

CURRICULUM VITAE

Eduard D. Akhunov
Department of Plant Pathology
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Education:

- 1999 Philosophy Doctor in Plant Molecular Biology
Institute of Genetics (Moscow, Russia)
- 1992 Master of Science in Biochemistry
Novosibirsk State University
- 1990 B.S. (Biochemistry), Bashkirian State University (Ufa, Russia)
- 1991 Teacher of Biology & Chemistry
Bashkirian State University (Ufa, Russia)

Employment:

- 07/2012 - present Associate Professor, Department of Plant Pathology, Kansas State University, Manhattan, KS
- 05/2007 – 07/2012 Assistant Professor, Department of Plant Pathology, Kansas State University, Manhattan, KS
- 07/2004 – 05/2007 Assistant Project Scientist, Department of Plant Sciences, University of California, Davis, CA, USA
- 02/2000 – 07/2004 Visiting Scientist, Department of Plant Sciences, University of California, Davis, CA, USA
- 06/1997 – 01/2000 Senior Research Scientist, Laboratory of Plant Molecular Biology, Institute of Biochemistry and Genetics of Russian Academy of Science
- 09/1994 – 06/1997 Graduate Student, Laboratory of Plant Molecular Biology, Institute of Biochemistry and Genetics of Russian Academy of Sciences (Ufa), Institute of Genetics (Moscow)
- 04/1993 – 09/1994 Research Scientist, Laboratory of Biotechnology, Institute of Biochemistry and Genetics of Russian Academy of Sciences
- 07/1992 – 04/1993 Research Scientist, Research and Development laboratory of "Bashbiotech" company, Ufa, Russia

Memberships:

- Member of the Genetics Society of America
- Member of American Association for Advancement of Science

Editorial Board:

- Frontiers in Plant Genetics and Genomics
- G3: Genes, Genomes, Genetics

Committees & advisory boards

Scientific Advisory Board of French BreedWheat project (2011 -present)
Coordinating Committee Member of the International Wheat Genome Sequencing Consortium, (2007-present)
National Wheat Genomics Committee, University Representative (2009-present)

Ad hoc reviewer:

Theoretical and Applied Genetics, Functional and Integrative Genomics, Genome Research, Genome, Plant Cell Reports, Genome, Nucleic Acids Research, Plant Cell, Nature Methods, Nature Biotechnology, Molecular Biology and Evolution, Journal of Molecular Evolution, BMC Genomics, BMC Genetics, G3, PLoS One, PLoS Genetics, Nature Plants

Areas of research:

1. Development and application of next-generation genotyping and sequencing tools and resources, comparative genomics, population genetics and bioinformatics for understanding wheat biology and improving wheat.
2. Development of genomic and genetic resources for functional analysis and cloning of wheat genes important for agriculture: BAC libraries, wheat genome and transcriptome sequences and TILLING populations.
3. Development of genomic resources for high-throughput screening of wheat TILLING populations by whole exome capture approach.
4. Development of high-throughput genotyping assays and strategies for genome-wide analysis of natural and chemically induced nucleotide sequence variation in wheat. For this purpose we developed high-throughput SNP genotyping assay including 90,000 SNPs and 110 Mb whole exome sequence capture assay. In addition, we use transcriptome sequencing and whole-genome sequencing of complexity reduced genomic libraries as genotyping strategy in wheat.
5. Application of genome-wide association scans for mapping agronomically important traits (disease resistance, development, abiotic stress response and yield).
6. Study of genome-wide patterns of nucleotide sequence variation across wheat genome in diversity panels and mapping populations to detect regions affected by selection and local adaptation resulting from domestication and breeding.
7. Molecular cloning and characterization of disease resistance genes and functional genomics of rust-wheat interaction.
8. Role of polyploidy in evolution of biochemical, physiological and phenotypic variation in wheat and its contribution to the origin of valuable agronomic phenotypes.
9. Application of next-generation sequencing to study the evolution of wheat gene function and genome structure.

Publications in peer-reviewed journals:

1. 2015 Kippes N, Debernardi JM, Vasquez-Grossa HA, Akpinarb BA, Budak H, Kato K, Chao S, **Akhunov E**, Dubcovsky J. Identification of the VERNALIZATION 4 gene reveals the origin of spring growth habit in

- ancient wheats from South Asia. *Proc Natl Acad Sci U S A*. doi: 10.1073/pnas.1514883112.
2. 2015 Jordan KW, Wang S, Lun Y, Gardiner L, MacLachlan R, Hucl P, Wiebe K, Wong D, Forrest KL, Sharpe AG, Sidebottom CHD, Hall N, Toomajian C, Close T, Dubcovsky J, Akhunova A, Talbert L, Bansal UK, Bariana HS, Hayden MJ, Pozniak C, Jeddelloh JA, Hall A, **Akhunov E**. A haplotype map of allohexaploid wheat reveals distinct patterns of selection on homoeologous genomes. *Genome Biology*, 2015, 16:48.
 3. 2015 Li G, Wang Y, Chen MS, Edae E, Poland J, **Akhunov E**, Chao S, Bai G, Carver BF, Yan L. Precisely mapping a major gene conferring resistance to Hessian fly in bread wheat using genotyping-by-sequencing. *BMC Genomics*. 2015, 16:108.
 4. 2015 Chen S, Rouse MN, Zhang W, Jin Y, **Akhunov E**, Wei Y, Dubcovsky J. Fine mapping and characterization of Sr21, a temperature-sensitive diploid wheat resistance gene effective against the *Puccinia graminis* f. sp. *tritici* Ug99 race group. *Theor Appl Genet*. 128:645-56.
 5. 2015 Kalous JR, Martin JM, Sherman JD, Heo HY, Blake NK, Lanning SP, Eckhoff JL, Chao S, **Akhunov E**, Talbert LE. Impact of the D genome and quantitative trait loci on quantitative traits in a spring durum by spring bread wheat cross. *Theor Appl Genet*. 2015 Sep;128(9):1799-811.
 6. 2015 Maccaferri M, Ricci A, Salvi S, Milner SG, Noli E, Martelli PL, Casadio R, **Akhunov E**, Scalabrin S, Vendramin V, Ammar K, Blanco A, Desiderio F, Distelfeld A, Dubcovsky J, Fahima T, Faris J, Korol A, Massi A, Mastrangelo AM, Morgante M, Pozniak C, N'Diaye A, Xu S, Tuberosa R. A high-density, SNP-based consensus map of tetraploid wheat as a bridge to integrate durum and bread wheat genomics and breeding. *Plant Biotechnol J*. 2015, 13(5):648-63.
 7. 2015 Bonman MJ, Babiker EM, Cuesta-Marcos A, Esvelt-Klos K, Brown-Guedira G, Chao S, See D, Chen M, **Akhunov E**, Zhang J, Bockelman HE, Gordon TC. Genetic Diversity among Wheat Accessions from the USDA National Small Grains Collection. *Crop Science*, 55, 1243-1253.
 8. 2015 Liu Z, El-Basyoni E, Kariyawasam G, Zhang G, Fritz A, Hansen J, Marais F, Friskop A, Chao S, **Akhunov E**, Baenziger PS. Evaluation and Association Mapping of Resistance to Tan Spot and *Stagonospora Nodorum* Blotch in Adapted Winter Wheat Germplasm, *Plant Disease*, PDIS-11-14-1131-RE.
 9. 2015 Turuspekov Y, Plieske J, Ganal M, **Akhunov E**, Abugalieva S. Phylogenetic analysis of wheat cultivars in Kazakhstan based on the wheat 90 K single nucleotide polymorphism array. *Plant Genet. Resources*, 1, 1-7, doi:10.1017/S1479262115000325.
 10. 2015 Guttieri MJ, Baenziger PS, Frels K, Carver B, Arnall B, Wang S, Akhunov E, Waters BM. Prospects for Selecting Wheat with Increased Zinc and Decreased Cadmium Concentration in Grain. *Crop Science* 2015 55: 4: 1712-1728.

