Much recent work has been done on the genomic impacts of hybridization as one spp. expands into the range of another species. Particukarly exciting for us hmans is work calculating the probability of hybridization between humans and other homo lineages as they expanded out of africa, both through contact with neanderthals in Europe and Denisovas in East asia. This work has helped to standardze a computational farmework for investigating expectations of genomic patterns of hybridization which may then me applied to non-model organisms.

Tamias chipmunks in the northwestern rocky mountains show a complex species history, including multiple hybridiazation events between both sister and non sister species. By applying genomoic techniques developed for investigating the impact of demography on gene tree discordance. As mitchondria are uniparentally inherited and have an effective population size of ¼ that of autosomes, the same demographic process on a species level can drive discordance between nuclear and cytogenetic population elements. However, it is also possible for selection to impact the spread of mitchondrial lineage, and this can also result in mtDNA nuc DNA discordance.

As Excoffier et al (????) showed the difference in poulation sizes between nuclear loci and mtDNA can drive different dynamics at the expansion

Summarize comparison to Sarah’s results and add in mtDNA genomes.

Look for selection in the mtDNA… but what about dealing with linkage. Can focus on dN/dS, and pull out targets of selection.

Sequenced taxa - Rfui 1,2 (12ish), aminus (12ish), quadrivitatus group (2), canapes, umbrinus (2) and dorsalas (2)

I need to get from Brice the list of samples.

Make a comparison of

Wait- is this what he meant by opposite direction? mtDNA has a smaller population size- more recent coalescence time- should show LESS introgression that nuc?

Sequence data will be 200-400bp…

Is the genetic architecure of divergence different across different parts of the phylogeny, and to what extent can we differentiate between different models of divergence?

reproductive proteins, X and Y linked markers, mtDNA

anonymous markers from cDNA

what fraction of the genome is involved and what fraction of the genome is introgressing-

and how often do we expect there to be that much of the genome

dN/dS ratios in multfarious selection vs hitchiking…

what if we include codon based models-

WHY are the sites diverged?

does it look neutral??

write out a mathematical model for our scenario models…

Trancriptoime seq…

12,000 exons.

10,500 contigs…

20K are found in the mouse genome?

10.5K contigs.

300 bp-3000

diploid seq with some missing data and a decent amount of hets

How much nuclear introgression is there and is it asymettric?

TA TAc Tas