community phylogeny and PD

# Miao and Hanyang will finish the PD analyses for US-CN community

GREAT!

# For US 6 sites, Ordway, Talladega, Harvard,and Coweeta, we use the species list that Mark complied; for  White Mountain (Bartlett)and Mountain\_Lake we are going to use own customized polygons based on yesterday's discussion.

YES, THANKS. ONE THING TO CHECK ON THE LISTS FROM MARK:  HE SENT DIFFERENT SETS:  FOR EXAMPLE, ONE TIME HE SENT BASICALLY THE ORDWAY SPECIES LIST BASED ON LUCAS’S AND KURT’S WORK, AND LATER HE SENT IT WITH THE 10-KM RADIUS THAT IS BIGGER THAN OSBS.  LET’S GO WITH THE ACTUAL SPECIES LISTS RATHER THAN THE ONES IN WHICH HE ADDED SPECIES BASED ON THE CIRCLES.

FOR WHITE MTN AND MTN LAKE, YES, LET’S USE THE POLYGONS, BUT NOT OUR OWN POLYGONS.  WE DECIDED TO USE THE OUTLINE OF MLBS FOR MTN LAKE AND OF BARTLETT EXPERIMENTAL FOREST FOR WHITE MTN.

ONE OPTION TO MAKE THE AREAS MORE LIKE CHINA WOULD BE TO USE THE CENTER OF EACH US AREA AND MAKE A CIRCLE SO THAT IT HAS THE SAME AREA AS CHINESE SITES (BUT THEY ALSO VARY).  THEN GET THE SPECIMEN RECORDS FROM THE CIRCLES. IT MIGHT BE A WAY TO APPROACH THE SPECIES RICHNESS ISSUE, BUT I LIKE HOW YOU DID IT, SO I’M NOT ADVOCATING THIS, JUST SUGGESTING IT AS ANOTHER OPTION FOR LATER ON, IN CASE WE WANT TO TRY OTHER OPTIONS.