

**SPEAKER ABSTRACTS**

**25–29 JUNE, 2012**  
**RAMADA PLAZA AND SUITES HOTEL–FARGO, ND, USA**

**SESSION I: GENOME SEQUENCING AND UTILIZATION**(Speakers denoted in **bold** lettering).***Sequences of 14,600 'gene-bearing' MTP BACs of Morex barley.*****Timothy J Close.** Department of Botany & Plant Sciences, University of California, Riverside, California, USA.

In a USDA–AFRI NIFA project entitled “Advancing the Barley Genome”, we applied combinatorial pooling and Illumina sequencing to ~14,600 BACs that constitute a minimal tiling path (MTP) from 83,831 gene-bearing BACs of Morex barley. The BAC library was developed by Yu et al. (2000. *Theor Appl Genet* 101:1093-99) and these BACs account for roughly 70% of all expressed genes but only about 30% of the entire genome. Identification of gene-bearing BACs, fingerprinting, BAC contig assembly, MTP definition and assignment of an initial subset of about 2,000 MTP BACs to the genetic map were the results of prior projects supported by NSF and USDA, and from contributions of many individuals. These individuals, and others involved in the BAC sequencing, will be cited during the presentation. Most of these ~14,600 newly generated BAC sequences have been anchored to the genetic map. Anchoring methods include Illumina GoldenGate assays to relate mapped SNP loci to BACs, BLAST of BAC sequences to flow-sorted chromosome 1H and the short and long arms of 2H–6H, and BLAST of BAC sequences to other grass genomes to enhance physical map resolution based on synteny. A consequence of the combinatorial sequencing method is that each BAC assembly is composed of about 100 unordered contigs with a N50 in the range of 6 kb; the result is not end-to-end finished BAC sequences. In addition, the BAC assemblies in general do not include highly repetitive sequences. The available BAC sequences are searchable by BLAST via [www.harvest-blast.org](http://www.harvest-blast.org) and can be retrieved from [www.harvest-web.org](http://www.harvest-web.org) as a single concatenated FASTA file for each BAC, with headers providing additional information. HarvEST:barley (<http://harvest.ucr.edu>) provides a Windows interface to facilitate retrieval of BAC sequences starting either with genetic map position or names of MTP BACs or other BACs contained in the same contigs from which gene-bearing MTP clones were selected for sequencing. Some example queries will be shown. Improvements of user interfaces and integration of these new BAC sequences with other International Barley Sequencing Consortium (IBSC) resources are in progress, with updates posted on the IBSC website ([www.barley-genome.org](http://www.barley-genome.org)).

***Same, same but different: complementary analytical approaches highlight the different shades of polyploidy in rye and wheat.***

Rachel Brenchley<sup>1</sup>, Manuel Spannagl<sup>2</sup>, Matthias Pfeifer<sup>2</sup>, Gary L.A. Barker<sup>3</sup>, Rosalinda D'Amore<sup>1</sup>, Alexandra M. Allen<sup>3</sup>, Neil McKenzie<sup>4</sup>, Melissa Kramer<sup>5</sup>, Dan Bolser<sup>6</sup>, Suzanne Kay<sup>1</sup>, Darren Waite<sup>4</sup>, Yong Gu<sup>7</sup>, Naxin Huo<sup>7</sup>, Ming-Cheng Luo<sup>8</sup>, Sunish Sehgal<sup>9</sup>, Sharyar Kianian<sup>10</sup>, Martin Trick<sup>4</sup>, Ian Bancroft<sup>4</sup>, Bikram S. Gill<sup>9</sup>, Olin Anderson<sup>7</sup>, Jan Dvorak<sup>8</sup>, Paul Kersey<sup>6</sup>, Richard McCombie<sup>5</sup>, Anthony Hall<sup>1</sup>, **Klaus F.X. Mayer**<sup>2</sup>, Keith J. Edwards<sup>3</sup>, Michael W. Bevan<sup>4</sup>, Neil Hall<sup>1</sup>, Mihaela Martis<sup>2</sup>, Hana Simkova<sup>11</sup>, Jan Vrana<sup>11</sup>, Jaroslav Dolezel<sup>11</sup>, Susanne König<sup>12</sup>, Ruonan Zhou<sup>12</sup>, Thomas Schmutzer<sup>12</sup>, Uwe Scholz<sup>12</sup>, Viktor Korzun<sup>13</sup>, Nils Stein<sup>12</sup>, Chris-Carolin Schön<sup>14</sup>, Eva Bauer<sup>14</sup>, and Grit Haseneyer<sup>14</sup>.

<sup>1</sup> Centre for Genome Research, University of Liverpool, Liverpool, UK; <sup>2</sup> MIPS/IBIS, Helmholtz- Zentrum München, Neuherberg, DE; <sup>3</sup> School of Biological Sciences, University of Bristol, Bristol, UK; <sup>4</sup> John Innes Centre, Norwich, UK; <sup>5</sup> Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA; <sup>6</sup> European Bioinformatics Institute, Hinxton, UK; <sup>7</sup> USDA Western Regional Laboratory, Albany, CA, USA; <sup>8</sup> Department of Agronomy and Range Science, University of California, Davis, CA, USA; <sup>9</sup> Department of Plant Pathology, Kansas State University, Manhattan, KS, USA; <sup>10</sup> Department of Plant Sciences, North Dakota State University, Fargo, ND, USA; <sup>11</sup> Centre of the Region Haná for Biotechnological and Agricultural Research, Institute of Experimental Botany, Olomouc, Czech Republic; <sup>12</sup> Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany; <sup>13</sup> KWS LOCHOW GmBH, Einbeck, Germany; and <sup>14</sup> Plant Breeding, Technische Universität München, Freising, Germany.