

Close

Print

◀ [1] ▶

Record 1 of 1**Title:** Comparative Analysis of Syntenic Genes in Grass Genomes Reveals Accelerated Rates of Gene Structure and Coding Sequence Evolution in Polyploid Wheat**Author(s):** Akhunov, ED (Akhunov, Eduard D.); Sehgal, S (Sehgal, Sunish); Liang, HQ (Liang, Hanquan); Wang, SC (Wang, Shichen); Akhunova, AR (Akhunova, Alina R.); Kaur, G (Kaur, Gaganpreet); Li, WL (Li, Wanlong); Forrest, KL (Forrest, Kerrie L.); See, D (See, Deven); Simkova, H (Simkova, Hana); Ma, YQ (Ma, Yaqin); Hayden, MJ (Hayden, Matthew J.); Luo, MC (Luo, Mingcheng); Faris, JD (Faris, Justin D.); Dolezel, J (Dolezel, Jaroslav); Gill, BS (Gill, Bikram S.)**Source:** PLANT PHYSIOLOGY **Volume:** 161 **Issue:** 1 **Pages:** 252-265 **DOI:** 10.1104/pp.112.205161 **Published:** JAN 2013**Times Cited in Web of Science Core Collection:** 49**Total Times Cited:** 49**Usage Count (Last 180 days):** 2**Usage Count (Since 2013):** 80**Cited Reference Count:** 91**Abstract:** Cycles of whole-genome duplication (WGD) and diploidization are hallmarks of eukaryotic genome evolution and speciation. Polyploid wheat (*Triticum aestivum*) has had a massive increase in genome size largely due to recent WGDs. How these processes may impact the dynamics of gene evolution was studied by comparing the patterns of gene structure changes, alternative splicing (AS), and codon substitution rates among wheat and model grass genomes. In orthologous gene sets, significantly more acquired and lost exonic sequences were detected in wheat than in model grasses. In wheat, 35% of these gene structure rearrangements resulted in frame-shift mutations and premature termination codons. An increased codon mutation rate in the wheat lineage compared with *Brachypodium distachyon* was found for 17% of orthologs. The discovery of premature termination codons in 38% of expressed genes was consistent with ongoing pseudogenization of the wheat genome. The rates of AS within the individual wheat subgenomes (21%-25%) were similar to diploid plants. However, we uncovered a high level of AS pattern divergence between the duplicated homeologous copies of genes. Our results are consistent with the accelerated accumulation of AS isoforms, nonsynonymous mutations, and gene structure rearrangements in the wheat lineage, likely due to genetic redundancy created by WGDs. Whereas these processes mostly contribute to the degeneration of a duplicated genome and its diploidization, they have the potential to facilitate the origin of new functional variations, which, upon selection in the evolutionary lineage, may play an important role in the origin of novel traits.**Accession Number:** WOS:000312964000021**PubMed ID:** 23124323**Language:** English**Document Type:** Article**KeyWords Plus:** MESSENGER-RNA DECAY; HEXAPLOID WHEAT; NUCLEOTIDE SUBSTITUTION; BRACHYPODIUM-DISTACHYON; PHYLOGENETIC ANALYSIS; DUPLICATE GENES; PLANT GENOMES; ORYZA-SATIVA; BREAD WHEAT; EXPRESSION**Addresses:** [Akhunov, Eduard D.; Sehgal, Sunish; Liang, Hanquan; Wang, Shichen; Akhunova, Alina R.; Kaur, Gaganpreet; Gill, Bikram S.] Kansas State Univ, Dept Plant Pathol, Manhattan, KS 66506 USA.

[Liang, Hanquan; Akhunova, Alina R.] Kansas State Univ, Integrated Genom Facil, Manhattan, KS 66506 USA.

[Li, Wanlong] S Dakota State Univ, Brookings, SD 57007 USA.

[Forrest, Kerrie L.; Hayden, Matthew J.] Victorian AgriBiosci Ctr, Dept Primary Ind Victoria, Bundoora, Vic 3083, Australia.

[See, Deven] Washington State Univ, USDA ARS, Western Reg Small Grains Genotyping Lab, Pullman, WA 99164 USA.

[Simkova, Hana; Dolezel, Jaroslav] Inst Expt Bot, Ctr Reg Hana Biotechnol & Agr Res, CZ-77200 Olomouc, Czech Republic.

[Ma, Yaqin; Luo, Mingcheng] Univ Calif Davis, Dept Plant Sci, Davis, CA 95616 USA.

[Ma, Yaqin] Univ Calif Riverside, Dept Bot & Plant Sci, Riverside, CA 92521 USA.

[Faris, Justin D.] USDA ARS, No Crop Sci Lab, Fargo, ND 58102 USA.

[Gill, Bikram S.] King Abdulaziz Univ, Fac Sci, Genom & Biotechnol Sect, Dept Biol Sci, Jeddah 21589, Saudi Arabia.

Reprint Address: Akhunov, ED (reprint author), Kansas State Univ, Dept Plant Pathol, Throckmorton Hall, Manhattan, KS 66506 USA.**E-mail Addresses:** eakhunov@ksu.edu**Author Identifiers:**

Author	ResearcherID Number	ORCID Number
Simkova, Hana	F-7734-2014	0000-0003-4159-7619
Dolezel, Jaroslav	B-7716-2008	0000-0002-6263-0492
Wang, Shichen	E-6213-2012	0000-0003-1441-2252
Fac Sci, KAU, Biol Sci Dept	L-4228-2013	
Faculty of, Sciences, KAU	E-7305-2017	

Publisher: AMER SOC PLANT BIOLOGISTS**Publisher Address:** 15501 MONONA DRIVE, ROCKVILLE, MD 20855 USA**Web of Science Categories:** Plant Sciences**Research Areas:** Plant Sciences**IDS Number:** 062ZP**ISSN:** 0032-0889**29-char Source Abbrev.:** PLANT PHYSIOL**ISO Source Abbrev.:** Plant Physiol.**Source Item Page Count:** 14**Funding:**

Funding Agency	Grant Number
U.S. Department of Agriculture National Institute of Food and Agriculture	2006-35604-17248 2008-35300-04588 CRIS0219050
Kansas Wheat Commission	
Grains Research and Development Corporation of Australia	
Ministry of Education, Youth, and Sports of the Czech Republic and the European Regional Development Fund (Operational Programme Research and Development for Innovations grant)	ED0007/01/01
Kansas Agricultural Experiment Station	
Integrated Genomics Facility	

This work was supported by the U.S. Department of Agriculture National Institute of Food and Agriculture (grant nos. 2006-35604-17248 to B.S.G., 2008-35300-04588 to B.S.G., and CRIS0219050 to E.D.A.), by the Kansas Wheat Commission (to E.D.A.), by the Grains Research and Development Corporation of Australia (to M.J.H.), by the Ministry of Education, Youth, and Sports of the Czech Republic and the European Regional Development Fund (Operational Programme Research and Development for Innovations grant no. ED0007/01/01 to H.S. and J.D.), and by Kansas Agricultural Experiment Station grants to the Wheat Genetics Resources Center (to B.S.G.) and the Integrated Genomics Facility (to A.R.A.).

Open Access: No**Output Date:** 2017-07-25

Close

Web of Science
Page 1 (Records 1 -- 1)

Print

◀ [1] ▶