**Suggested outline for the OWB linkage mapping exercise – designed for online delivery**

**Items in green highlight are special instructions for using RQTL to map the *Nud*, *Kap*, and *Lks2* phenotypes as QTLs.**

This exercise assumes students have facility with linkage map construction software, familiarity with molecular markers, and familiarity with QTL mapping.

All resources are at the BarleyWorld education page (or hyperlinked from there): <https://barleyworld.org/education>

* Go to University/Archives/Linkage mapping and dissection of the hooded phenotype

**Session (class) 1**

[Overview slides](https://barleyworld.org/sites/barleyworld.org/files/owb_mapping_2018_1.pptx)  provides background on the OWBs and focuses on considerations relevant to adding a new type of marker to an existing linkage map.

[Phase 1 slides](https://barleyworld.org/sites/barleyworld.org/files/owb_nud_kap_-1.pptx) describe doubled haploid production, and introduce the phenotypes associated with *Nud* and *Kap*.

1. Present slides 1 - 9.
2. Participants go to breakout rooms to map *Nud*.
	1. The genotype data are hyperlinked in the slide and at the education page in Excel format.
	2. Participants score the *Nud* phenotypes (following the hyperlink provided to the images) and add these allele scores to the marker data sheet for subsequent mapping.
		1. If using RQTL, the *Nud* alleles are scored as 1 and 0, with 1= the OWB-D allele and 0 = the OWB-R allele.
3. Instructor(s) join breakout rooms to:
	1. Assist in phenotyping calls.
	2. Explain data entry.
	3. Prepare data sets for mapping.
	4. Assist in mapping (using software of choice).
4. Next steps depend on status of *Nud* mapping.
	1. ***If*** *participants map Nud in the breakout rooms, they rejoin the full class.*
		1. *Present slides 10 – 13 and participants map Kap (based on hooded vs. awned phenotype) as homework.*
	2. ***If*** *participants are not able to finish mapping Nud in the breakout rooms, they complete the following (as homework)*
		1. *Finish mapping of Nud.*
		2. *Review slides 10 – 13.*
		3. *Map Kap based on hooded vs. awned phenotype.*

**Session (class) 2**

[Phase 2 slides](https://barleyworld.org/sites/barleyworld.org/files/owb_nud_kap_-_2.pptx) focus on the hooded vs. awned phenotypes and epistasis.

1. Present slides 1 - 6.
2. Participants go to breakout rooms to map *Lks2 and Hvknox3*.
	1. As in Session 1, the genotype data are hyperlinked in the slide and at the education page Excel.
	2. Participants score the *Lks2* phenotypes (following the hyperlink provided to the images and paying close attention to Slide 6) and add these allele scores to the data sheet for subsequent mapping.
		1. If using RQTL, the *Lks2* alleles are scored as 1 and 0, with 1= the OWB-D allele and 0 = the OWB-R allele.
	3. *Hvknox3* is in the marker data set – participants ensure that this linkage map position corresponds to that reported in the literature.
3. Instructor(s) join breakout rooms to:
	1. Assist in phenotyping calls.
	2. Explain data entry.
	3. Prepare data sets for linkage mapping
	4. Assist in mapping (using software of choice).
	5. Stimulate discussion on implications of phenotype vs. genotype data for mapping qualitative traits.
4. Next steps depend on status of *Lks2* and *Kap* mapping.
	1. ***If*** *participants map Lks2 and Kap in the breakout rooms, they rejoin the full class.*
		1. *Present slide 8.*
		2. *Open discussion*
	2. ***If*** *participants are not able to finish mappingLks2 and Kap in the breakout rooms, they complete the exercise as homework.*
		1. *They review slide 8 on their own.*
		2. *The open discussion can be the focus of a third session and/or a written assignment.*