11. 2014 Marcussen T, Sandve SR, Heier L, Spannagl M, Pfeifer M; International Wheat Genome Sequencing Consortium, Jakobsen KS, Wulff BB, Steuernagel B, Mayer KF, Olsen OA. Ancient hybridizations among the ancestral genomes of bread wheat. *Science*. 2014 Jul 18;345(6194):1250092. doi: 10.1126/science.1250092. PubMed PMID: 25035499.
12. 2014 Pfeifer M, Kugler KG, Sandve SR, Zhan B, Rudi H, Hvidsten TR; International Wheat Genome Sequencing Consortium, Mayer KF, Olsen OA. Genome interplay in the grain transcriptome of hexaploid bread wheat. *Science*. 2014 Jul 18;345(6194):1250091. doi: 10.1126/science.1250091. PubMed PMID: 25035498.
13. 2014 Zytnicki M, Akhunov E, Quesneville H. Tedna: a transposable element de novo assembler. *Bioinformatics*. 2014 Jun 3. pii: btu365. [Epub ahead of print] PubMed PMID: 24894500.
14. 2014 Bruce M, Neugebauer KA, Joly DL, Migeon P, Cuomo C, Wang S, **Akhunov E**, Bakkeren G, Kolmer JA, Fellers JP. Using transcription of six *Puccinia triticina* races to identify the effective secretome during infection of wheat, *Frontiers in Plant-Microbe Interaction*, *Front. Plant Sci*. 2014 Jan 13;4:520.
15. 2014 Middleton C, Kilian B, **Akhunov E**, Keller B, Wicker T. Sequencing of chloroplast genomes from wheat, barley, rye and their relatives provides a detailed insight into the evolution of the Triticeae tribe *PLoS One*. 2014 Mar 10;9(3):e85761.
16. 2014 Wang S, Wong D, Forrest K, Allen A, Chao S, Huang B, Maccaferri M, Salvi S, Milner S, Cattivelli L, Mastrangelo A, Whan A, Stephen S, Barker G, Wieseke R, Plieske J, (IWGSC) Wheat Genome Sequencing Consortium, Lillemo M, Mather D, Appels R, Dolferus R, Brown-Guedira G, Korol A, Akhunova A, Feuillet C, SALSE J, Morgante M, Pozniak C, Luo MC, Dvorak J, Morell M, Dubcovsky J, Ganal M, Tuberosa R, Lawley C, Mikoulitch I, Cavanagh C, Edwards K, Hayden M, **Akhunov E***. Characterization of polyploid wheat genomic diversity using a high-density 90,000 SNP array. *Plant Biotechnol J*. 2014 Mar 20. doi: 10.1111/pbi.12183.
17. 2014 Tiwari VK, Wang S, Sehgal S, Vrána J, Friebe B, Kubaláková M, Chhuneja P, Dole El J, **Akhunov E**, Kalia B, Sabir J, Gill BS. SNP Discovery for mapping alien introgressions in wheat. *BMC Genomics*. 2014, 1:273.
18. 2014 Henry IM, Nagalakshmi U, Lieberman M. C., Ngo K. J, Krasileva KV, Vasquez-Gross H, Akhunova A, **Akhunov E**, Dubcovsky J, Tai H, Comai L Efficient Genome-Wide Detection and Cataloging of EMS-Induced Mutations Using Exome Capture and Next-Generation Sequencing. *Plant Cell*, 2014, 26:1382-1397.
19. 2013 Mascher M, Richmond TA, Gerhardt DJ, Himmelbach A, Clissold L, Sampath D, Ayling S, Steuernagel B, Pfeifer M, D'Ascenzo M, **Akhunov ED**, Hedley PE, Gonzales AM, Morrell PL, Kilian B, Blattner FR, Scholz U, Mayer KF, Flavell AJ, Muehlbauer GJ, Waugh R, Jeddelloh JA, Stein N. Barley whole exome capture: a tool for genomic research in the genus *Hordeum* and beyond. *Plant J*. 2013 Jul 24. doi: 10.1111/tpj.12294. [Epub ahead of print]

20. 2013 Saintenac C, Zhang W, Salcedo A, Rouse MN, Trick HN, **Akhunov E**, Dubcovsky J. Identification of Wheat Gene Sr35 That Confers Resistance to Ug99 Stem Rust Race Group. *Science*. 341:783-786.
21. 2013 Krasileva KV, Buffalo V, Bailey P, Pearce S, Ayling S, Tabbita F, Soria M, Wang S, Consortium I, **Akhunov E**, Uauy C, Dubcovsky J. Separating homeologs by phasing in the tetraploid wheat transcriptome. *Genome Biol*. 14:R66.
22. 2013 Saintenac C, Jiang D, Wang S, **Akhunov E**. Sequence-based mapping of the polyploid wheat genome. *G3 (Bethesda)*. 3:1105-1114.
23. 2013 Cavanagh CR, Chao S, Wang S, Huang BE, Stephen S, Kiani S, Forrest K, Saintenac C, Brown-Guedira GL, Akhunova A, See D, Bai G, Pumphrey M, Tomar L, Wong D, Kong S, Reynolds M, da Silva ML, Bockelman H, Talbert L, Anderson JA, Dreisigacker S, Baenziger S, Carter A, Korzun V, Morrell PL, Dubcovsky J, Morell MK, Sorrells ME, Hayden MJ, **Akhunov E**. Genome-wide comparative diversity uncovers multiple targets of selection for improvement in hexaploid wheat landraces and cultivars. *Proc Natl Acad Sci U S A*. 110:8057-8062.
24. 2013 Würschum T, Langer SM, Longin CF, Korzun V, **Akhunov E**, Ebmeyer E, Schachschneider R, Schacht J, Kazman E, Reif JC. Population structure, genetic diversity and linkage disequilibrium in elite winter wheat assessed with SNP and SSR markers. *Theor Appl Genet*. 126:1477-1486.
25. 2013 **Akhunov E**, Sehgal S, Liang H, Wang S, Akhunova A, Kaur G, Li W, Forrest K, See D, Simkova H, Hayden M, Luo M, Farris JD, Dolezel J, Gill BS. Comparative analysis of syntenic genes in grass genomes reveals accelerated rates of gene structure and coding sequence evolution in polyploid wheat. *Plant Phys*. 161:252-265.
26. 2012 Philippe R, Choulet F, Paux E, van Oeveren J, Tang J, Wittenberg AH, Janssen A, van Eijk MJ, Stormo K, Alberti A, Wincker P, **Akhunov E**, van der Vossen E, Feuillet C. Whole Genome Profiling provides a robust framework for physical mapping and sequencing in the highly complex and repetitive wheat genome. *BMC Genomics* 13:47.
27. 2012 **Akhunov E**, Chao S, Saintenac C, Kiani S, See D, Brown-Guedira G, Sorrells M, Akhunova A, Dubcovsky J, Cavanagh C, Hayden M. High-throughput approaches to genome-wide analysis of genetic variation in polyploid wheat. *Canadian Journal of Plant Sciences* 3:596.
28. 2011 Saintenac C, Jiang D, Akhunov E. Targeted analysis of nucleotide and copy number variation by exon capture in allotetraploid wheat genome. *Genome Biol* 12:R88.
29. 2011 Dario C, Pearce SP, Distelfeld A, Christiansen MW, Uauy C, **Akhunov E**, Fahima F, Dubcovsky J. Effect of the down-regulation of the high Grain Protein Content (GPC) gene on the wheat transcriptome during monocarpic senescence. *BMC Genomics* 12:492.
30. 2011 Dvorak J, Luo MC, **Akhunov E**. N.I. Vavilov's theory of centers of diversity in the light of current understanding of wheat domestication and evolution. *Czech J Genet Plant Breeding*, 47: S20–S27.

