The data:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Type** | **# samples** | **Sequence status** | **Description** | **Source/Location** |
| Exon capture | 260 | Complete | 1400 exon capture; goal is for all murine species (~700) | Kevin’s lab |
| Exome | 48 | Complete | Across murinae; used in Emily’s paper and by Gregg | Kevin’s lab; Gregg |
| Exome | 48 | Complete | Focused on division Pseudomys | Kevin’s lab; Carl |
| Exome | 10 | Complete | Mus samples from Jeff’s 2017 paper | Jeff’s lab |
| Exome | 73 | In progress | Across murinae | Jeff’s lab |
| Genome | 9 | Complete | 8 Mus strains/species and *Rattus norvegicus* | Ensembl; Gregg |
| Genome | 6 | Complete | Mostly African murinae | Mike Lampson and Mia Levine at Upenn; Gregg |
| Genome | 2 | Complete | Mastacomys and Pseudomys | Kevin’s lab |
| Genome | 6 | Proposed | Body size/longevity contrasts and convergence | Samples somewhere |

\* Note that Ensembl has many other non-murine rodents that I will use in whole genome analyses.

The plan:

1. Carl and I will combine our exome data and work on the best assembly/mapping method. Carl will focus on assembly with Spades and I will develop an iterative mapping approach. We will need to figure out a way to compare approaches

Carl: I will set us up a Box folder and email you in the next day or so.

1. Response requested: If no one objects, I would like to compile all data in a single location (Box folder?) preferably with the top of the directory tree being the three folders *exon-capture*, *exomes*, and *genomes*, and sub-folders for each species sampled which would contain reads, mappings, and assemblies. What do you all think?
2. For exomes, we are freezing the sampling at what is listed above. Though there was talk of sequencing all species of some genera. What would the timeframe of that be?
3. For now, I would only use a few Pseudomys exomes from the 48 Carl is using so the sampling is not to heavy from that single division. Carl and I can discuss which ones would be best for my analyses.
4. For whole genome sequencing, we are proposing to sequence:
   1. Phloeomys, Musseromys, Papagomys, and Komodomys for body size/longevity contrasts
   2. Crossomys and Waiomys for amphibousness convergence
   3. Paucidentomys for worm-sucking convergence (Mastacomys is already sequenced)

For this sampling, I want to confirm that we will have the proper sister comparisons for convergence tests in the next couple of days.

We also mentioned sequencing Notomys, but I’m not sure if that was for a specific reason or just a possibility.

1. Whole genome sequencing will be simple shotgun sequencing
2. I will be finishing an NIH NRSA in the next couple of weeks that will be centered on the whole genome sequencing. The aims focus on phylogenetic discordance, molecular evolution (rate variation), and molecular convergence, and how sampling genomes compares to sampling exomes. We didn’t get around to discussing this, but it would be great to have Jake and Kevin as co-sponsors or collaborators!
3. We will have a Skype call on Tuesday November 26th!