

Barley CAP Association Genetics, Marker-Assisted Selection Workshop

REGISTRATION



August 19-21, 2009

Cargill Building, University of Minnesota, St. Paul, MN

- Presenters:** Kevin Smith and Rex Bernardo (University of Minnesota), Jean-Luc Jannink (USDA-ARS, Ithaca, NY), Shiaoman Chao (USDA-ARS, Fargo, ND)
- Registration:** Registration forms are due July 15, 2009. Space is limited so be sure to register early. Registration form is available online at www.barleycap.org (Click on calendar)
- Cost:** Free for Barley CAP participants and their students and postdocs; \$100 for non Barley CAP participants to cover three lunches, a reception and coffee breaks. We cannot accept credit cards. You may send a check or money order by mail made out to "University of Minnesota."
- Student stipend:** A limited number of \$500 student stipends will be provided. To apply send a 1-page description on how attending this workshop will benefit your research and a letter of support from your advisor to Lynne Medgaarden (see address below).
- Mail forms to:** Lynne Medgaarden, University of Minnesota, Agronomy and Plant Genetics, 1991 Upper Buford Circle, 411 Borlaug Hall, St. Paul, MN 55108. Questions: (612) 625-4742, FAX: (612) 625-1268, medga001@umn.edu,
- Lodging:** Rooms have been reserved at the Radisson University Hotel, 615 Washington Ave S.E., Minneapolis, MN 55414, phone: 612-379-8888, Fax: 612-379-8682, website: <http://www.radisson.com/barley> Please reserve your room by July 15. Ask for group: Barley CAP Workshop. Rate is \$119 plus tax. Hotel shuttle will bring you to campus.
- Note:** **Workshop will last 2 ½ days and end at noon on Friday Aug 21.** Participants are asked to bring along laptop computers. You will load the new program into your computer and learn how to use it during the workshop.

NAME: _____ ORGANIZATION: _____

ADDRESS: _____

ADDRESS: _____

CITY: _____ STATE: _____ ZIP: _____

PHONE: () _____ EMAIL: _____

- I am a barley CAP participant or barley CAP graduate student or barley CAP post-doc
- Check enclosed for \$100
- Dietary restrictions or special needs What? _____

You will receive a confirmation of your registration. Please provide an email address



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WORKSHOP AGENDA

Session I QTL mapping

1. Traditional approaches
 - i. Populations
 - ii. QTL detection methodologies
2. Association mapping
 - i. Population structure
 - ii. Linkage disequilibrium
 - iii. Haplotype structure
 - iv. Markers, marker density, minor allele frequency
 - v. Hands on – QTL Miner Simulator, Haploview, THT/Germinate tools

Session II Genome-Wide Association Mapping

1. Hands on – Tassel, QTL Miner
2. Interpreting QTL mapping results
3. Identifying targets for MAS

Session III Designing MAS Strategies

1. Review phenotypic selection in barley breeding
2. Overview of various MAS strategies - BC, allele enrichment, single locus, multiple loci, whole genome selection
3. Marker Platforms: SSRs, Illumina Bead Station SNP, Florescent polarization SNP detection,
4. High-throughput SNPs to markers that can be implemented in a breeding program