31. 2011 Alo F, Furman BJ, **Akhunov E**, Dvorak J, Gepts P. Leveraging Genomic Resources of Model Species for the Assessment of Diversity and Phylogeny in Wild and Domesticated Lentil. *J Heredity* 102:315-29.
32. 2010 Chao S, Dubcovsky J, Dvorak J, Luo MC, Baenziger SP, Matnyazov R, Clark DR, Talbert LE, Anderson JA, Dreisigacker S, Glover K, Chen J, Campbell K, Bruckner PL, Rudd JC, Haley S, Carver BF, Perry S, Sorrells ME, **Akhunov E**. Population- and genome-specific patterns of linkage disequilibrium and SNP variation in spring and winter wheat (*Triticum aestivum* L.). *BMC Genomics* 11:727.
33. 2010 **Akhunov ED**, Akhunova AR, Anderson OD, Anderson JA, Blake N, Clegg MT, Coleman-Derr D, Conley EJ, Crossman CC, Deal KR, Dubcovsky J, Gill BS, Gu YQ, Hadam J, Heo HY, Huo N, Lazo GR, Luo MC, Ma YQ, Matthews DE, McGuire PE, Morrell P, Qualset CO, Renfro J, Tabanao D, Talbert LE, Tian C, Toleno D, Warburton M, You FM, Zhang W, Dvorak J. Nucleotide diversity maps reveal variation in diversity among wheat genomes and chromosomes. *BMC Genomics* 11:702.
34. 2010 Akhunova AR, Matnyazov RT, Liang H, **Akhunov E**. Homoeolog-specific transcriptional bias in allopolyploid wheat. *BMC Genomics* 11:505.
35. 2010 Sharma S, Sreenivasulu N, Harshavardhan VT, Seiler C, Sharma S, Khalil ZN, **Akhunov E**, Sehgal SK, Röder MS. Delineating the structural, functional and evolutionary relationships of sucrose phosphate synthase gene family II in wheat and related grasses. *BMC Plant Biology* 10:134.
36. 2010 Zhang W, Olson E, Saintenac C, Rouse M, Abate Z, Jin Y, **Akhunov ED**, Pumphrey M, Dubcovsky J. Genetic maps of stem rust resistance gene Sr35 in diploid and hexaploid wheat. *Crop Science* 50:2464-2474.
37. 2009 **Akhunov E**, C Nicolet, J Dvorak. Single nucleotide polymorphism genotyping in polyploid wheat with Illumina GoldenGate assay. *Theor Appl Genet* 119:507-517.
38. 2009 Luo MC, Deal KR, **Akhunov ED**, Akhunova AR, Anderson OD, Anderson JA, Blake N, Clegg MT, Coleman-Derr D, Conley EJ, Crossman CC, Dubcovsky J, Gill BS, Gu YQ, Hadam J, Heo HY, Huo N, Lazo G, Ma Y, Matthews DE, McGuire PE, Morrell PL, Qualset CO, Renfro J, Tabanao D, Talbert LE, Tian C, Toleno DM, Warburton ML, You FM, Zhang W, Dvorak J. Genome Comparisons Reveal a Dominant Mechanism of Chromosome Number Reduction in Grasses and Accelerated Genome Evolution in Triticeae. *Proc Natl Acad Sci U S A* 106:15780-15785.
39. 2009 Chao S, Zhang W, **Akhunov E**, Sherman J, Ma Y, Luo M, Dubcovsky J. Analysis of gene-derived SNP marker polymorphism in wheat (*Triticum aestivum* L.) *Mol Breeding* 23:23–33.
40. 2007 **Akhunov E**, Akhunova A, Dvorak J. Birth and death of dispersed duplicated genes in a large plant genome: mechanisms and rates in a multigene family. *Mol Biol Evol* 24:539–550.
41. 2006 Dvorak J, **Akhunov ED**, Akhunov AR, Deal KR, Luo MC. Molecular Characterization of a Diagnostic DNA Marker for Domesticated Tetraploid Wheat Provides Evidence for Gene Flow from Wild Tetraploid Wheat to Hexaploid Wheat. *Mol Biol Evol* 23:1386-1396.

42. 2005 **Akhunov ED**, Akhunova AR, Dvorak J. BAC libraries of diploid progenitors of hexaploid wheat. *Theor Appl Genet* 111:1617-1622.
43. 2005 Dvorak J, Akhunov ED. Tempos of deletions and duplications of gene loci in relation to recombination rate during diploid and polyploid evolution in Aegilops-Triticum alliance. *Genetics* 171:323-332.
44. 2004 Qi LL, Echalié B, Chao S, Lazo GR, Butler GE, Anderson OD, **Akhunov ED**, Dvorák J, Linkiewicz AM, Ratnasiri A, Dubcovsky J, Bermudez-Kandianis CE, Greene RA, Kantety R, La Rota CM, Munkvold JD, Sorrells SF, Sorrells ME, Dilbirligi M, Sidhu D, Erayman M, Randhawa HS, Sandhu D, Bondareva SN, Gill KS, Mahmoud AA, Ma XF, Miftahudin, Gustafson JP, Conley EJ, Nduati V, Gonzalez-Hernandez JL, Anderson JA, Peng JH, Lapitan NLV, Hossain KG, Kalavacharla V, Kianian SF, Pathan MS, Zhang DS, Nguyen HT, Choi DW, Fenton RD, Close TJ, McGuire PE, Qualset CO, Gill BS. A Chromosome Bin Map of 16,000 Expressed Sequence Tag Loci and Distribution of Genes Among the Three Genomes of Polyploid Wheat. *Genetics* 168:701-712.
45. 2004 Hossain KG, Kalavacharla V, Lazo GR, Hegstad J, Wentz MJ, Kianian PM, Simons K, Gehlhar S, Rust JL, Syamala RR, Obeori K, Bhamidimarri S, Karunadharma P, Chao S, Anderson OD, Qi LL, Echalié B, Gill BS, Linkiewicz AM, Ratnasiri A, Dubcovsky J, **Akhunov ED**, Dvorák J, Miftahudin, Ross K, Gustafson JP, Radhawa HS, Dilbirligi M, Gill KS, Peng JH, Lapitan NL, Greene RA, Bermudez-Kandianis CE, Sorrells ME, Feril O, Pathan MS, Nguyen HT, Gonzalez-Hernandez JL, Conley EJ, Anderson JA, Choi DW, Fenton D, Close TJ, McGuire PE, Qualset CO, Kianian SF. A chromosome bin map of 2148 expressed sequence tag loci of wheat homoeologous group 7. *Genetics* 168:687-699.
46. 2004 Randhawa HS, Dilbirligi M, Sidhu D, Erayman M, Sandhu D, Bondareva S, Chao S, Lazo GR, Anderson OD, Miftahudin, Gustafson JP, Echalié B, Qi LL, Gill BS, **Akhunov ED**, Dvorák J, Linkiewicz AM, Ratnasiri A, Dubcovsky J, Bermudez-Kandianis CE, Greene RA, Sorrells ME, Conley EJ, Anderson JA, Peng JH, Lapitan NL, Hossain KG, Kalavacharla V, Kianian SF, Pathan MS, Nguyen HT, Endo TR, Close TJ, McGuire PE, Qualset CO, Gill KS. Deletion mapping of homoeologous group 6-specific wheat expressed sequence tags. *Genetics* 168:677-686.
47. 2004 Linkiewicz AM, Qi LL, Gill BS, Ratnasiri A, Echalié B, Chao S, Lazo GR, Hummel DD, Anderson OD, **Akhunov ED**, Dvorák J, Pathan MS, Nguyen HT, Peng JH, Lapitan NL, Miftahudin, Gustafson JP, La Rota CM, Sorrells ME, Hossain KG, Kalavacharla V, Kianian SF, Sandhu D, Bondareva SN, Gill KS, Conley EJ, Anderson JA, Fenton RD, Close TJ, McGuire PE, Qualset CO, Dubcovsky J. A 2500-locus bin map of wheat homoeologous group 5 provides insights on gene distribution and colinearity with rice. *Genetics* 168:665-676.
48. 2004 Conley EJ, Nduati V, Gonzalez-Hernandez JL, Mesfin A, Trudeau-Spanjers M, Chao S, Lazo GR, Hummel DD, Anderson OD, Qi LL, Gill BS, Echalié B, Linkiewicz AM, Dubcovsky J, **Akhunov ED**, Dvorák J, Peng JH, Lapitan NL, Pathan MS, Nguyen HT, Ma XF, Miftahudin, Gustafson JP, Greene RA, Sorrells ME, Hossain KG, Kalavacharla V, Kianian SF, Sidhu

