

An Explanatory Note On CAP Maps

February 9, 2007

CAP mapping scope:

- The CAP project proposes to map SNP loci represented on Pilot OPA's 2 and 3. (Pilot OPA 1 data were generated via a prior NSF grant). With 1,536 SNPs represented per OPA, the goal is to map at least 3,000 SNPs.
- The SNPs will be mapped using three mapping populations: Morex x Barke, Oregon Wolfe Barley, and Stepto x Morex
- In addition, the Triticarte DArT markers will be mapped.

The process:

Four groups are collaborating on the first phase of the mapping and the following responsibilities have been delegated to each group.

- Tim Close et al. use mapping as an iterative process of SNP allele calling in all populations – their evolving maps are currently available at <http://138.23.191.142/hweb/bin/wc.dll?hwebProcess~hmain~&versid=4> and represent a consensus map sign a minimal number of non-SNP markers and a maximum number of SNPs.
- Tim Close et al. are preparing a paper on the P-OPA 1 map.
- Nils Stein et al. at the IPK have primary responsibility for the Morex x Barke map and will write a paper on the mapping of this population including SNPs, prior, and new data.
- Robbie Waugh, Luke Ramsay et al. at the SCRI have primary responsibility for the Steptoe x Morex map and will write a paper on the mapping of this population including SNPs, prior, and new data.
- Pat Hayes and Peter Szucs at OSU have primary responsibility for the Oregon Wolfe Barley map and will write a paper on the mapping of this population including SNPs, prior, and new data.

In the second and final (?) phase, Abraham Korol et al at the University of Haifa will develop a consensus barley map integrating all possible data (e.g. AFLP, DArT, NEO, RFLP, SNP, SSR, STS, etc).

Data availability:

- The UC- Riverside is periodically updating their map viewer
- The OSU group has posted, on the CAP webpage, the OWB-based P-OPA 2 SNP map integrated with prior data and will do the same for P-OPA 1 and 3 as these work spaces are closed.
- In the future, more comprehensive data sets and powerful tools will be available at THT, GrainGenes, and any plant genetics database interesting in making these data available.