

2016-02-10 Meeting notes

Date

Location: <https://connect.unl.edu/tcap3/>

09 Feb 2016

Attendees

- [Clayton L Birkett](#)
- [Jean-Luc Jannink](#)
- [Peter James Bradbury](#)
- [David Hane](#)
- [Unknown User \(cdl67\)](#)
- [@crs289](#)

Goals

Discussion items

Time	Item	Who	Notes
	combine genotype experiments	Jean-Luc	This could be done in the select lines by "genotype" page. Limit combining to same platform (9K, 90K, GBS). In cases where lines duplicate, the name can be altered (_duplicate) Decided to combine 2 genotype experiments into 1 experiment then we will not need to change tools
	schedule dates of operating system upgrade	Clay Birkett, David Hane	install Ubuntu 14.04 on tcap machine. We need to allocate several days when no updates are allowed on production machine operating system upgrade scheduled for weekend of Feb 19th
	new TCAP hardware?		plan on adding a new server this summer
	genotype data loading		1. merging lines with 50% genotype conflicts (these are not the same line) 2. Nick/Shiaoman (haplotag) will submit VCF file (Oat) 3. others? Jeffery (Kevin from MN), Rich (Barley 9K ND)
	harvesting QTLs		1. added link for JBrowse, marker, and trial count 2. added trait description and ontology 3. added QTLs from imputed genotypes 4. added grouping by marker and gene 5. how to combine p values? Do you through out disease trials? Do we need confidence interval for qtl loci?
	problems with DNS and email on T3 machines	Clay Birkett, David Hane	1. email still not delivered to some sites because of USDA limitations

Action items

- ✓ Clayton L Birkett combine TCAP90K_HWWAMP and TCAP90K_HWWAMP_R
- ✓ Clayton L Birkett remove TCAP90K_HWW_Panel