- D, Dilbirligi M, Gill KS, Choi DW, Fenton RD, Close TJ, McGuire PE, Qualset CO, Anderson JA. A 2600-locus chromosome bin map of wheat homoeologous group 2 reveals interstitial gene-rich islands and colinearity with rice. *Genetics* 168:625-637.
49. 2004 Peng JH, Zadeh H, Lazo GR, Gustafson JP, Chao S, Anderson OD, Qi LL, Echalié B, Gill BS, Dilbirligi M, Sandhu D, Gill KS, Greene RA, Sorrells ME, **Akhunov ED**, Dvorák J, Linkiewicz AM, Dubcovsky J, Hossain KG, Kalavacharla V, Kianian SF, Mahmoud AA, Miftahudin, Conley EJ, Anderson JA, Pathan MS, Nguyen HT, McGuire PE, Qualset CO, Lapitan NL. Chromosome bin map of expressed sequence tags in homoeologous group 1 of hexaploid wheat and homoeology with rice and Arabidopsis. *Genetics* 168:609-623.
50. 2004 Zhang D, Choi DW, Wanamaker S, Fenton RD, Chin A, Malatrasi M, Turuspekov Y, Walia H, **Akhunov ED**, Kianian P, Otto C, Simons K, Deal KR, Echenique V, Stamova B, Ross K, Butler GE, Strader L, Verhey SD, Johnson R, Altenbach S, Kothari K, Tanaka C, Shah MM, Laudencia-Chingcuanco D, Han P, Miller RE, Crossman CC, Chao S, Lazo GR, Klueva N, Gustafson JP, Kianian SF, Dubcovsky J, Walker-Simmons MK, Gill KS, Dvorák J, Anderson OD, Sorrells ME, McGuire PE, Qualset CO, Nguyen HT, Close TJ. Construction and evaluation of cDNA libraries for large-scale expressed sequence tag sequencing in wheat (*Triticum aestivum* L.). *Genetics* 168:595-608.
51. 2004 Miftahudin, Ross K, Ma XF, Mahmoud AA, Layton J, Milla MA, Chikmawati T, Ramalingam J, Feril O, Pathan MS, Momirovic GS, Kim S, Chema K, Fang P, Haule L, Struxness H, Birkes J, Yaghoubian C, Skinner R, McAllister J, Nguyen V, Qi LL, Echalié B, Gill BS, Linkiewicz AM, Dubcovsky J, **Akhunov ED**, Dvorák J, Dilbirligi M, Gill KS, Peng JH, Lapitan NL, Bermudez-Kandianis CE, Sorrells ME, Hossain KG, Kalavacharla V, Kianian SF, Lazo GR, Chao S, Anderson OD, Gonzalez-Hernandez J, Conley EJ, Anderson JA, Choi DW, Fenton RD, Close TJ, McGuire PE, Qualset CO, Nguyen HT, Gustafson JP. Analysis of expressed sequence tag loci on wheat chromosome group 4. *Genetics* 168:651-663.
52. 2004 Munkvold JD, Greene RA, Bermudez-Kandianis CE, La Rota CM, Edwards H, Sorrells SF, Dake T, Bensché D, Kantety R, Linkiewicz AM, Dubcovsky J, **Akhunov ED**, Dvorák J, Miftahudin, Gustafson JP, Pathan MS, Nguyen HT, Matthews DE, Chao S, Lazo GR, Hummel DD, Anderson OD, Anderson JA, Gonzalez-Hernandez JL, Peng JH, Lapitan N, Qi LL, Echalié B, Gill BS, Hossain KG, Kalavacharla V, Kianian SF, Sandhu D, Erayman M, Gill KS, McGuire PE, Qualset CO, Sorrells ME. Group 3 chromosome bin maps of wheat and their relationship to rice chromosome 1. *Genetics* 168:639-650.
53. 2004 Lazo GR, Chao S, Hummel DD, Edwards H, Crossman CC, Lui N, Matthews DE, Carollo VL, Hane DL, You FM, Butler GE, Miller RE, Close TJ, Peng JH, Lapitan NL, Gustafson JP, Qi LL, Echalié B, Gill BS, Dilbirligi M, Randhawa HS, Gill KS, Greene RA, Sorrells ME, **Akhunov ED**, Dvorák J, Linkiewicz AM, Dubcovsky J, Hossain KG, Kalavacharla V, Kianian SF, Mahmoud AA, Miftahudin, Ma XF, Conley EJ, Anderson JA,

- Pathan MS, Nguyen HT, McGuire PE, Qualset CO, Anderson OD. Development of an expressed sequence tag (EST) resource for wheat (*Triticum aestivum* L.). EST generation, unigene analysis, probe selection and bioinformatics for a 16,000-locus bin-delineated map. *Genetics* 168:585-593.
54. 2004 Caldwell KS, Dvorak J, Lagudah ES, **Akhunov E**, Luo MC, Wolters P, Powell W. Sequence polymorphism in polyploid wheat and their d-genome diploid ancestor. *Genetics* 167:941-947.
55. 2003 **Akhunov ED**, Goodyear AW, Geng S, Qi LL, Echalié B, Gill BS, Miftahudin, Gustafson JP, Lazo G, Chao S, Anderson OD, Linkiewicz AM, Dubcovsky J, La Rota M, Sorrells ME, Zhang D, Nguyen HT, Kalavacharla V, Hossain K, Kianian SF, Peng J, Lapitan NL, Gonzalez-Hernandez JL, Anderson JA, Choi DW, Close TJ, Dilbirligi M, Gill KS, Walker-Simmons MK, Steber C, McGuire PE, Qualset CO, Dvorak J. The organization and rate of evolution of wheat genomes are correlated with recombination rates along chromosome arms. *Genome Research* 13:753-763.
56. 2003 **Akhunov ED**, Akhunova AR, Linkiewicz AM, Dubcovsky J, Hummel D, Lazo G, Chao S, Anderson OD, David J, Qi L, Echalié B, Gill BS, Miftahudin, Gustafson JP, La Rota CM, Sorrells ME, Zhang D, Nguyen HT, Kalavacharla V, Hossain K, Kianian SF, Peng J, Lapitan NL, Wennerlind EJ, Nduati V, Anderson JA, Sidhu D, Gill KS, McGuire PE, Qualset CO, Dvorak J. Synteny perturbations between wheat homoeologous chromosomes caused by locus duplications and deletions correlate with recombination rates along chromosome arms. *Proc Natl Acad Sci U S A* 100:10836-10841.
57. 2003 Sorrells ME, La Rota CM, Bermudez-Candianis CE, Greene RA, Kantety R, Munkvold JD, Miftahudin, Mahmoud A, Gustafson JP, Qi L, Echalié B, Gill BS, Matthews D, Lazo GR, Chao S, Anderson OD, Edwards H, Linkiewicz AM, Dubcovsky J, **Akhunov ED**, Dvorak J, Zhang D, Nguyen HT, Peng J, Lapitan NL, Gonzalez-Hernandez JL, Anderson JA, Hossain K, Kalavacharla V, Kianian SF, Choi DW, Close TJ, Dilbirligi M, Gill KS, Steber C, Walker-Simmons MK, McGuire PE, Qualset CO. Comparative DNA sequence analysis of wheat and rice genomes. *Genome Res* 13:1818-1827.
58. 2003 Vakhitov VA, Chemeris AV, Sabirzhanov BE, **Akhunov ED**, Kulikov AM, Nikonorov IuM, Gimalov FR, Bikbulatova SM, Baimiev AKh. Phylogeny of *Triticum* L. and *Aegilops* L. genera inferred from a comparative analysis of nucleotide sequences in promoter rDNA regions of individual species. *Russian Journal of Genetics* 39:5-17.
59. 2001 **Akhunov ED**, Chemeris AV, Kulikov AM, Vakhitov VA. Functional analysis of diploid wheat rRNA promoter by transient expression. *Biochim Biophys Acta* 1522:226-229.
60. 2001 Nijevitch AA, **Akhunov ED**. Host-bacterial interaction: what role does *Helicobacter pylori* urease play? *Dig Dis Sci* 46:75-77.
61. 2000 Nijevitch AA, **Akhunov ED**, Khasanov R, Yelitcheva Z, Ousmanova. I Childhood duodenal ulcer: is there any pathogenetic association with *Helicobacter pylori* urease? *J Gastroenterol* 35: 254-255.

62. 2000 Nijeitch AA, Farztdinov KM, Sataev VU, Khasanov RSh, Katayev VA, Khusnutdinov SM, **Akhunov ED**, Kazykhanov NS. Helicobacter pylori infection in childhood: results of management with ranitidine bismuth citrate plus amoxicillin and tinidazole. *J Gastroenterol Hepatol* 15:1243-1250.
63. 1998 Mavziutov AR, **Akhunov ED**, Bondarenko VM, Gabidullin ZG, Tuigunov MM. Conservative regions of the gene of thermostable enterotoxin in Enterobacteriaceae-the principal possibility of their practical use. *Zh Mikrobiol Epidemiol Immunobiol* 5:36-39.
64. 1998 **Akhunov ED**, Bondarenko VM, Tuigunov MM, Mavziutov AR, Gabidullin ZG. The use of random amplification of polymorphous bacterial DNA for the typing of bacteria in the genus Citrobacter. *Zh Mikrobiol Epidemiol Immunobiol* 4:61-63.
65. 1997 **Akhunov ED**, Chemeris AV, Vakhitov VA. Unusual motifs of the nucleotide sequence adjacent to the putative transcription initiation site in the rDNA intergenic spacer of diploid wheat *Triticum urartu* Thum. ex Gandil, *T. boeoticum* Boiss, and *T. monococcum* L. *Russian Journal of Genetics* 33:1593-1595.

Non peer-reviewed publications:

1. 2011 Akhunov E, Chao S, Catana V, See D, Brown-Guedira G, Sorrells M, Akhunova A, Dubcovsky J, Cavanagh C, Hayden M (2011) New tools for wheat genetics and breeding: genome-wide analysis of SNP variation. Proceedings of BGRI Technical Workshop, June 13-16, St. Paul, MN, USA.
2. 2008 Akhunov ED, Akhunova AR, Anderson OD, Anderson JA, Blake N, Clegg MT, Coleman-Derr D, Conley EJ, Crossman CC, Deal KR, Dubcovsky J, Gill BS, Gu YQ, Hadam J, Heo HY, Huo N, Lazo GR, Luo MC, Ma YQ, Matthews DE, McGuire PE, Morrell P, Qualset CO, Renfro J, Reynolds S, Tabanao D, Talbert LE, Tian C, Toleno D, Warburton M, You FM, Zhang W, Dvorak J (2008) Purifying Selection and Gene Conversion in Polyploid Wheat Evolution. Proceedings of the 11th International Wheat Genetics Symposium, Aug 24-29, Brisbane, Australia.
3. 2003 Gill BS, Qi L, Echaliier S, Chao S, Lazo G, Anderson OD, Akhunov ED, Dvorak J. et al. A transcriptome map of wheat. Proceedings of the 10th International Wheat Genetics Symposium, Paestum, Italy, 1:261-264.
4. 2003 Dvorak J, Akhunov ED, Akhunova AR, Luo MC, Linkiewicz AM, Dubcovsky J, Hummel D, Lazo G, Chao S, Anderson OD, David J, Qi L, Echaliier B, Gill BS, Miftahudin, Gustafson JP, La Rota M, Sorrells M, Zhang D, Nguyen HT, Kalavacharla V, Hossain K, Kianian SF, Peng JH, Lapitan NLV, Wennerlind EJ, Nduati V, Anderson JA, Sidhu D, Gill KS, Choi DW, Close TJ, McGuire PE, Qualset CO. New Insights into the Organization and Evolution of Wheat Genomes. Proceedings of the 10th International Wheat Genetics Symposium, Paestum, Italy, 1:248-253.
5. 2003 Akhunov ED, David JL, Chao S, Lazo G, Anderson OD, Qi L, Echaliier B, Gill BS, Linkiewicz AM, Dubcovsky J, Miftahudin, Gustafson JP, La Rota CM, Sorrells ME, Zhang D, Nguyen HT, Hossain K, Kianian SF, Peng J, Lapitan NLV, Sidhu D, Gill KS, McGuire PE, Qualset CO, Dvorak J. GC

composition and codon usage in genes of inbreeding and outcrossing Triticeae species. Proceedings of the 10th International Wheat Genetics Symposium, Paestum, Italy, 1:203-206.

Book chapters:

1. 2013 Kiani S, Akhunova A, **Akhunov E**. Application of next-generation sequencing technologies for genetic diversity analysis in cereals. Cereal Genomics II. Editors: Gupta PK and Varshney RK, Springer, 2nd ed. VII, 598 p.
2. 2011 Gill BS, Sehgal SK, Friebe B, Akhunov E. Wheat Genome and Gene Analysis. In: Wheat Science Dynamics: Challenges and opportunities (eds. Chibbar RN and Dexter JE) Agrobios (International) Jodhpur, India. pp 483-491.
3. 1999 Chemeris AV, Akhunov ED, Vakhitov VA. DNA sequencing. ed. Vakhitov, VA, Nauka, Moscow, 429 pages (Russian).

Invited oral presentations and seminars:

1. 2015 Johnson L, Gray M, Amand P, Galliard M, Brown S, Poland J, Garrett K, Akhunov E, Bello N, Morgan T, Baer S, Maricle B. Genetic Differentiation, Transcriptome Variation, and Local Adaptation of Dominant Prairie Grass *Andropogon gerardii* along the Climate Gradient of the US Midwest: Implications for Climate Change and Restoration. Plant and Animal Genome meeting, Jan 10-14, San Diego, CA, USA.
2. 2015 Kippes N, Akpinar B, Vasquez-Gross H, Chao S, Akhunov E, Budak H, Kato K, Dubcovsky J. Positional Cloning of the Wheat Vernalization Gene VRN-D4 Reveals the Origin of Spring Growth Habit in Ancient Hexaploid Wheats from India. Plant and Animal Genome meeting, Jan 10-14, San Diego, CA, USA.
3. 2015 Jordan K, Wang S, Lun Y, Chao S, Dubcovsky J, Sherman J, Akhunova A, Talbert L, Akhunov E. Sequence-Based Map Development of Wheat NAM Populations. Plant and Animal Genome meeting, Jan 10-14, San Diego, CA, USA.
4. 2015 Akhunov E. Population Genomics of Allopolyploid Wheat Adaptation. Plant Biology Meeting, July 26-30, Minneapolis, MN, USA.
5. 2015 Akhunov E. Wheat natural diversity. CSHL meeting, April 25-27, Banbury, NY, USA.
6. 2015 Akhunov E. Population Genomics of Allopolyploid Wheat Adaptation. UC Davis Spring Seminar Series, February 17-18, Davis, CA, USA.
7. 2014 Akhunov E, Salcedo A, Lou Y, Zhang W, Li C, Akhunova A, Rutter W, Wang S, Cantu D, Rouse MN, Dubcovsky J. Functional genomics of stem rust - wheat pathosystem. USDA Project Director meeting for Plant Biology Programs, May 14-15, Washington DC, USA.
8. 2014 Jordan K, Wang S, Gardiner L, Lun Y, Hall N, Dubcovsky J, Pozniak C, Akhunova A, Talbert L, Hall A, Akhunov E. A First Generation Haplotype

- Map of Wheat Genome. Plant and Animal Genome meeting, Jan 11-15, San Diego, CA, USA.
9. 2014 Wang S, Jordan K, Lun Y, Akhunova A, Hall A, Pozniak C, Cavanagh C, Chao S, Hayden M, Talbert L, Akhunov E. Application of Haplotype-Based Genetics in Wheat. Plant and Animal Genome meeting, Jan 11-15, San Diego, CA, USA.
 10. 2014 Akhunov E, Sehgal S, Jordan K, Akhunova A, Lun Y, Liang H, Gill B, Wang S. Genomic Redundancy in Young Polyploids: Does It Play an Important Role in Adaptation? Plant and Animal Genome meeting, Jan 11-15, San Diego, CA, USA
 11. 2014 Wang S, Jordan K, Kiani SP, Hayden MJ, Liu S, Baenziger PS, Bowden RL, Akhunov E. Genetic Architecture of Quantitative Disease Resistance Revealed By Genome-Wide Association Scan in Wheat. Plant and Animal Genome meeting, Jan 11-15, San Diego, CA, USA
 12. 2014 Akhunov ED, Wans S, Jordan K, Lun Y, Akhunova A, Chao S, Pozniak C, Cavanagh C, Dubcovsky J, Talbert L, Hayden M. A haplotype map of wheat and its utility for wheat genetics and breeding. The 12th International Wheat Genetics Symposium, Sept 8- 14, Yokohama, Japan.
 13. 2013 Akhunov E. Next Generation DNA Sequencing. What to Do with a Genome Sequence? Laboratory Workshop on FUSARIUM. June 23-28, KSU, Manhattan, KS, USA.
 14. 2013 Akhunov E. RNA-Seq Data Analysis. Gene Expression Analysis Workshop. June 10-14, KSU, Manhattan, KS, USA.
 15. 2013 Akhunov E. Genomic patterns of SNP variation in worldwide wheat populations. Illumina Workshop: Accelerating the Impact of Genomics in Agriculture. Plant and Animal Genome meeting, Jan 12-16, San Diego, CA, USA.
 16. 2013 Akhunov E, Liang H, Saintenac C, Zhang W, Salcedo A, Lun Y, Xu SS, Bowden RL, Szabo LJ, Cantu D, Akhunova A, Rouse M, Dubcovsky J. Genomic Architecture Of Rust-Wheat Interaction: Implications For Breeding Disease-Resistant Crops. W773. Plant and Animal Genome meeting, Jan 12-16, San Diego, CA, USA.
 17. 2013 Akhunov E. Sequence capture. Roche - Advancing Agricultural Genomics Research using Roche NimbleGen Sequence Capture and 454 Long-Read Sequencing Roche workshop. Plant and Animal Genome meeting, Jan 12-16, San Diego, CA, USA.
 18. 2013 Akhunov E. What have we learned from the genotyping efforts? TCAP annual meeting, Jan 13, San Diego, CA, USA.
 19. 2012 Analysis of genetic variation in polyploid wheat by whole-exome capture. Oct 21-24, 2012, ASA-CSSA-SSSA International Annual Meetings, Cincinnati, Ohio, USA.
 20. 2012 Akhunov E. Understanding structural and functional diversity of wheat genome Feb 28, Cornell University, Department of Plant Breeding and Genetics, Ithaca, NY, USA.
 21. 2012 Akhunov E. Next-generation tools for studying genomics of wheat evolution and improvement. Modern Tools in Plant Breeding, April 20, Davis, CA, USA.

22. 2012 Akhunov E. The structural and functional diversity of polyploid wheat genome, John Innes Center seminar series, June 15, Norwich, UK.
23. 2012 Akhunov E, Wang S, Chao S, Stephen S, Huang E, Saintenac C, See D, Carter A, Brown-Guedira G, Forrest K, Wong D, Pumphrey M, Bai G, Bowden R, Baenzinger PS, Talbert L, Anderson JA, Dreisigacker S, Chen J, Campbell K, Akhunova A, Korzun V, Sorrells M, Dubcovsky J, Cavanagh C, Hayden M. Nonparametric tests reveal multiple selection events in the wheat genome. International Triticeae Mapping Initiative meeting, June 24-29, Fargo, North Dakota, USA.
24. 2012 Akhunov E. Usage of genome-wide genotyping approaches to understand the genetics of agronomically important traits in wheat, Triticeae CAP online seminar series, March 29.
25. 2012 Akhunov E. Statistical approaches to analysis of microarray data, June 18-21, Microarray Workshop, KSU, Manhattan, KS, USA.
26. 2012 Akhunov E, Sehgal S, Liang H, Wang S, Akhunova A, Li W, Forrest K, See D, Simkova H, Hayden M, Luo MC, Faris J, Dolezel J, Gill BS. Alternative splicing and coding sequence evolution in polyploid wheat. Plant and Animal Genome meeting, Jan 14-18, San Diego, CA, USA.
27. 2012 Akhunov E. Understanding structural and functional diversity of wheat genome. University of Minnesota, St. Paul, Department of Biology Seminar Series, Feb 7, USA.
28. 2012 Akhunov E. Functional genomics of Sr35-based resistance in wheat. 13th International Cereal Rusts and Powdery Mildews Conference, Aug 28 –Sept 1, Beijing, China.
29. 2012 Saintenac C, Jiang D, Ezrati S, Korol A, Dubcovsky J, Breiman A, Dvorak J, Akhunov E. Targeted Analysis of Polyploid Wheat Genome by Exon Capture. Plant and Animal Genome meeting, Jan 14-18, San Diego, CA, USA.
30. 2012 Dubcovsky J, Saintenac C, Zhang W, Li C, Cantu D, Akhunova A, Liang H, Rouse M, Akhunov E. New approaches to rust resistance in wheat. Plant and Animal Genome meeting, Jan 14-18, San Diego, CA, USA.
31. 2012 Alo F, Furman B, Akhunov E, Dvorak J, Gepts P. Leveraging genomic resources of model species for the assessment of phylogeny in wild and domesticated lentil. Plant and Animal Genome meeting, Jan 14-18, San Diego, CA, USA.
32. 2012 Tsai H, Nitcher R, Howell T, Akhunov E, Tai T, Dubcovsky J, Comai L. High-throughput sequencing makes TILLING more fun. Plant and Animal Genome meeting, Jan 14-18, San Diego, CA, USA.
33. 2012 Jones M, Akhunov E, Peart J, Yip R, Lawley CT. Sequencing and Genotyping in a Complex Genome: Current Status and Future Possibilities. Plant and Animal Genome meeting, Jan 14-18, San Diego, CA, USA.
34. 2012 Akhunov E. Using SureSelect Sequence Capture Assay for Targeted Exon Re-sequencing in Polyploid Wheat. Plant and Animal Genome meeting, Jan 14-18, San Diego, CA, USA.
35. 2012 Akhunov E, Wang S, Catana V, Kiani S, Saintenac C, Hayden M, Cavanagh C, Forrest K, Akhunova A, Dubcovsky J, Brown-Guedira G, Coram T, Sorrells M, See D, Chao S. Genome-wide patterns of SNP variation in

- wheat: tools and resources for breeding and studying genetics of agronomic traits. USDA program directors meeting, Jan 13th, San Diego, CA, USA.
36. 2012 Akhunov E. Gene Capture and Genotyping-By-Sequencing. Annual Triticeae CAP meeting, Jan 15, San Diego, CA, USA.
 37. 2011 Akhunov E., Chao S, Saintenac C, Kiani S, See D, Brown-Guedira G, Sorrels M, Akhunova A, Dubcovsky J, Cavanagh C, Hayden M. (2011) High-throughput approaches to genome-wide analysis of genetic variation in polyploidy wheat. 1st Canadian Wheat Symposium, Nov. 30- Dec. 2, Manitoba, Canada.
 38. 2011 Akhunov E, Chao S, Catana V, See D, Brown-Guedira G, Sorrels M, Akhunova A, Dubcovsky J, Cavanagh C, Hayden M. (2011) Genome-wide analysis of SNP variation in wheat. Development and use of molecular markers for crop improvement meeting. Oct 29-31, New Delhi, India.
 39. 2011 Akhunov E. Wheat chromosome 3A physical mapping and sequencing (update). 21st International Triticeae Mapping Initiative (21st-ITMI), Sept 4-9, Mexico City, Mexico.
 40. 2011 Saintenac C, Zhang W, Rouse M, Akhunov E, Dubcovsky J. Map based cloning and characterization of Ug99 resistance gene Sr35. 21st International Triticeae Mapping Initiative (21st-ITMI), Sept 4-9, Mexico City, Mexico.
 41. 2011 Akhunov E. Next generation tools for wheat genetics and breeding: high-throughput SNP genotyping assays and sequence-based genotyping. 21st International Triticeae Mapping Initiative (21st-ITMI), Sept 4-9, Mexico City, Mexico.
 42. 2011 Hansen M, Akhunov E, Davis T, Haas J, Dvorak J, Hayden M, Jacobs J, Luo M, Deynze AV, Royce T, Hodgson R, Peart J, Yip R, Lawley C. Refining software tools for calling genotypes using high density SNP panels (>10,000 markers) in polyploid species. 21st International Triticeae Mapping Initiative (21st-ITMI), Sept 4-9, Mexico City, Mexico.
 43. 2011 Akhunov E. Sequencing and analysis of the wheat chromosome 3A gene space. Plant and Animal Genome meeting, Jan 14-17, San Diego, CA, USA.
 44. 2011 Akhunov E. Statistical approaches to analysis of microarray data. IGF Microarray workshop, June 24-27, Manhattan, KS, USA.
 45. 2011 Akhunov E. New tools for wheat genetics and breeding: genome-wide analysis of SNP variation. Proceedings of BGRI Technical Workshop, June 13-16, St. Paul, MN, USA.
 46. 2011 Akhunov E. Patterns of SNP variation in wheat breeding populations and genome-wide association mapping. Eastern Wheat Workers/Southern Small Grain Workers Meeting, Apr 17–20, Dallas, TX, USA.
 47. 2011 Akhunov E. Analysis of polyploid wheat genome by exon capture. UC Davis, Dept. Plant Sciences seminar series, Feb 8, Davis, CA, USA.
 48. 2010 Akhunov E. Genome-wide patterns of SNP variation in polyploid wheat. 2nd International Symposium on Genomics of Plant Genetic Resources, Apr 24-27, Bologna, Italy.
 49. 2010 Akhunov E. Genomic technologies and resources for wheat genetics and breeding. International Wheat Conference, June 1–4, Saint-Petersburg, Russia.

50. 2010 Akhunov E. Statistical approaches to the analysis of Affymetrix microarray data. IGF Microarray workshop, July 12-15, Manhattan, KS, USA.
51. 2010 Akhunov E. Assessment of genetic variation in spring and winter wheat populations using Illumina high-throughput SNP genotyping assay. ASA, CSSA, and SSSA International Annual Meetings, Oct 31-Nov 3, Long Beach, CA, USA.
52. 2010 Akhunov E. The patterns of SNP variation and linkage disequilibrium in wheat: moving toward genome-wide association mapping. 20th International Triticeae Mapping Initiative (20th-ITMI), Sept 1-5, Beijing, China.
53. 2010 Akhunov E. Development of global SNP resource for wheat. 20th International Triticeae Mapping Initiative (20th-ITMI), Sept 1-5, Beijing, China.
54. 2009 Akhunov E. Sequencing the wheat genome: lessons from simulation and next-generation sequencing studies. GS FLX SEQUENCING WORKSHOP, Integrated Genomics Facility, KSU Targeted Excellence Program, November 10, Manhattan, KS, USA.
55. 2009 Akhunov E. Next-generation sequencing of flow-sorted wheat chromosomes, 454 Sequencing Workshop, Nov 15, Saint-Louis, MO, USA.
56. 2009 Akhunov E. Wheat Genome Sequencing: Testing The Utility Of Next Generation Sequencing Technologies. Plant and Animal Genome meeting, Jan 10-14, San Diego, CA, USA.
57. 2009 Akhunov E. High-throughput genotyping of wheat using Illumina Golden Gate Assay. Plant and Animal Genome meeting, Wheat CAP Workshop, Jan 10-14, San Diego, CA, USA.
58. 2009 Akhunov E. Using next-generation sequencing technology to characterize the gene space of the wheat chromosome 3A. International Triticeae Mapping Initiative meeting, Aug 31-Sept 4, Clermont-Ferrand, France.
59. 2009 Akhunov E. SNP resources for wheat genome mapping. International Triticeae Mapping Initiative meeting, Aug 31-Sept 4, Clermont-Ferrand, France.
60. 2008 Akhunov E. SNP discovery in complex genomes using 454. Wheat SNP markers workshop, Aug 23, Brisbane, Australia.
61. 2008 Akhunov E. High-Throughput SNP Genotyping Of Polyploid Wheat: Resources And Technologies. Plant and Animal Genome meeting, Jan 12-16, San Diego, CA, USA.
62. 2008 Dvorak J, Akhunov ED, Akhunova AR, Anderson OD, Anderson JA, Blake N, Clegg MT, Coleman-Derr D, Conley EJ, Crossman CC, Deal KR, Dubcovsky J, Gill BS, Gu YQ, Hadam J, Heo HY, Huo N, Lazo GR, Lundy KE, Luo MC, Ma YQ, Matthews DE, McGuire PE, Morrell P, Qualset CO, Renfro J, Reynolds S, Dindo T, Talbert LE, Tian C, Toleno D, Warburton M, You FM, Zhang W. Wheat diversity map. International Durum Wheat Symposium, June 30-July 3, Bologna, Italy.
63. 2007 Akhunov E. Plant Genotyping Using the Illumina Platform. DNA Technologies Symposium, UC Davis, Nov 28, Davis, CA, USA.
64. 2007 Akhunov E. Plant Genotyping Using the Illumina Platform. Workshop "Wheat SNP utilization and deployment", UC Davis, Aug 30, Davis, CA, USA.

65. 2007 Akhunov E. The patterns of genetic diversity in polyploid wheat and its diploid ancestors. Ecology and Evolutionary Biology seminar series, Division of Biology, KSU, Nov 5, Manhattan, KS, USA.
66. 2007 Akhunov E. Mechanisms and rates of acireductone deoxygenase gene family evolution provide insights into the evolution of large plant genomes. International Triticeae Mapping Initiative meeting, Apr 16-20, Tiberias, Israel.
67. 2007 Akhunov E. Wheat SNP markers: discovery and utilization. National Wheat Genomics Conference, Nov 30 – Dec2, Kansas City, MO, USA.
68. 1998 Akhunov ED, Chemeris AV, Vakhitov VA. RDNA transcription in diploid wheats with weak nucleolar organizers does not require the TATA motif just upstream of the transcription initiation site. Proceedings of the 9th International Wheat Genetic Symposium, ed. A.E.Slinkard, Saskatoon, Canada, V.1, p. 99-102.

Abstracts at professional meetings:

1. 2015 Maccaferri M, Ricci A, Salvi S, Milner S, Noli E, Martelli P, Casadio R, Akhunov E, Scalabrin S, Vendramin V, Ammar K, Blanco A, Desiderio F, Distelfeld A, Dubcovsky J, Fahima T, Faris J, Korol A, Massi A, Mastrangelo A, Morgante M, Pozniak C, N'Diaye A, Xu S, Tuberosa R. A High-Density SNP-Based Consensus Map of Tetraploid Wheat (*Triticum turgidum* L.). Useful for Durum and Bread Wheat Genomics and Breeding. Plant and Animal Genome meeting, Jan 10-14, San Diego, CA, USA.
1. 2015 Klocova B, Frenkel Z, Kumar A, Chao S, Abrouk M, Wang S, Kianian S, Simkova H, Korol A, Akhunov E, Dolezel J, Valarik M. Construction of High Density Radiation Hybrid Map of Bread Wheat Chromosome 4A. Plant and Animal Genome meeting, Jan 10-14, San Diego, CA, USA.
1. 2015 Guttieri M, Frels K, Waters B, Baenziger S, Akhunov E, Wang S. Genome-Wide Association Mapping of Nitrogen Use Efficiency Traits in Hard Winter Wheat. Plant and Animal Genome meeting, Jan 10-14, San Diego, CA, USA.
1. 2014 H Sela, S Ezrati, J Manisterski, E Akhunov, J Dvorak, A Breiman, A B Korol. Linkage disequilibrium and association analysis of stripe rust resistance in wild emmer wheat (*Triticum turgidum* ssp. *dicoccoides*) population in Israel. EUCARPIA Cereals Section – I T M I Joint Conference Wernigerode, Germany, June 29 – July 4, 2014
2. 2014 E Komínková, B Klocová, M Abrouk, D Posti, I Jakobson, H Peusha, K Järve, L Timofejeva, A Kumar, S F Kianian, Y Hu, M Luo, Z Frenkel, A B Korol, J Carling, A Kilian, H Šimková, J Šafář, S Wang, E Akhunov, J Doležel, M Valárik Construction of physical map for the locus introgressed to bread wheat from *Triticum militinae* conferring powdery mildew resistance. EUCARPIA Cereals Section – I T M I Joint Conference Wernigerode, Germany, June 29 – July 4, 2014
3. 2014 Y Turuspekov, J Plieske, M W Ganal, E Akhunov, S Abugalieva. SNP genotyping of wheat accessions from Kazakhstan. EUCARPIA Cereals

Section – I T M I Joint Conference Wernigerode, Germany, June 29 – July 4, 2014

4. 2014 B Klocová, M Abrouk, Z Frenkel, A Kumar, S F Kianian, H Šimková, J Šafař, Y Hu, M Luo, J Carling, A Kilian, A B Korol, S Wang, E Akhunov, J Doležel, M Valárik. Sequence ready physical map of bread wheat chromosome 4A. EUCARPIA Cereals Section – I T M I Joint Conference Wernigerode, Germany, June 29 – July 4, 2014
5. 2014 M Maccaferri, A Ricci, S Salvi, K Ammar, E Akhunov, A Blanco, L Cattivelli, A Distelfeld, J Dubcovsky, J Dvorak, T Fahima, A B Korol, A Massi, M Morgante, R Papa, C Pozniak, S S Xu, J Faris, R Tuberosa Towards an SNP-based consensus map of durum wheat. EUCARPIA Cereals Section – I T M I Joint Conference Wernigerode, Germany, June 29 – July 4, 2014
6. 2014 Gray M, Shelton J, Chellapilla S, Bello N, Brown S, Akhunova A, Liang H, Garrett K, Akhunov E, Morgan T, Johnson L. Transcriptional differences of mesic and xeric ecotypes of an ecologically-dominant prairie grass *Andropogon gerardii* to abiotic stress. Plant and Animal Genome meeting, Jan 11-15, San Diego, CA, USA.
7. 2014 Jordan K, Wang S, Gardiner L, Lun Y, Hall N, Dubcovsky J, Pozniak C, Akhunova A, Talbert L, Hall A, Akhunov E. A Diversity Map of the Hexaploid Wheat Genome. Plant and Animal Genome meeting, Jan 11-15, San Diego, CA, USA.
8. 2014 Maccaferri M, Ricci A, Salvi S, Ammar K, Akhunov E, Blanco A, Cattivelli L, Distelfeld A, Dubcovsky J, Dvorak J, Fahima T, Korol A, Morgante M, Papa R, Pozniak C, Xu S, Tuberosa R. Towards an SNP-Based Consensus Map of Durum Wheat. Plant and Animal Genome meeting, Jan 11-15, San Diego, CA, USA
9. 2014 Klocova B, Abrouk M, Frenkel Z, Kumar V, Kianian SF, Simkova H, Safar J, Hu Y, Luo M, Carling J, Kilian A, Korol AB, Wang S, Akhunov E, Doležel J, Valarik M. Construction of Ready-to-Sequence Physical Map of Bread Wheat Chromosome 4A. Plant and Animal Genome meeting, Jan 11-15, San Diego, CA, USA
10. 2014 Tiwari VK, Wang S, Sehgal S, Friebe B, Vrana J, Kubalaková M, Doležel J, Chhuneja P, Akhunov E, Rawat N, Kalia B, Sabir J, Gill BS. Sequence Based Analysis of Flow-Sorted *Aegilops geniculata* Chromosome 5Mg using a Next Generation Sequencing Approach. Plant and Animal Genome meeting, Jan 11-15, San Diego, CA, USA
11. 2014 Wang S, Jordan K, Kiani S, Lowry E, Akhunov E. Association Studies in Polyploid Wheat Using Imputation-Based Analyses of Genotyping-By-Sequencing Data. Plant and Animal Genome meeting, Jan 11-15, San Diego, CA, USA
12. 2014 Guttieri M, Frels K, Waters BM, El-Basyoni IS, Akhunov E, Baenziger PS. Genetic Variation for Grain Cadmium in Hard Winter Wheat. Plant and Animal Genome meeting, Jan 11-15, San Diego, CA, USA
13. 2014 Salcedo A, Wang S, Bowden RL, Wang X, Cantu D, Liang H, Dubcovsky J, Akhunov E. Evaluation of Pathogen-Protein Effectors Candidates Responsible for Triggering the Sr35-mediated Response to Puccinia

- graminis f. sp. tritici (Pgt) Infection. Plant and Animal Genome meeting, Jan 11-15, San Diego, CA, USA
14. 2014 Wang S, Jordan K, Kiani SP, Hayden MJ, Liu S, Baenziger PS, Bowden RL, Akhunov E. Genetic Architecture of Quantitative Disease Resistance Revealed By Genome-Wide Association Scan in Wheat. Plant and Animal Genome meeting, Jan 11-15, San Diego, CA, USA
 15. 2013 Akhunov E, Saintenac C, Zhang W, Salcedo A, Liang H, Cantu D, Akhunova A, Rouse M, Trick H, Dubcovsky J. Functional Genomics of stem rust-wheat pathosystem. USDA Project Director meeting for Plant Biology Programs, May 22-23, Washington DC, USA.
 16. 2013 Jordan K, Wang S, Akhunova A, Lun Y, Saintenac C, Pozniak C, Hall A, Talbert L, Akhunov E. Targeted Re-Sequencing Of Polyploid Wheat Genome. Plant and Animal Genome meeting, Jan 12-16, San Diego, CA, USA.
 17. 2013 Akhunov E, Wang S, Chao S, Brown-Guedira G, See D, Akhunova A, Forrest K, Allen AM, Tuberosa R, Morgante M, Cattivelli L, Dvorak J, Luo M, Sorrells M, Feuillet C, Salse J, Dubcovsky J, Edwards KJ, Ganai MW, Cavanagh C, Hayden MJ. Analysis of Genome-Wide Patterns of Genetic Variation Across Wheat Genome using 90,000 SNP iSelect Assay. Plant and Animal Genome meeting, Jan 12-16, San Diego, CA, USA.
 18. 2013 Akhunov E, Liang H, Saintenac C, Zhang W, Salcedo A, Lun Y, Xu SS, Bowden RL, Szabo LJ, Cantu D, Akhunova A, Rouse M, Dubcovsky J. Genomic Architecture of Rust-Wheat Interaction: Implications for Breeding Disease-Resistant Crops. P0258. Plant and Animal Genome meeting, Jan 12-16, San Diego, CA, USA.
 19. 2013 Wang S, Akhunova A, Lun Y, Chao S, See D, Brown-Guedira G, Chalhoub B, Akhunov E. Homoeologous imbalance of gene expression in polyploid wheat. Plant and Animal Genome meeting, Jan 12-16, San Diego, CA, USA.
 20. 2013 Shelton J, Gray M, Brown SJ, Chellapilla S, Akhunova A, Akhunov E, Liang H, Johnson L. De novo transcriptome profiling of two edaphically and phenotypically divergent grasses: dominant forage grass big bluestem *Andropogon gerardii* and drought- sand bluestem *Andropogon gerardii* ssp. *Hallii*. Plant and Animal Genome meeting, Jan 12-16, San Diego, CA, USA.
 21. 2013 Johnson L, Gray M, Akhunova A, Brown SJ, Chellapilla S, Morgan TJ, Garrett K, Liang H, Akhunov E. Phenotypic and genetic variation in a dominant forage and biofuel grass along the Great Plains' precipitation gradient: a reciprocal garden approach. Plant and Animal Genome meeting, Jan 12-16, San Diego, CA, USA.
 22. 2013 Pozniak C, MacLachlan R, McCartney C, Sharpe AG, Akhunov ED, Hucl PJ. Combining Exome Capture and Bulk Segregant Analysis for Marker Discovery in Durum Wheat. Plant and Animal Genome meeting, Jan 12-16, San Diego, CA, USA.
 23. 2013 Hofstad AN, Jia H, Millett BP, Akhunov ED, Muehlbauer G. Identifying FHB Resistance Genes in Wheat Using a Next-Generation Sequencing Approach. Plant and Animal Genome meeting, Jan 12-16, San Diego, CA, USA.

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